ASKeD-BN: Automatic Synthesis of Boolean Networks from Biological Knowledge and Data

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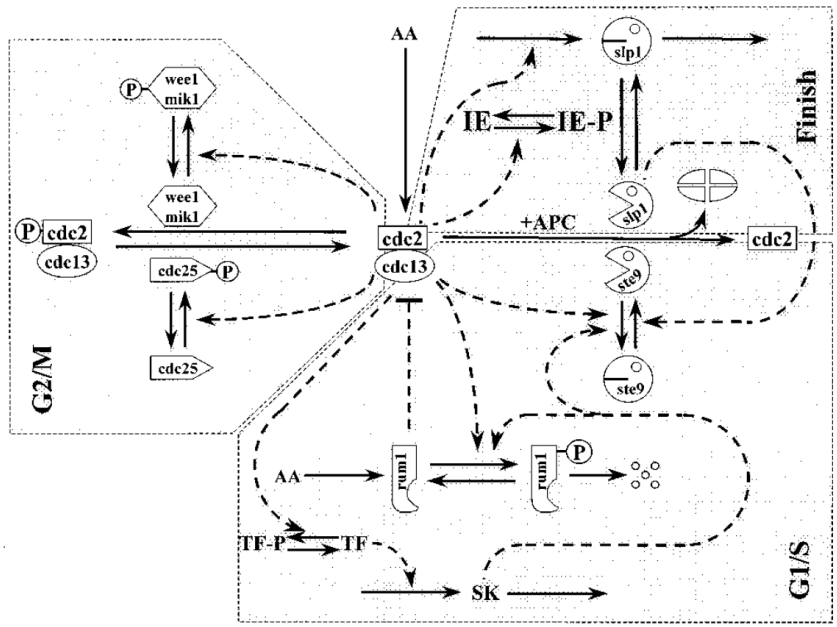
Modeling Biological Systems with Boolean Networks

Boolean Networks (BN) are:

- qualitative formalism, well-suited for biological systems
- built from experimental data and knowledge from literature
- the **automatic** synthesis of BNs from biological data and knowledge is still a challenge



from Novak et al. 2001

Boolean Networks – Generalities

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in the Boolean world: $\mathbb{B} = \{0, 1\}$

n Boolean **components**

BN = set of n **update functions**

negation: $\neg$ disjunction: $\vee$ conjunction: $\wedge$

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Boolean Networks – Their Structure and Dynamics

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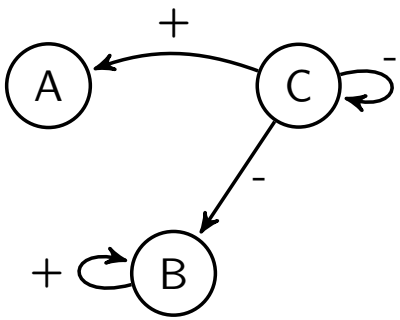

Interaction Graph (IG)

nodes: components of the BN

edges: influences + polarity

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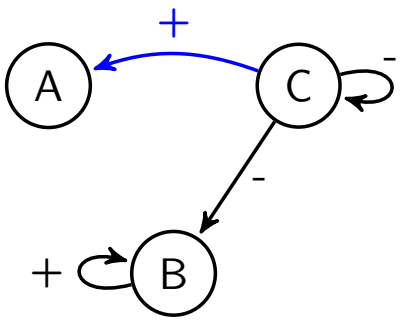

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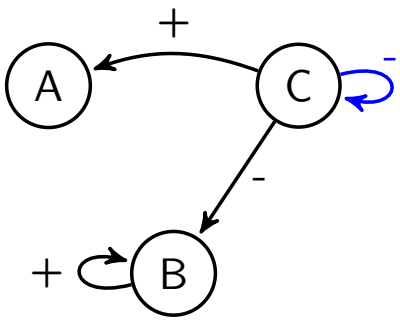

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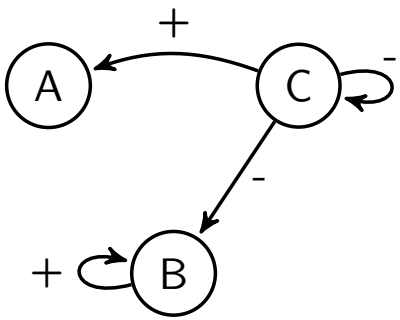

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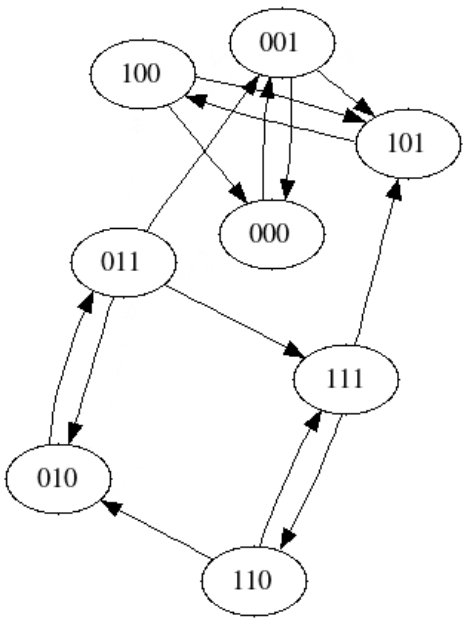
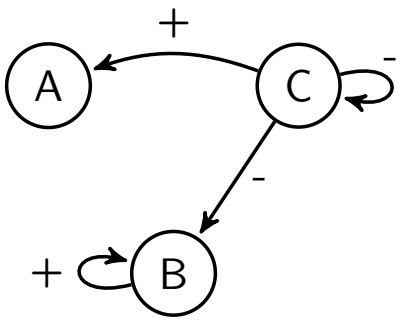


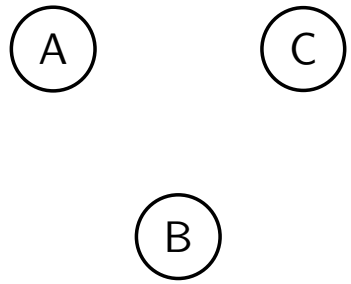
State Transition Graph (STG)

nodes: configurations of the BN (vector $\in \mathbb{B}^n$)
e.g. 001, 010, 111, ...

edge from c to c' if c' = f(c)

Boolean Networks – Synthesis from Knowledge and Data





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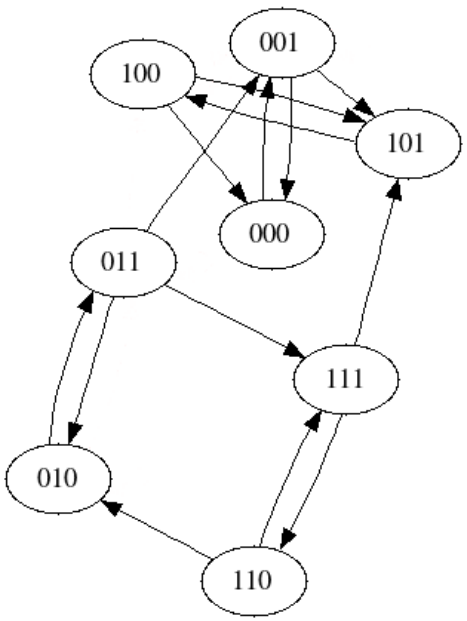

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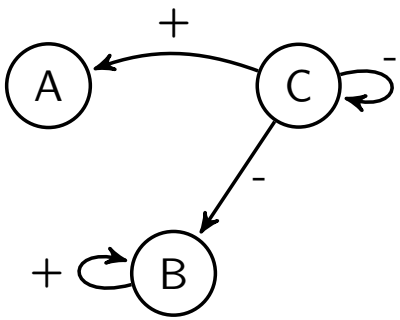

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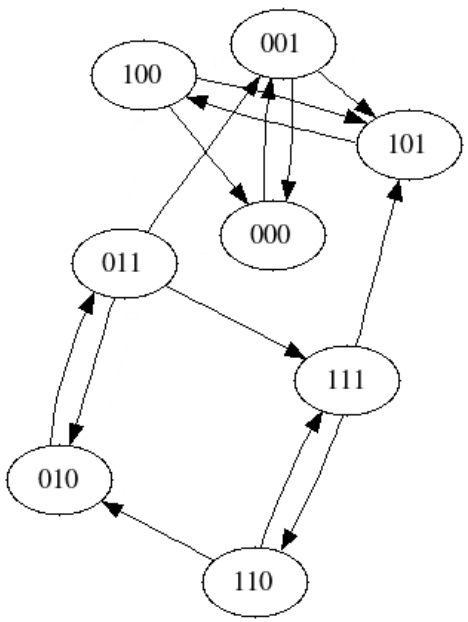

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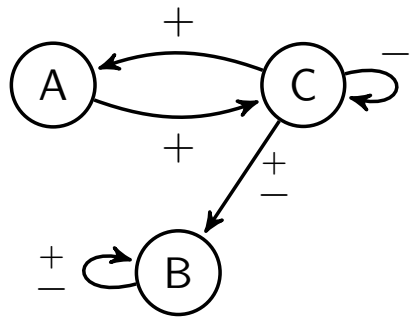

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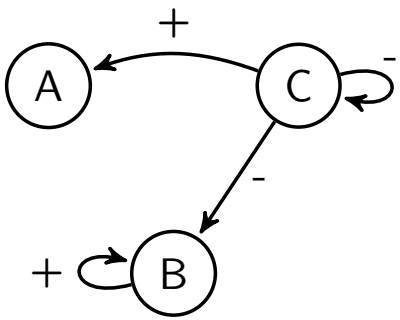

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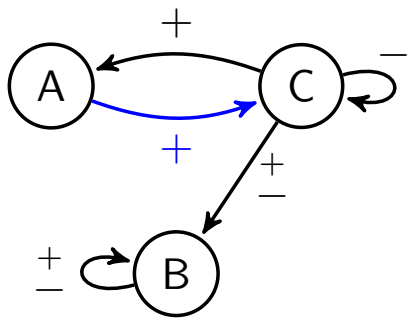

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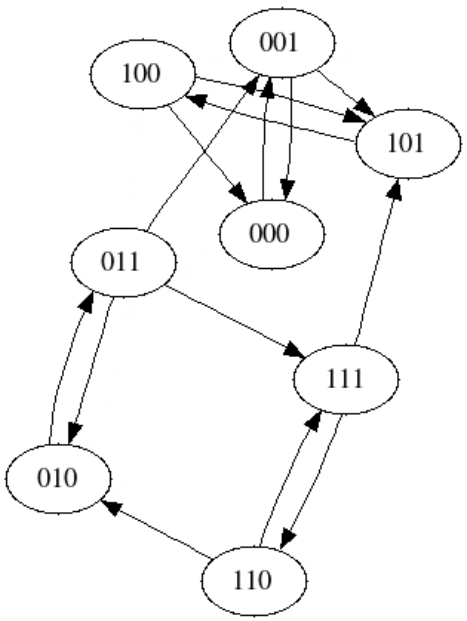

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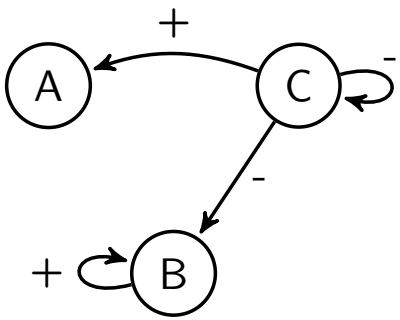

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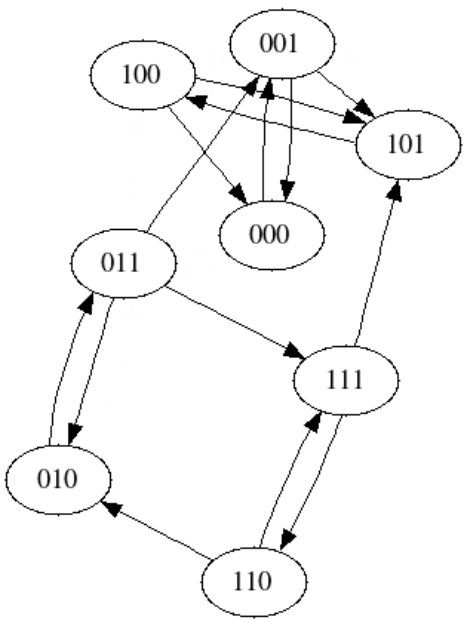

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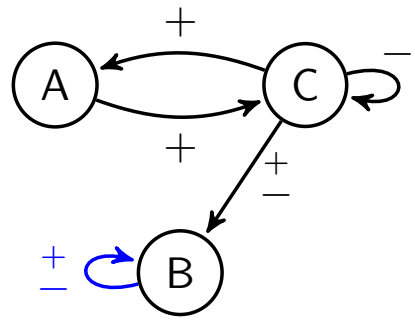

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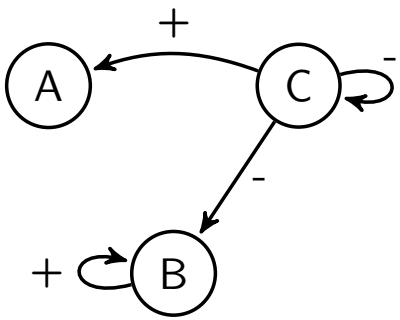

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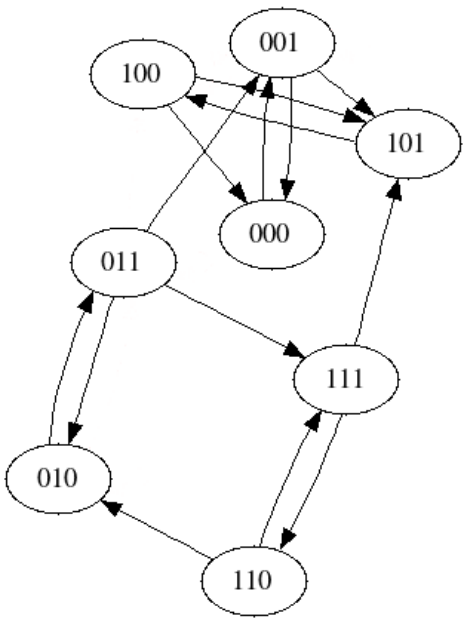

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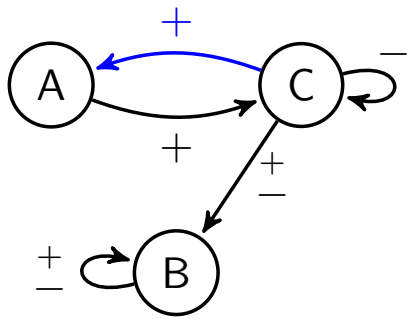

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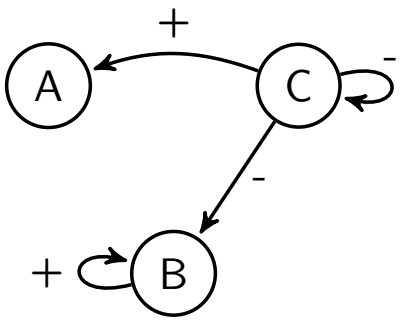

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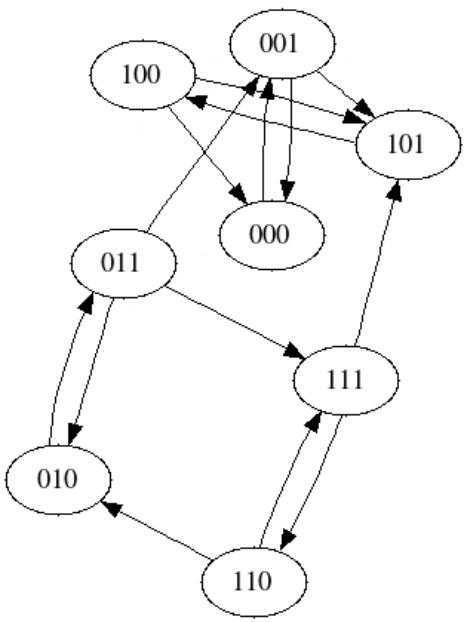

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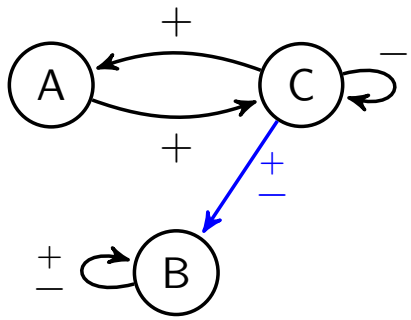

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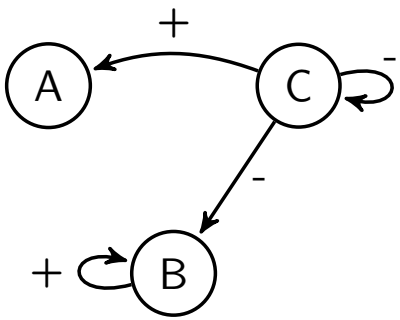

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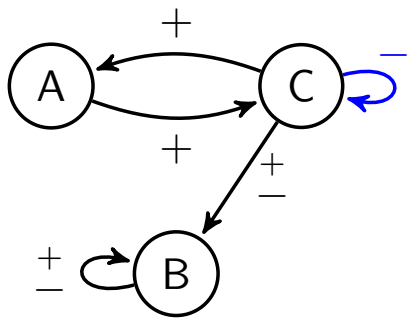

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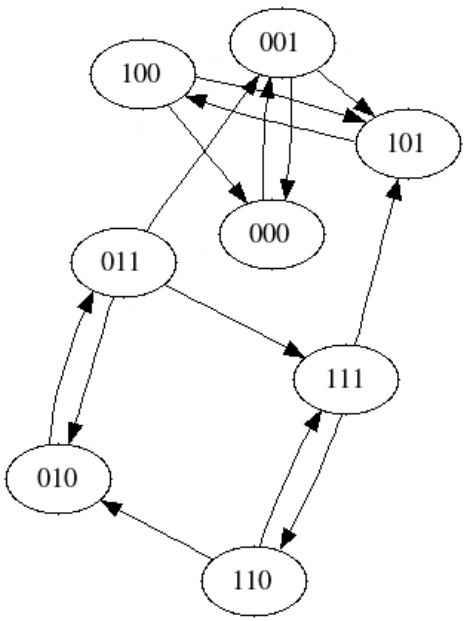

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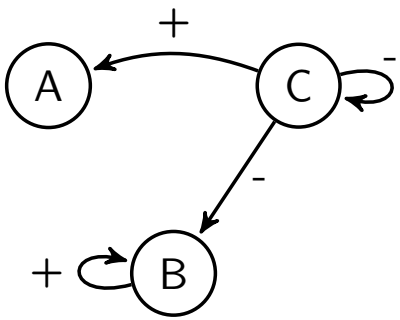

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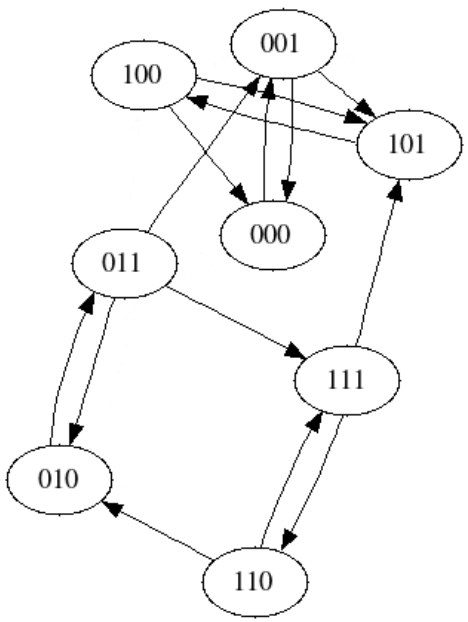

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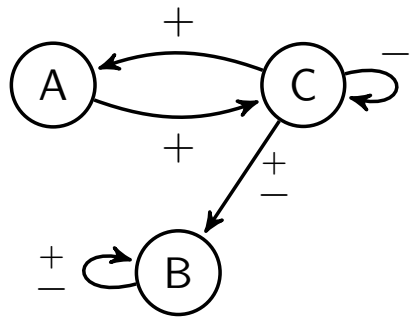

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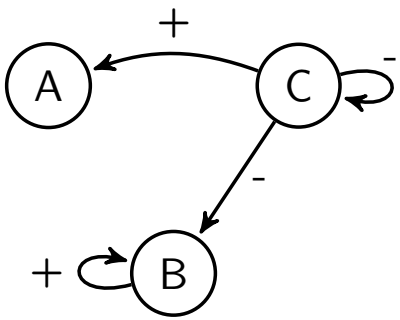

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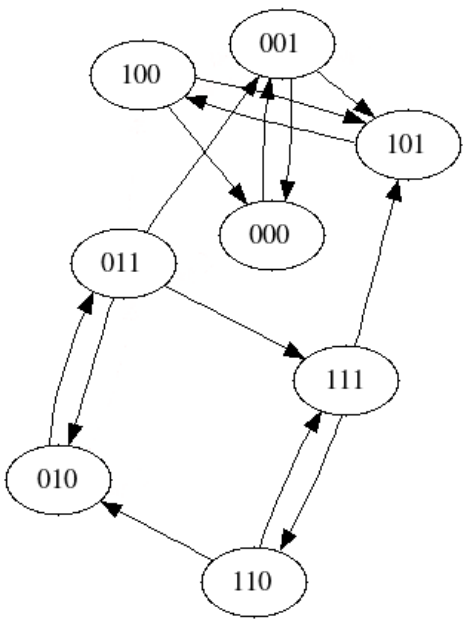

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Super-set of influences allowed

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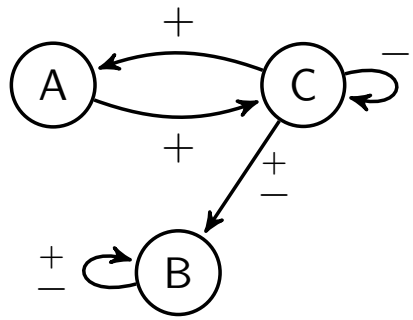

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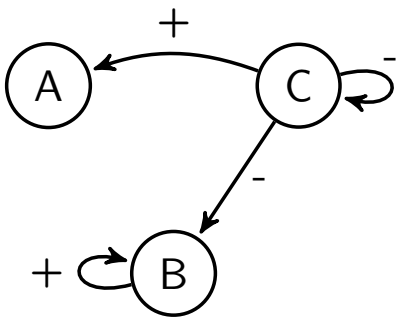

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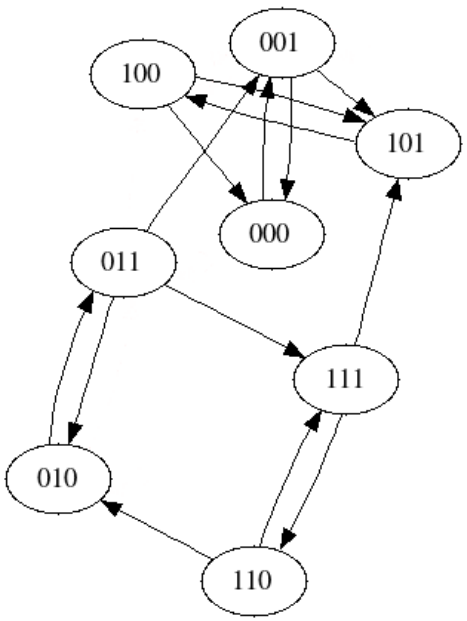

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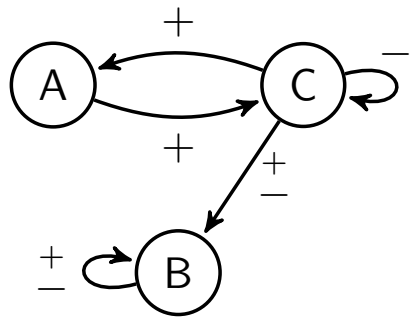

Multivariate Time Series (TS)

Concentrations of the components over time

t	1	2	3	4	5	6	7	8	9	10	11	12	13	...
A	0	3	7	13	20	30	49	61	100	63	36	25	2	...
B	100	86	64	57	54	53	51	49	45	37	33	28	22	...
C	0	27	36	42	60	75	54	44	38	48	60	72	88	...

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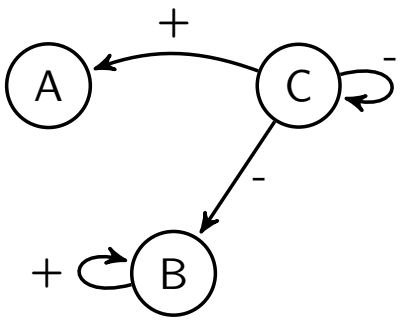

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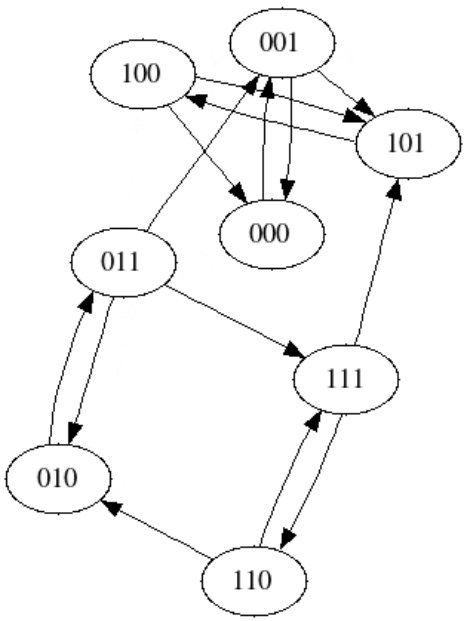

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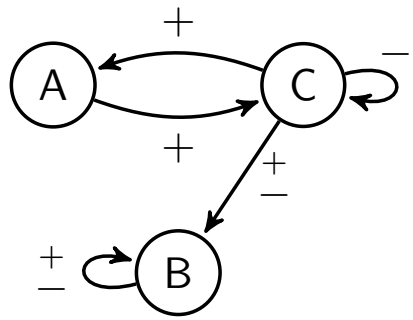

Multivariate Time Series (TS)

Concentrations of the components over time

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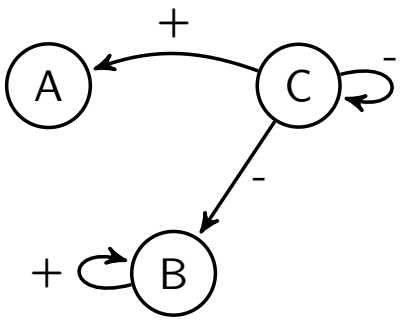

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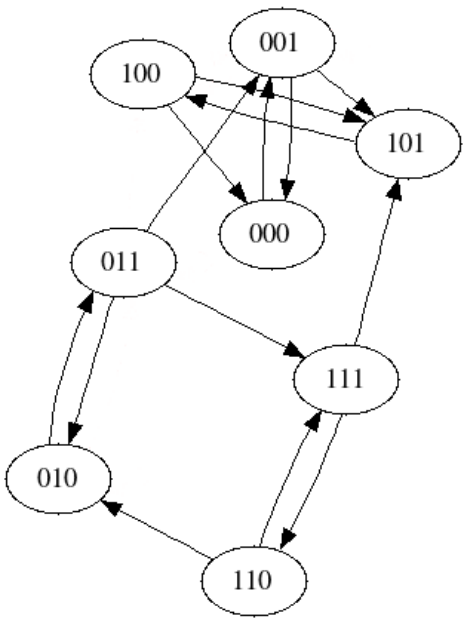

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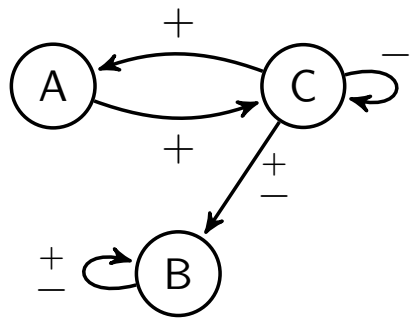

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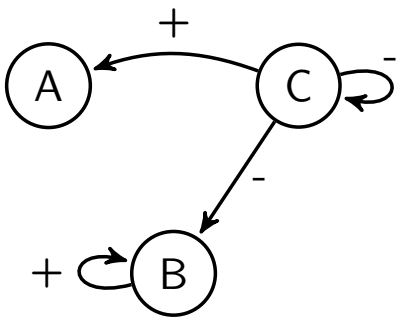

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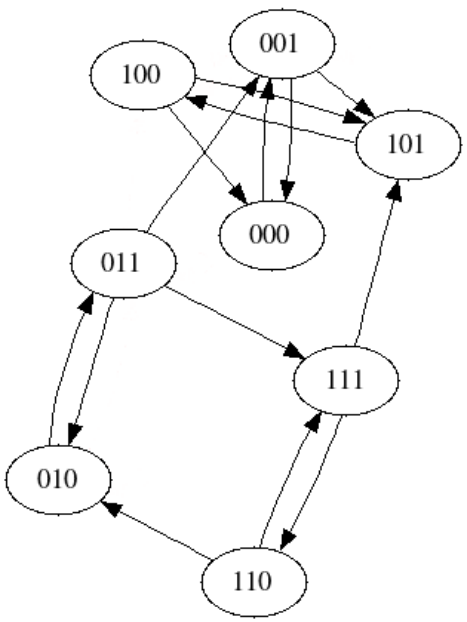

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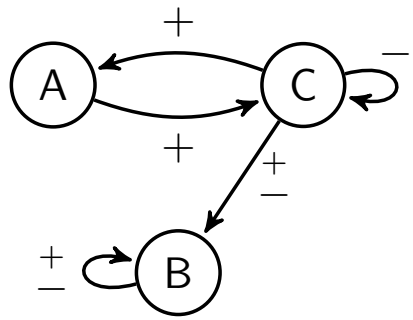

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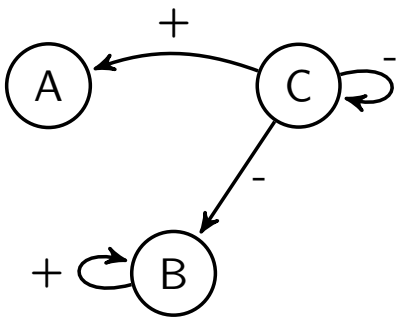

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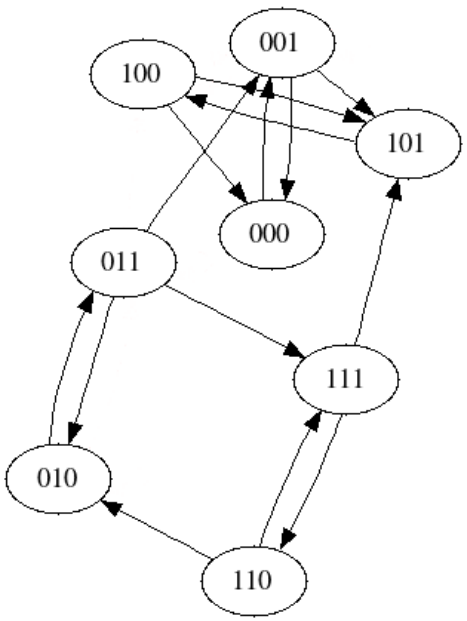

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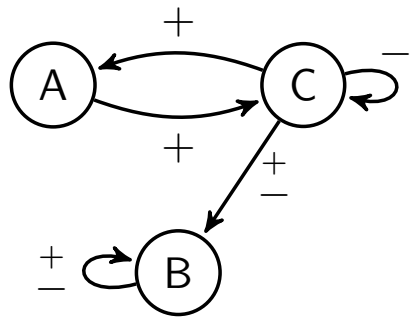

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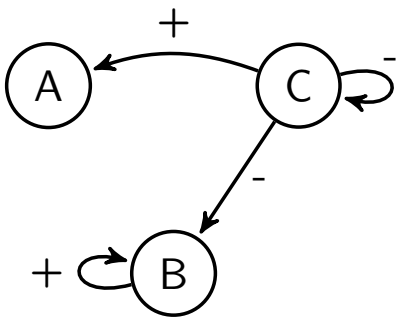

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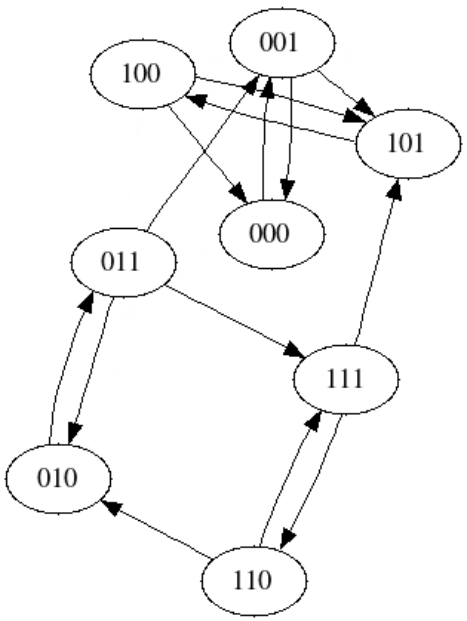

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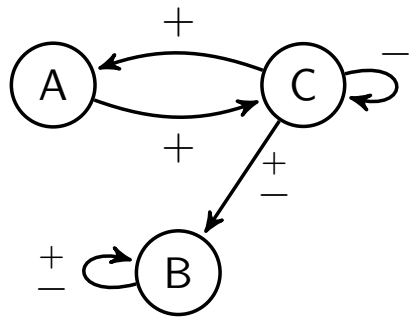

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A														...
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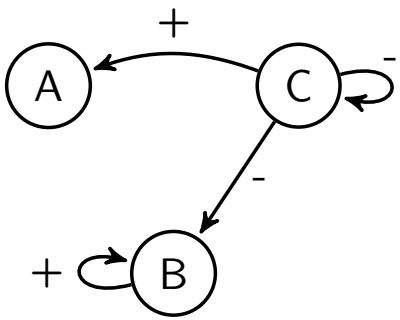

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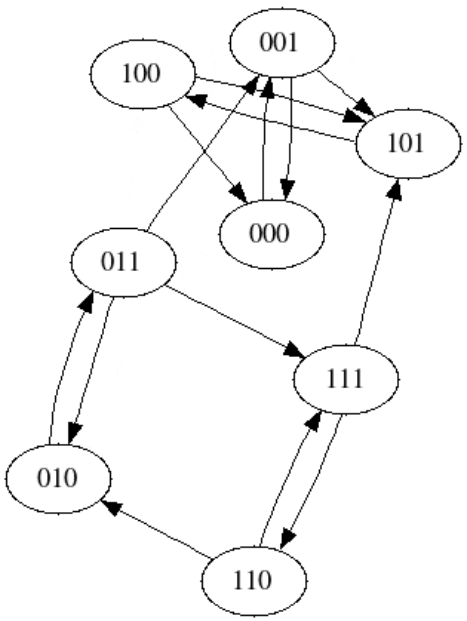

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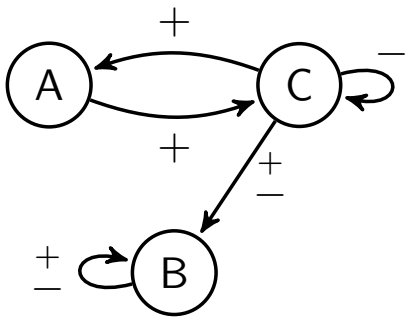

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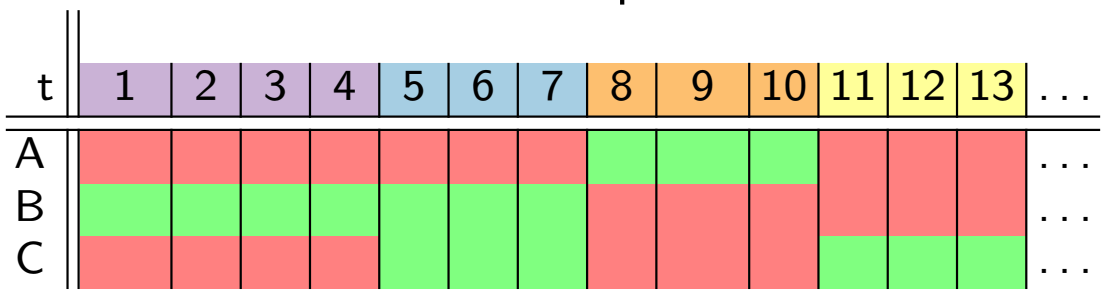

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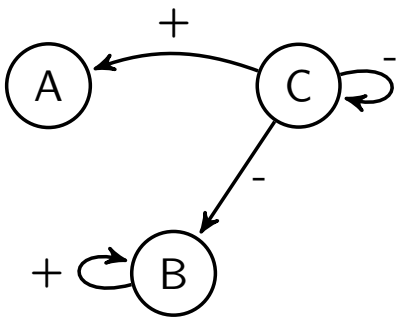

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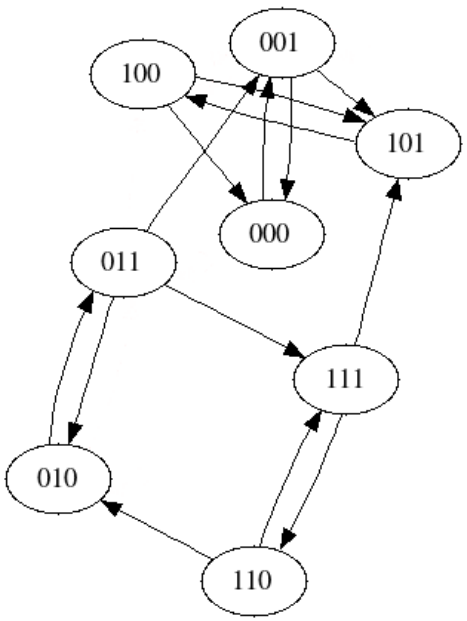

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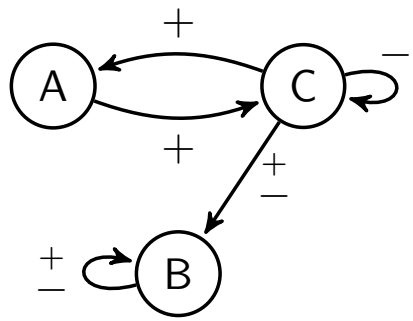

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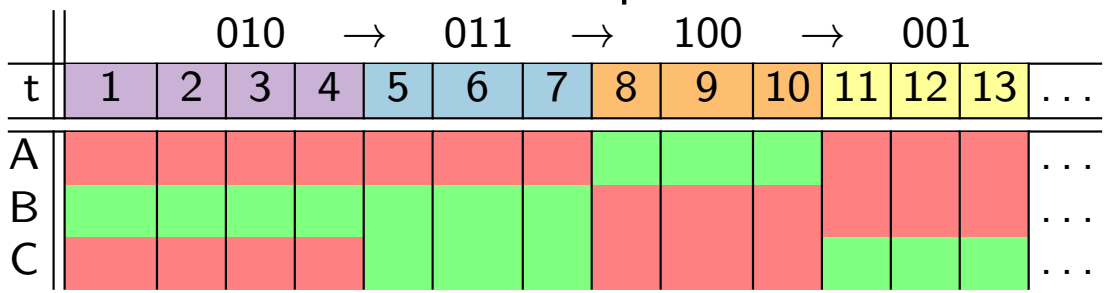

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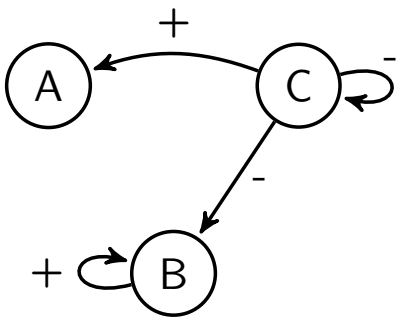

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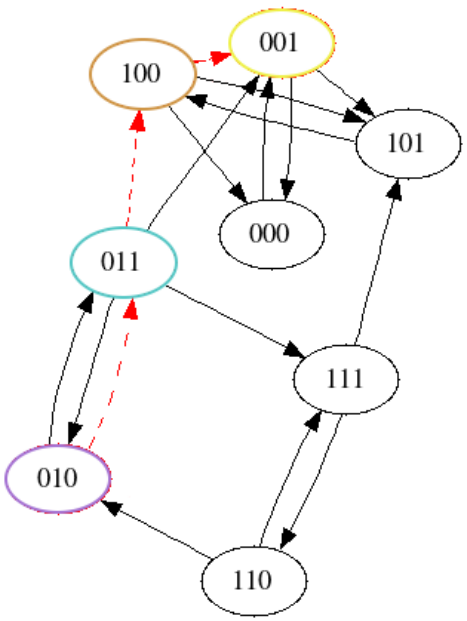

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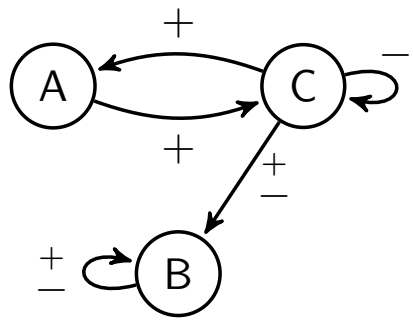

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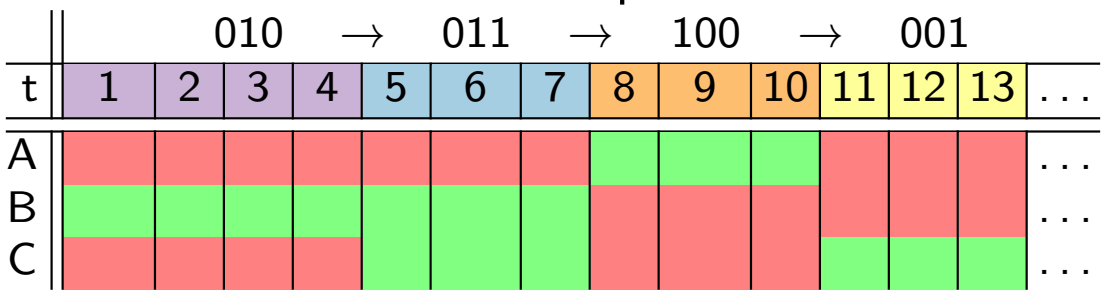

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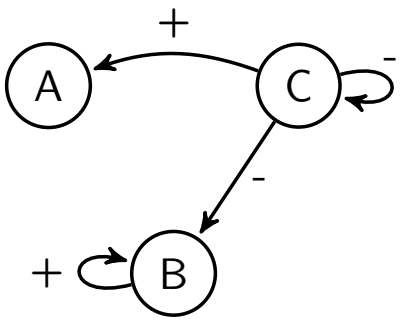

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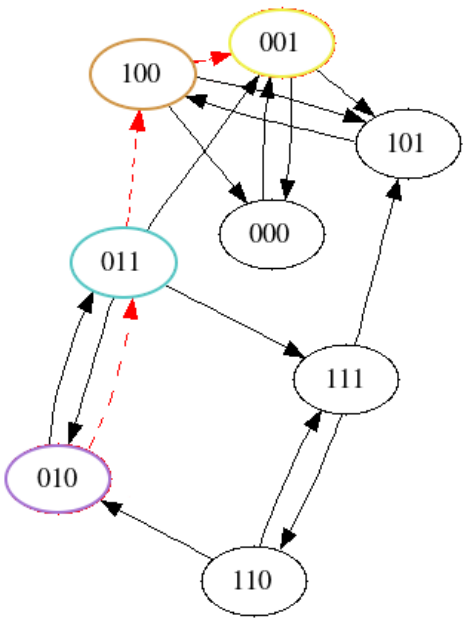

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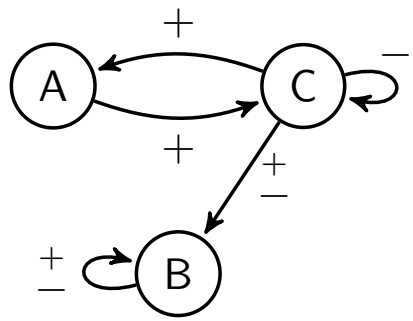

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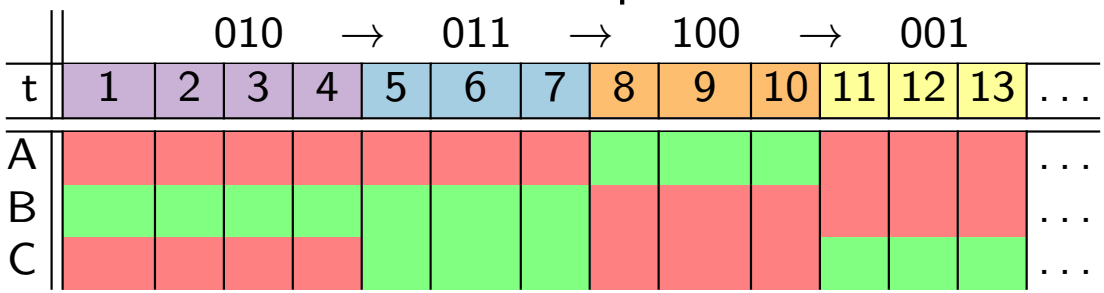

Get the best coverage possible

Existing tools

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Automatic synthesis of BNs from a Prior Knowledge Network (PKN)
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= hard problem (combinatorial explosion)

`REVEAL`
`Best-Fit`
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	PKN	TS	assumptions
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1. delimitation of the search space using the PKN as constraint
2. optimization of a criteria which measure the adequacy of the synthesized BNs with the TS (coverage)

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Multiple optimal solutions are all returned

ASKeD-BN

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Formulation the BN synthesis problem as a logic program with the Answer Set Programming (ASP) framework

ASKeD-BN

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Main parts of the logic program:

1. generates all the possible candidate functions
2. removes the ones that do not respect the PKN
3. acts like an exhaustive evaluation of all the candidates and returns the *parsimonious* candidates which explain best the *binarized* observations from the given time series

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ASP solvers are designed to solve hard combinatorial satisfaction problem. They prune the search space *efficiently* (heuristic from SAT solvers).

Evaluation Procedure

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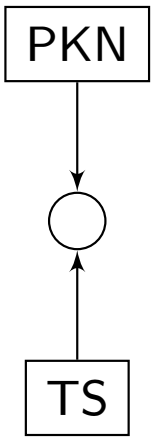

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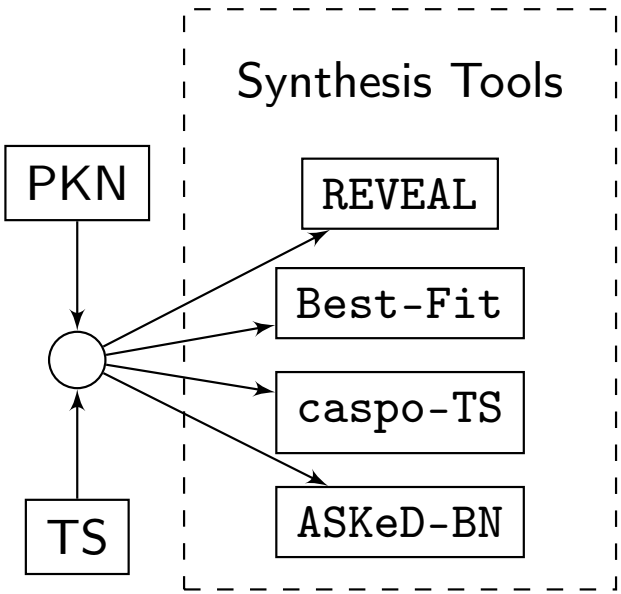

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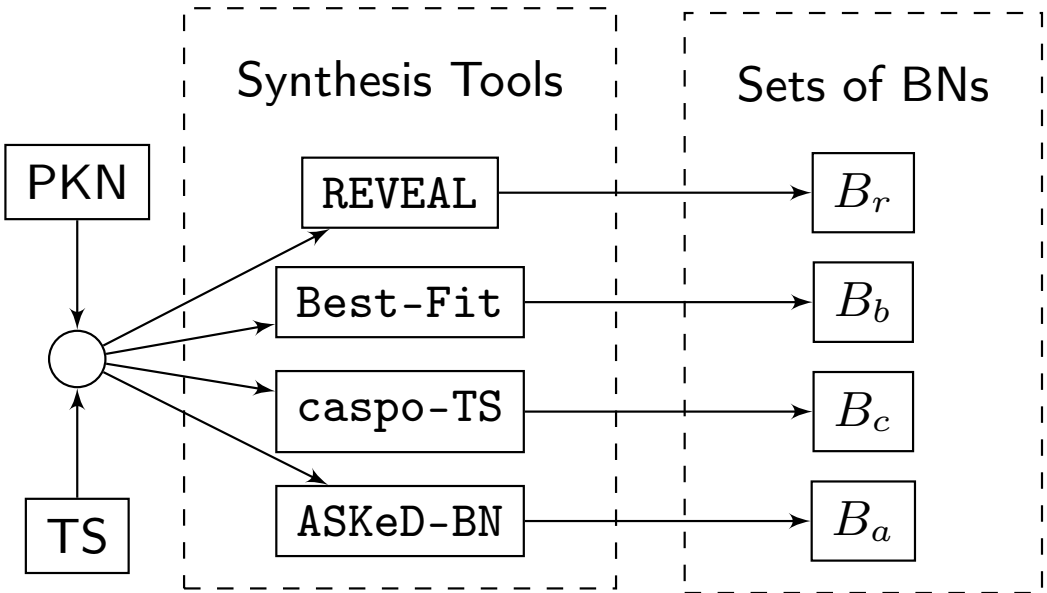

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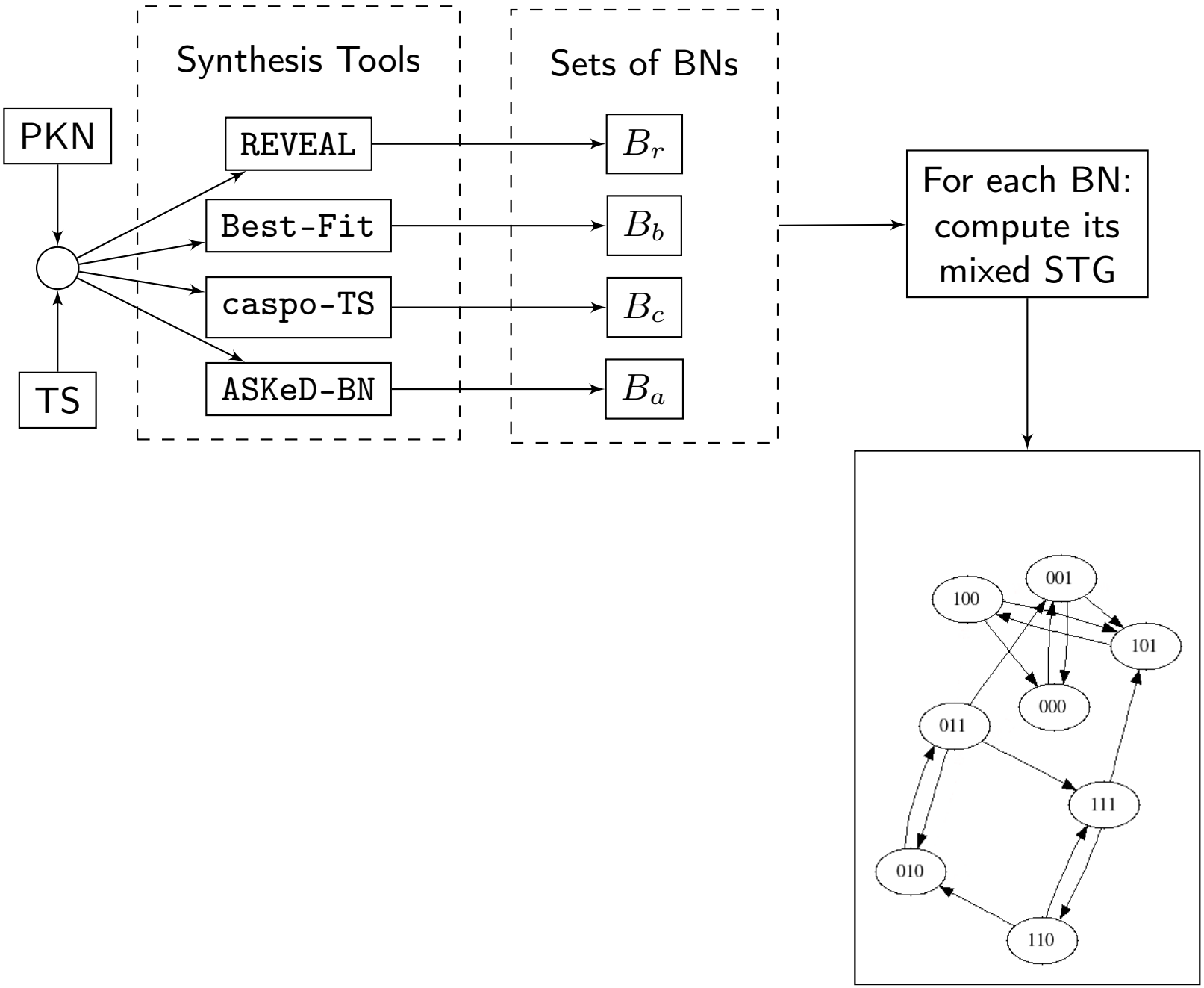

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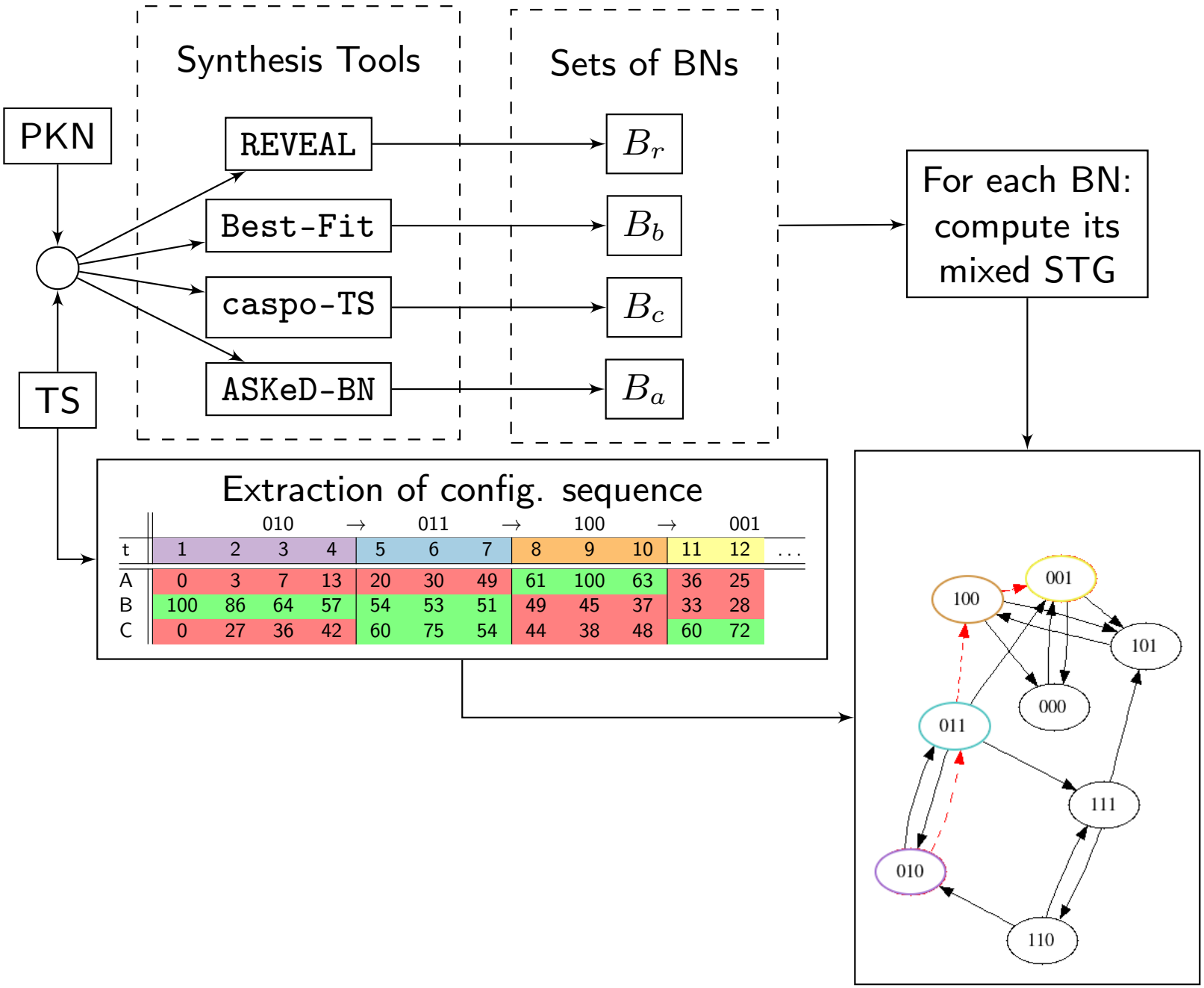

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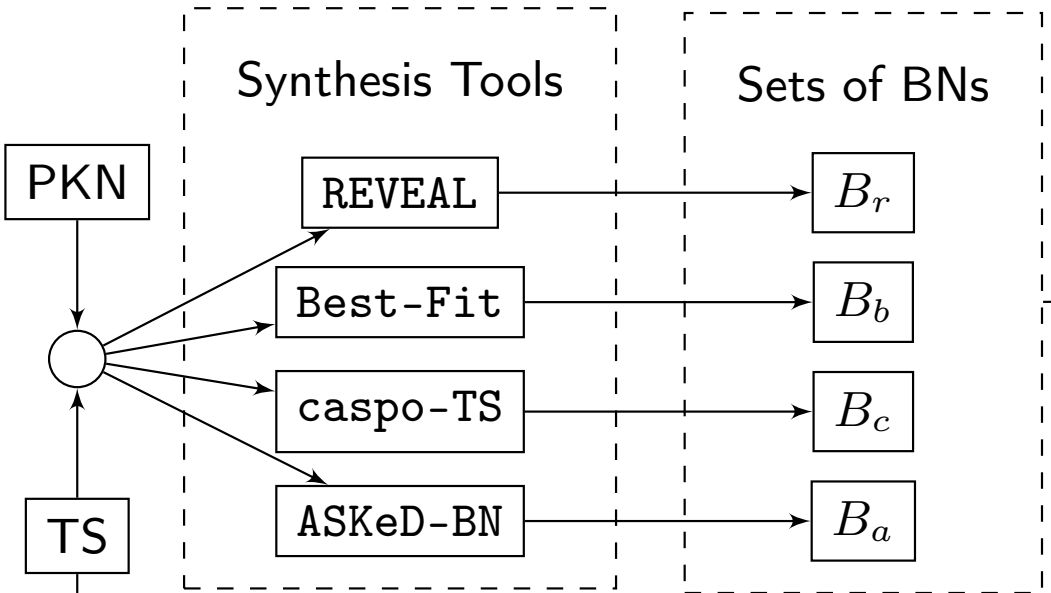

For each BN: compute its mixed STG

Extraction of config. sequence

					010			→	011			→	100			→	001	
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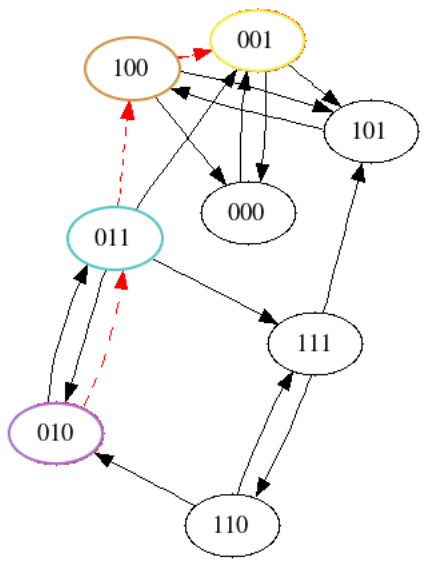
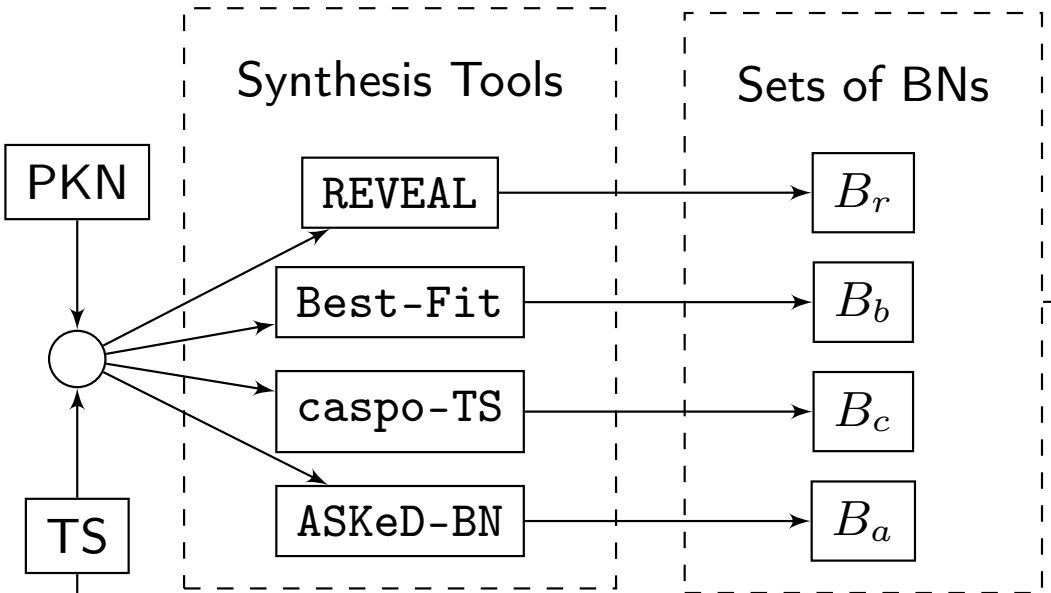
For each BN: compute its **coverage**



Evaluation Procedure

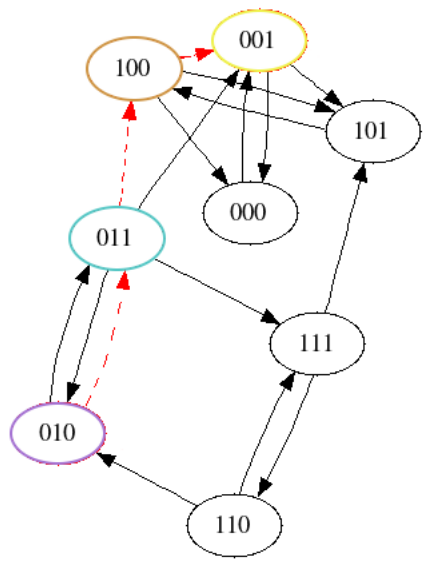


For each BN: compute its mixed STG

Extraction of config. sequence

				010	→		011	→		100	→		001
t	1	2	3	4	5	6	7	8	9	10	11	12	...
A	0	3	7	13	20	30	49	61	100	63	36	25	
B	100	86	64	57	54	53	51	49	45	37	33	28	
C	0	27	36	42	60	75	54	44	38	48	60	72	

For each BN: compute its **coverage**



Ideally: only BNs with good coverage

Datasets for Evaluation

2 real datasets:

System	PKN		TS	
	# nodes	# edges	# time steps	# transitions
yeast (cell cycle)	4	28	14	6
A. thaliana (circadian clock)	5	8	50	11

6 synthetic datasets:

Various complexity: from 3 to 10 nodes.
Various conditions: synch. or async. update scheme, with or without repetition, with or without noise

336 experiments at total including 42 with the ARN setting.

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Evaluation – Quality of the Synthesised BNs

REVEAL Best-Fit caspo-TS ASKeD-BN

Evaluation – Quality of the Synthesised BNs

`REVEAL` `Best-Fit` `caspo-TS` `ASKeD-BN`

schematic representation of the coverage ratio
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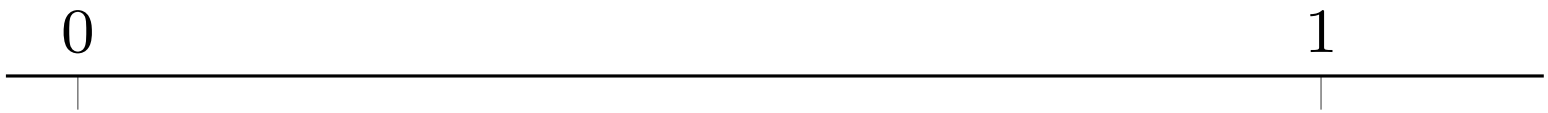
Points are jittered



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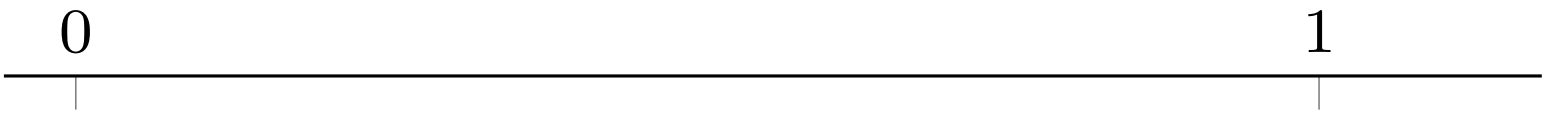

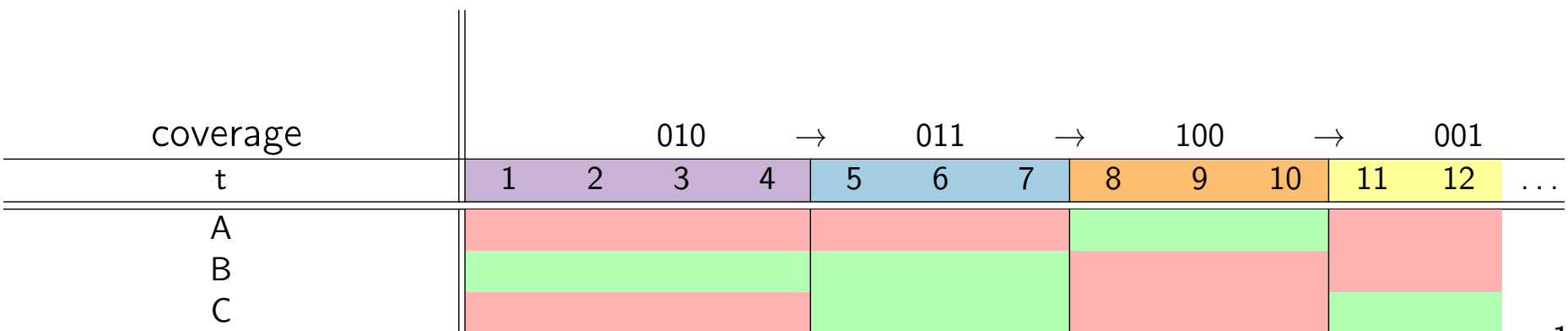

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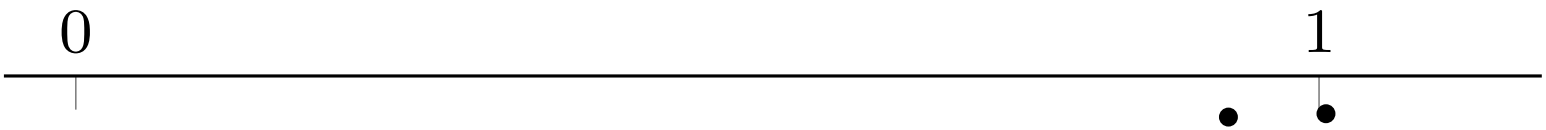

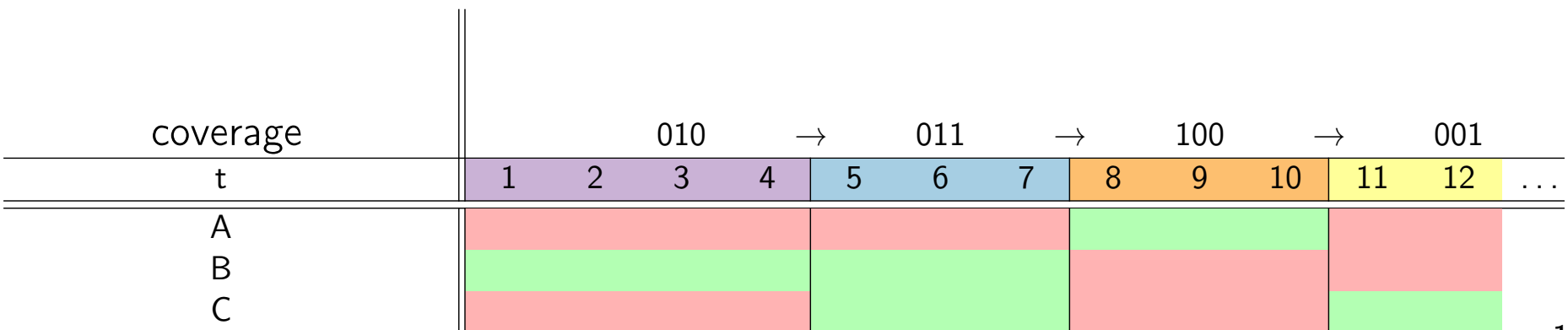

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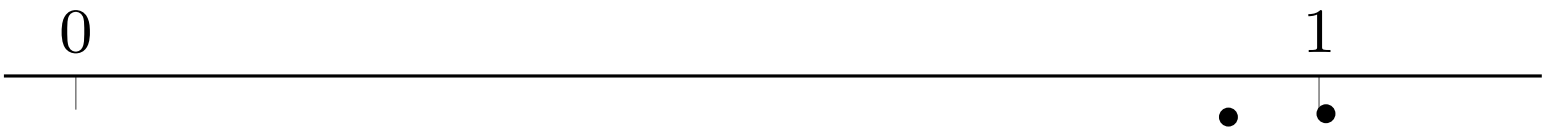

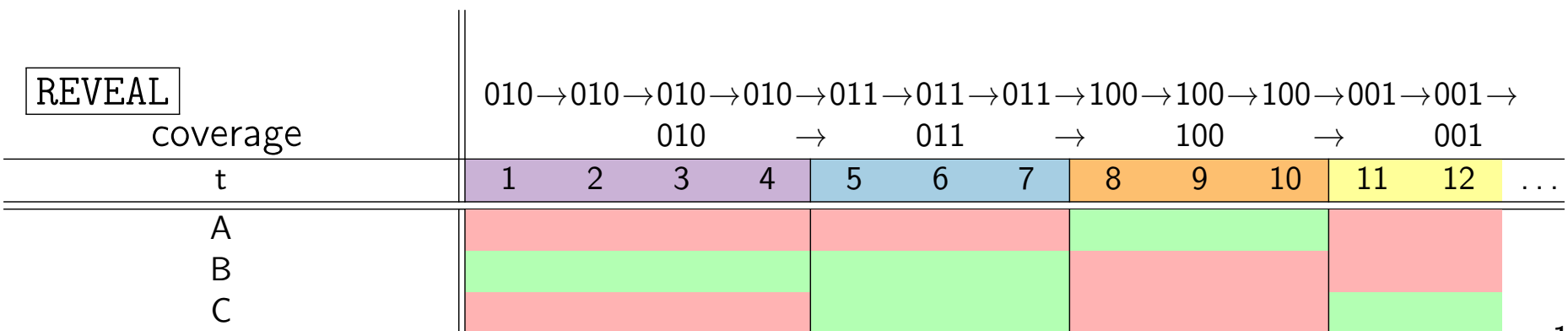

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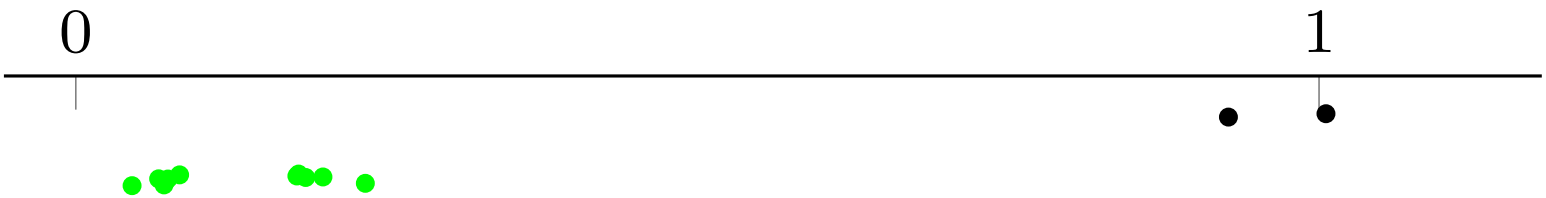

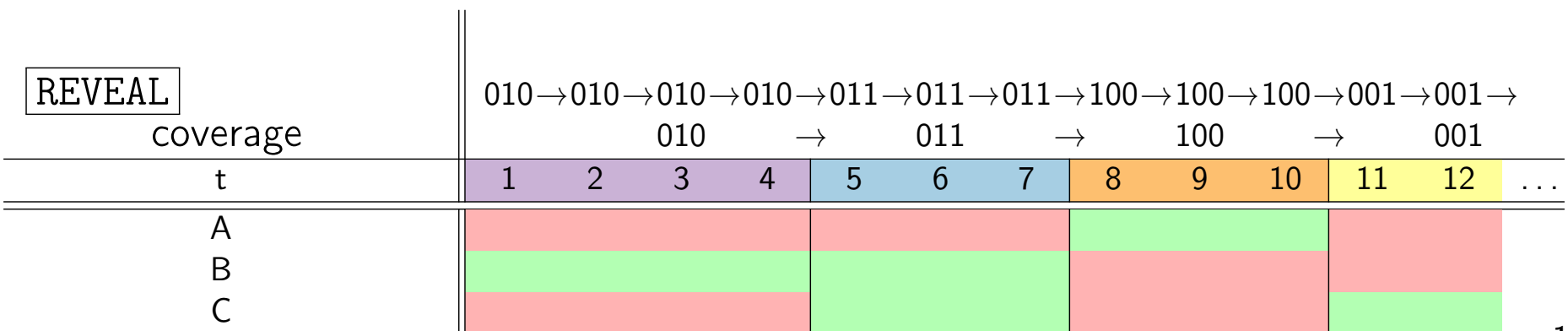

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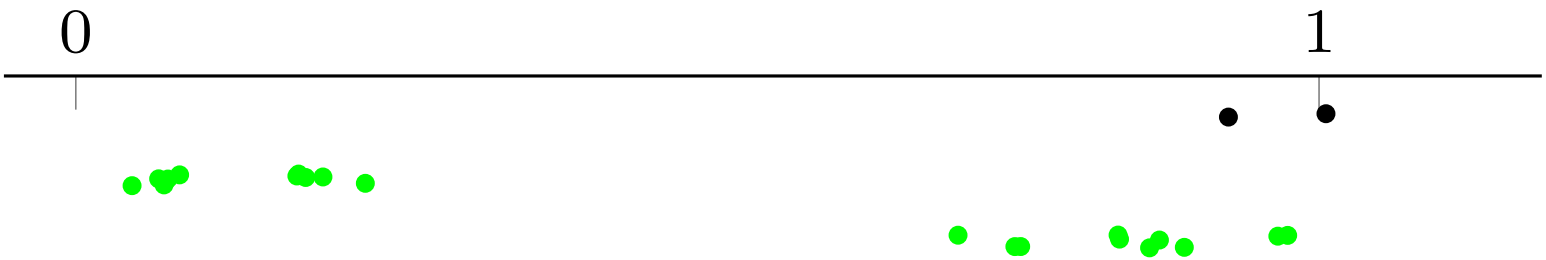

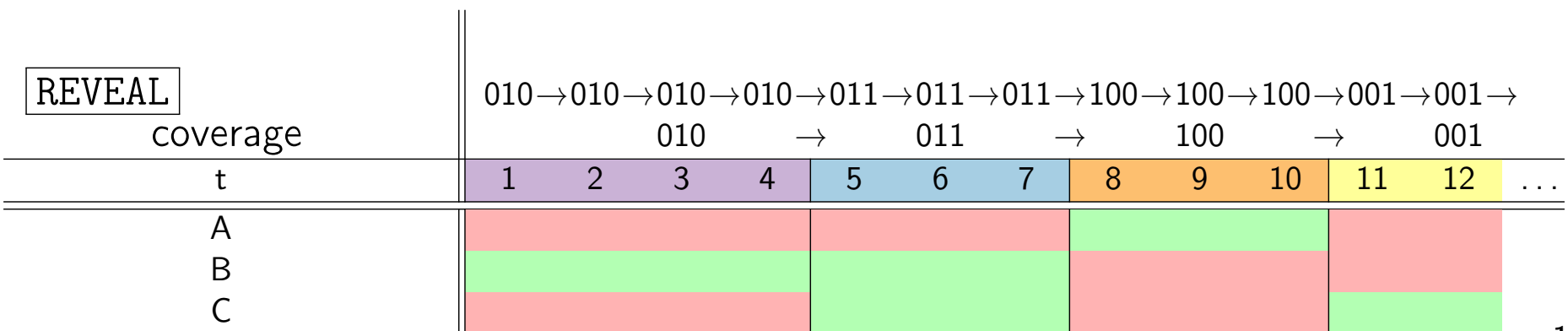

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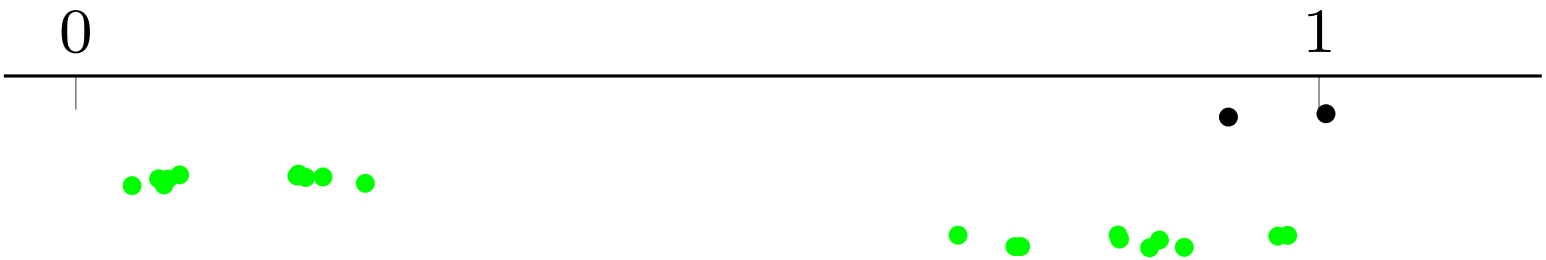

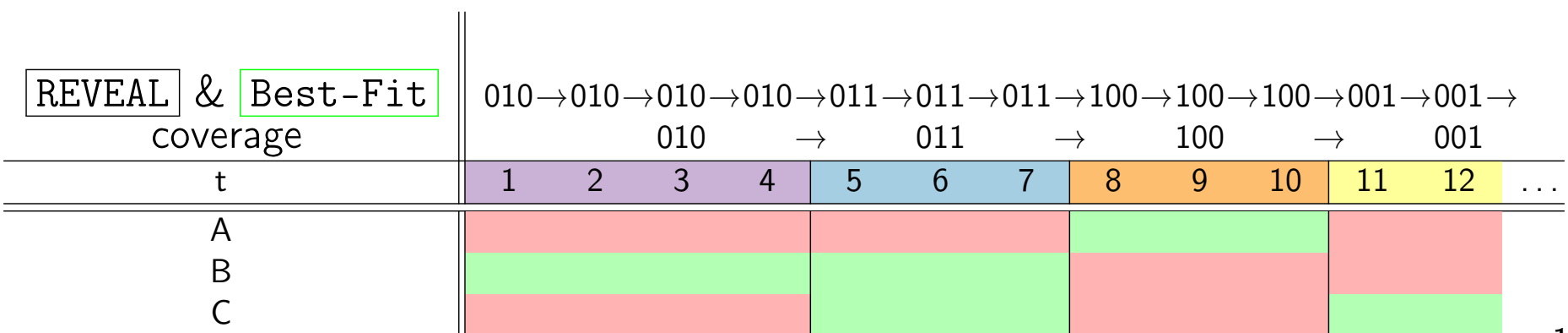

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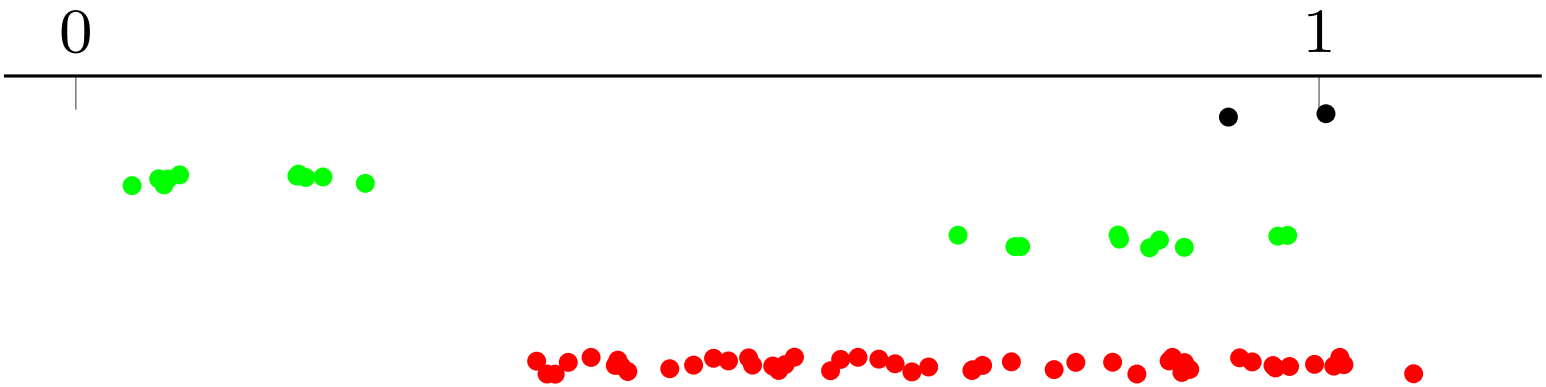

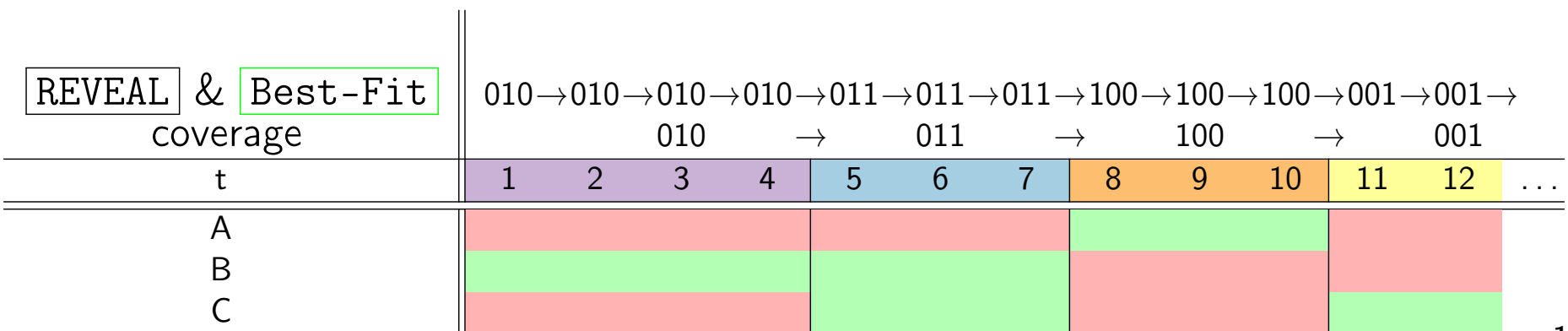

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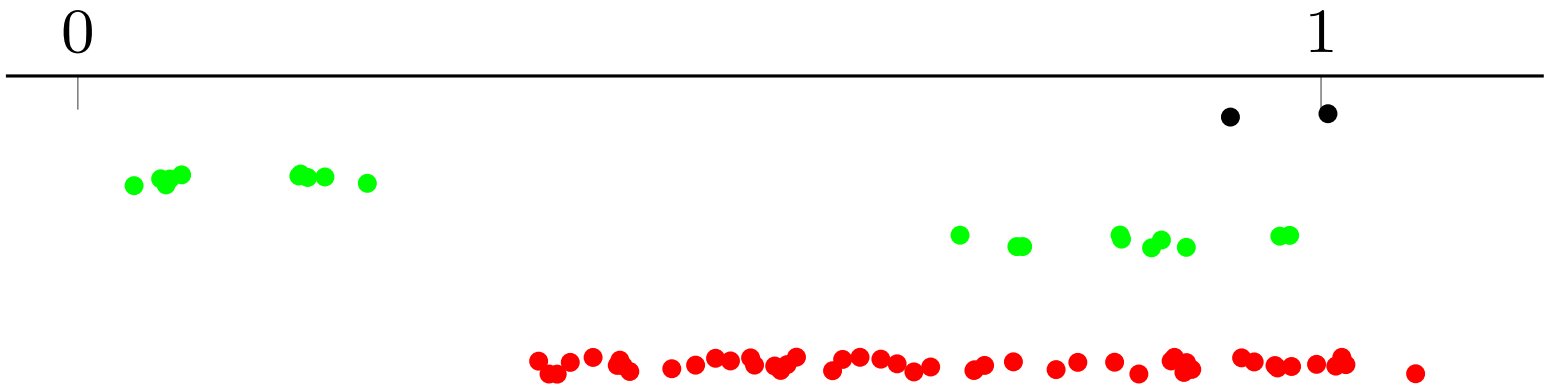

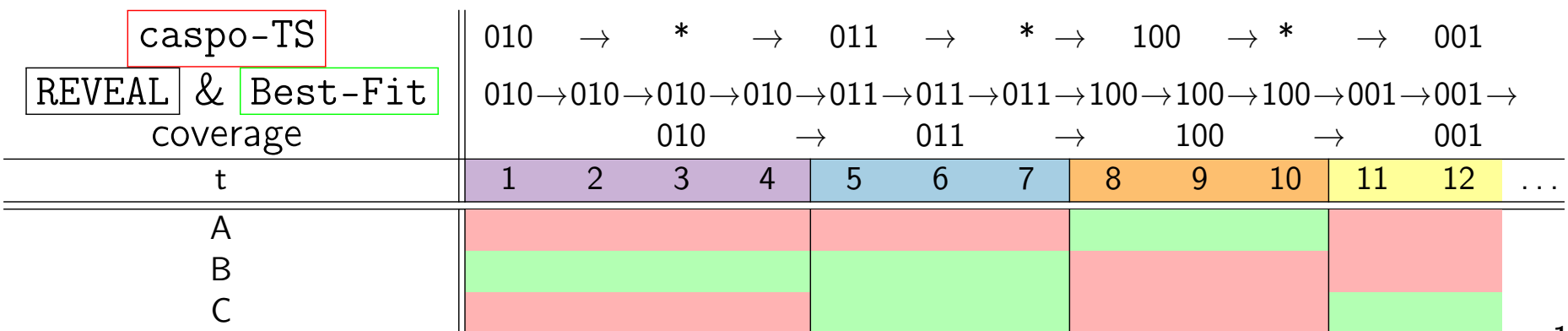

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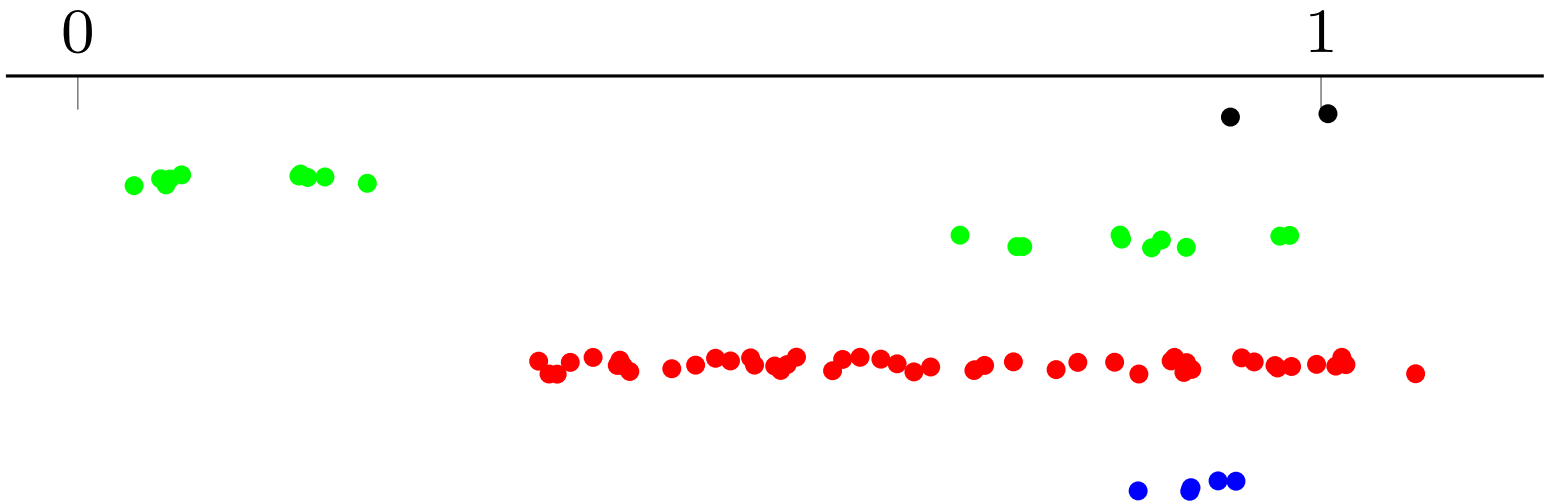

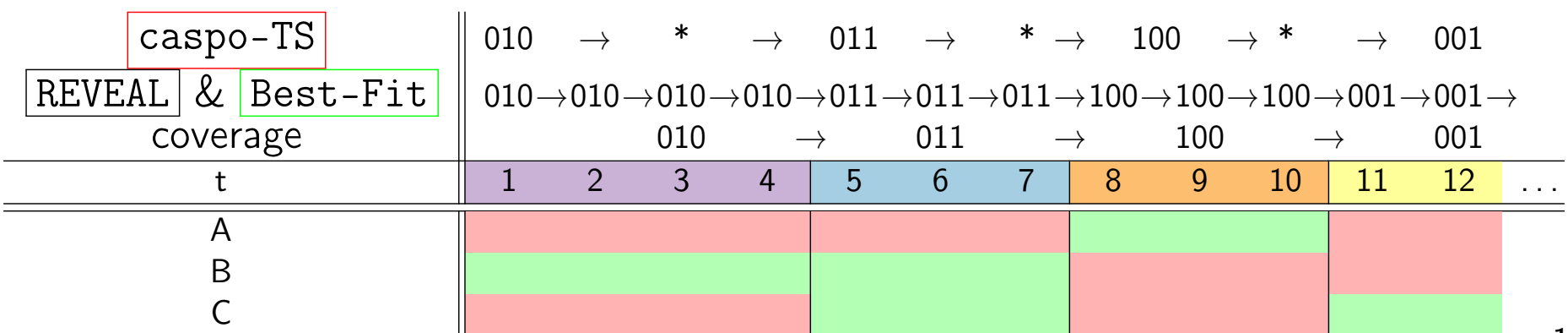

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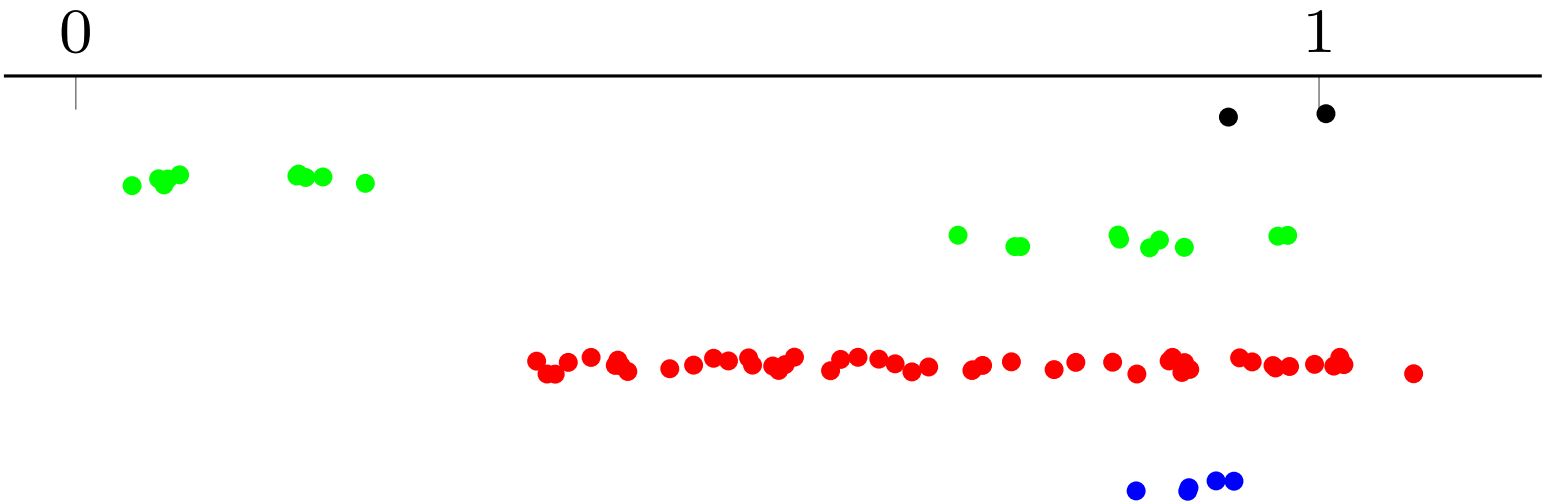
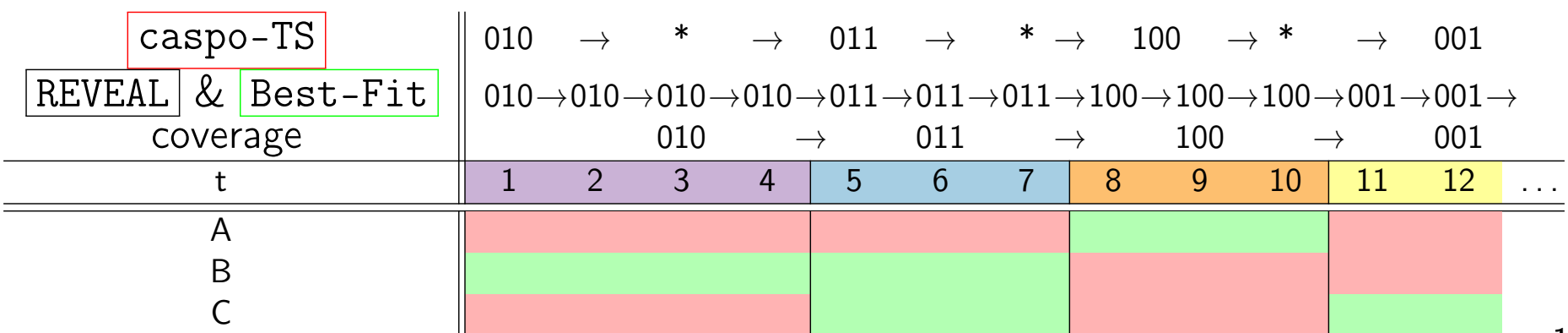
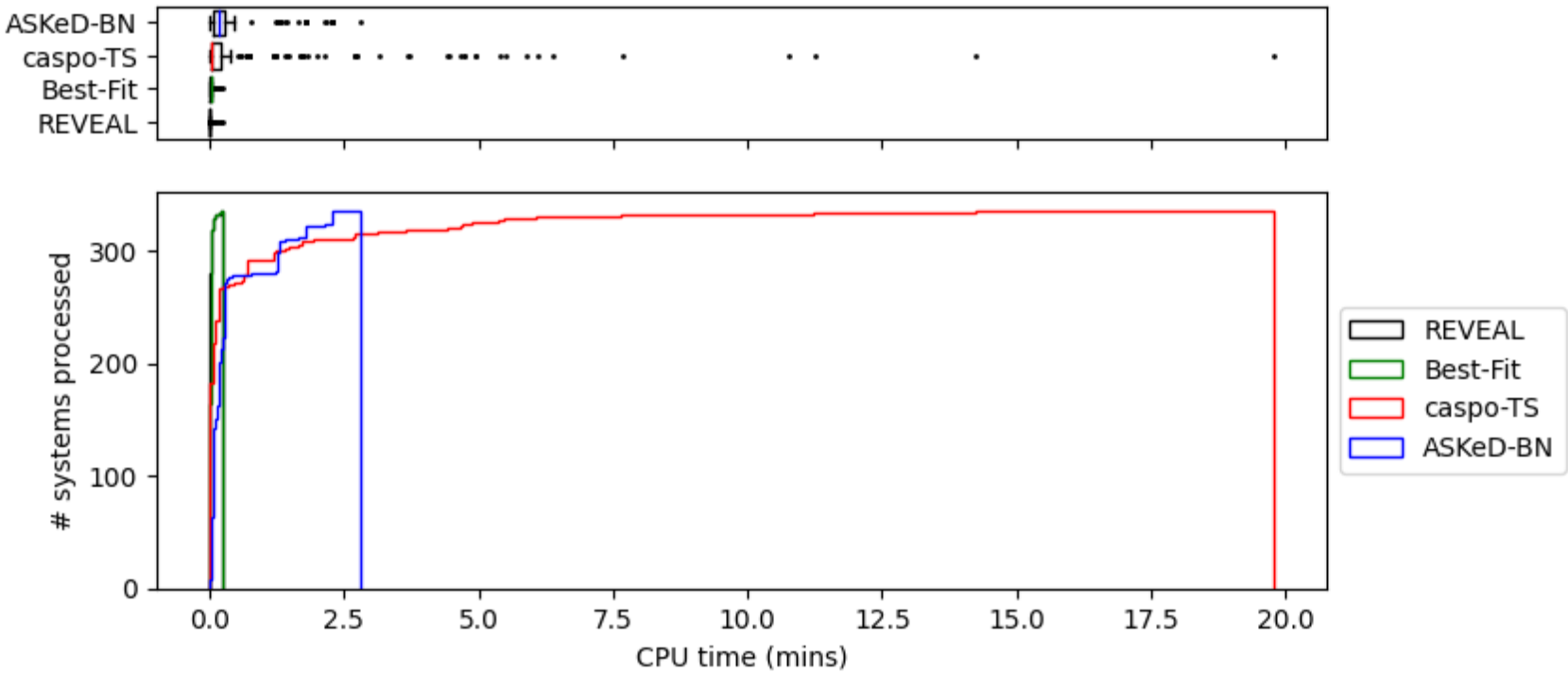




Evaluation - Comparison Runtime



336 experiments at total

fails

`REVEAL`: 240, `Best-Fit`: 64, `caspo-TS`: 20, `ASKeD-BN`: 0

Conclusion

Contribution:

- `ASKeD-BN`: Automatic Synthesis of Boolean Networks constrained in their structure (PKN knowledge) and their dynamics (TS data)
- Approach free of strong / restraining assumptions
- Formulation as a logic program (Answer-Set Programming)
- `ASKeD-BN` gives good results

All data + code available at:
`https://gitlab.inria.fr/avaginay/OLA2021`

Work in progress:

- Apply `ASKeD-BN` on PKN and TS directly extracted from existing biological models (ODE-like)

The end. Any question?

Automatic Synthesis of Boolean Networks
from Biological Knowledge and Data
Athénaïs Vaginay, Taha Boukhobza, and Malika Smaïl-Tabbone

International Conference on Optimization and Learning

21-23 June 2021, Catania, Italia

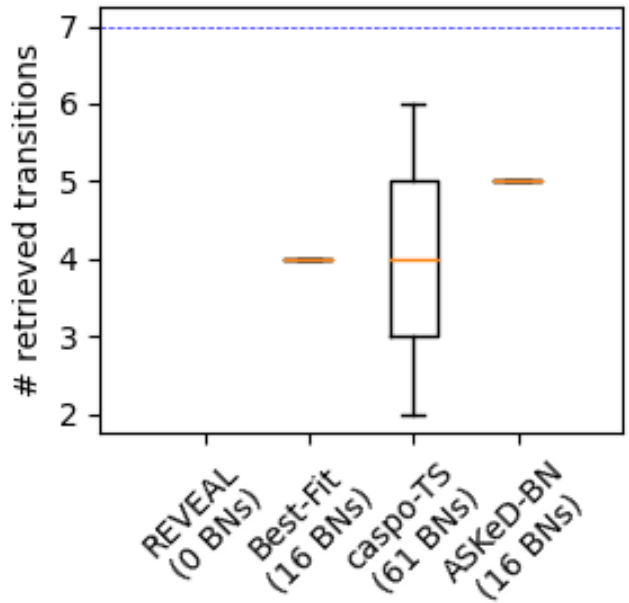
`https://ola2021.sciencesconf.org/data/pages/book_ola2021_en.pdf`

Annexe

Evaluation on Real Datasets

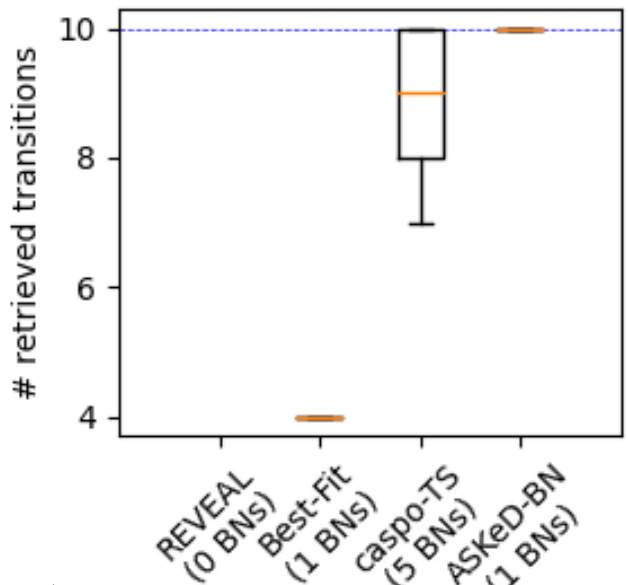
yeast

4 components, 7 transitions



A. thaliana

5 components, 10 transitions



- `REVEAL` fails
- `Best-Fit` lacks consistency
- `caspo-TS` and `ASKeD-BN` find good BNs
- `caspo-TS` returns more BNs, some of them with poor coverage

} confirmed on synthetic datasets

→ `ASKeD-BN` returns a small number of BN, with good coverage and low variance ✓

Synthetic Data – Complexity

system	# node	# edges	# hyperedges (caspo-TS)
raf	3	8	17
randomnet_n7k3	7	35	125
xiao_wnt5a	7	12	19
arellano_rootstem	9	18	60
davidich_yeast	10	27	117
faure_cellcycle	10	35	194

Synthetic Data – Comparison of the # of BN Returned

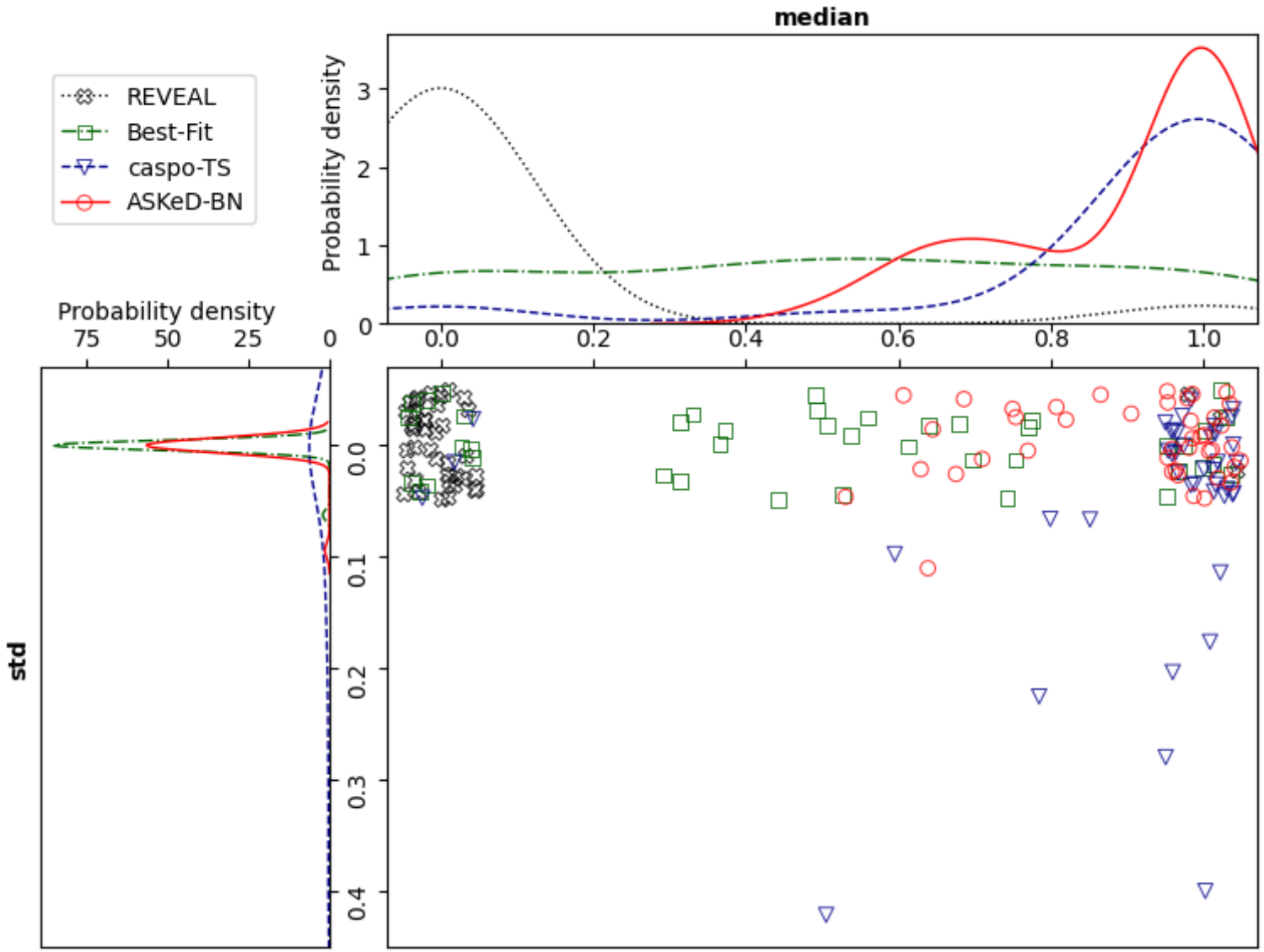
336 experiments at total including 42 with the ARN* setting.

		REVEAL		Best-Fit		caspo-TS	ASKeD-BN
	setting	before filter	after filter	before filter	after filter		
# failing xp	all	230	240	0	64	20	0
# total returned BNs	all	100 677 500	406	100 678 198	724	8481	1210
# total returned BNs	ARN	3	3	51	35	720	85

- `REVEAL` often fails
- `REVEAL` and `Best-Fit` return a lots of BNs which are not respecting the PKN
- `caspo-TS` returns in average between 5 and 7 times more BNs than `ASKeD-BN` (depending on the setting)

*: ARN = Asyn. update scheme, with repetition and noise

Synthetic data, ARN setting – Quality of the BNs



Evaluation - Comparison time and RAM

yest

method	running time (s)	cputime (s)	max_rss (MB)
`REVEAL`	1.0095	0.55	72.97
`Best-Fit`	1.4069	1.10	92.77
`caspo-TS`	24.6545	12.91	183.08
`ASKeD-BN`	5.4209	4.90	186.80

A. thaliana

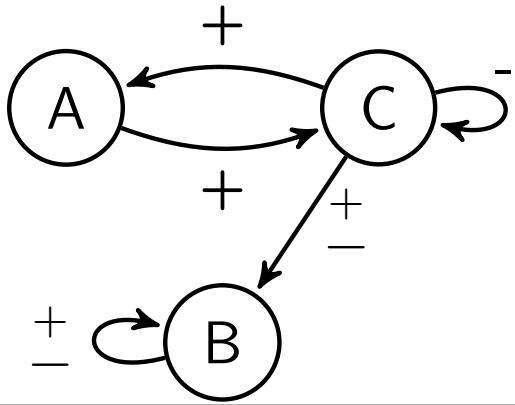
method	running time (s)	cputime (s)	max_rss (MB)
`caspo-TS`	7.0394	1.85	139.93
`ASKeD-BN`	8.5820	8.19	163.38

observed in general:

- `ASKeD-BN` faster in general, but does not scale
- `caspo-TS` is using less RAM

ASKeD-BN: Hard Constraints

"A activates C"
"B interacts with itself"
"C activates A"
"C interacts with B"
"C inhibits itself"



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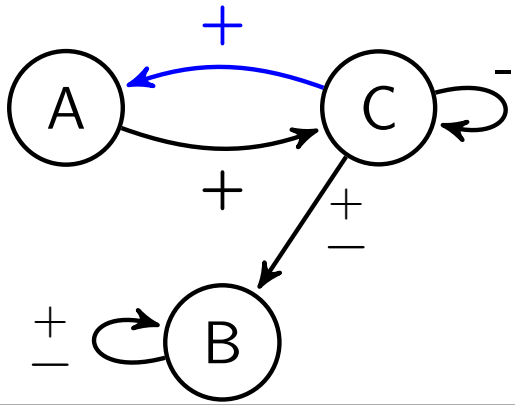

For A:

3 choices:
A := C
A := 0
A := 1

but not:
A := B
A := ¬C

ASKeD-BN: Hard Constraints

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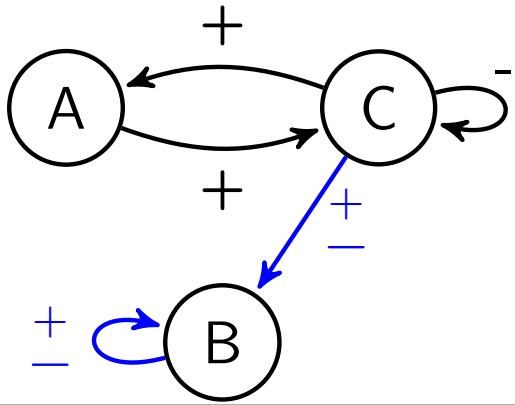

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$A := C$
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but not:
$A := B$
$A := \neg C$

For B:

16 choices:
$B := B \wedge \neg C$
$B := (B \wedge \neg C) \vee (\neg B \wedge C)$;
...
$B := 0$
$B := 1$

but not:
$B := A$

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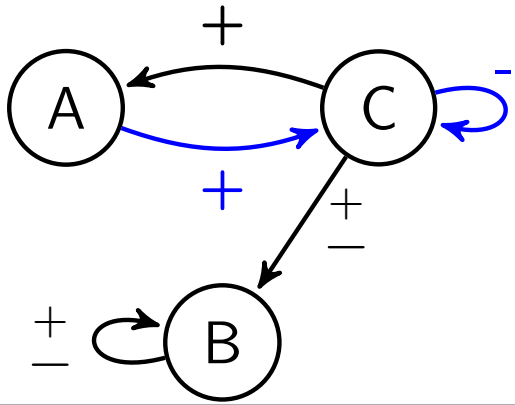

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For C:

6 choices:
$C := \neg C$
$C := A$
...
$C := 0$
$C := 1$

but not:
$C := A \wedge B$

ASKeD-BN: Hard Constraints

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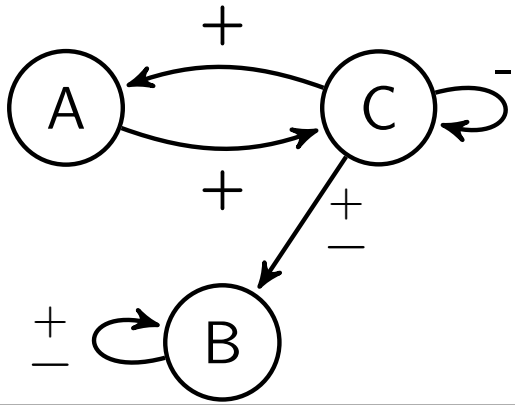

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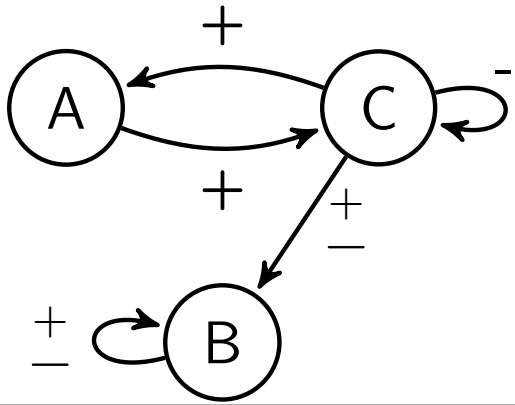

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ASKeD-BN: Soft constraints — Example 1

	010			→	011			→	100			→	001							
t	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
A	0	3	7	13	20	30	49	61	100	63	36	25	2	3	1	1	3	0	0	0
B	100	86	64	57	54	53	51	49	45	37	33	28	22	19	14	12	9	5	2	0
C	0	27	36	42	60	75	54	44	38	48	60	72	88	90	100	100	100	100	100	100

$\mathscr{U}$ set of unexplained timesteps

Mean Absolute Error $\text{MAE}_{\mathsf{X}} = \frac{\sum_{t' \in \mathscr{U}} |\theta_{\mathsf{X}} - x_{t'}|}{T}$

	$a_{t+1} = c_t$	✓	$a_{t+1} = 0$
$\mathscr{U}$	$\emptyset$		$\{8\}$
MAE	0	✓	0.55

ASKeD-BN: Soft constraints — Example 2

	010			→	011		→	100		→	001									
t	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
A	0	3	7	13	20	30	49	61	100	63	36	25	2	3	1	1	3	0	0	0
B	100	86	64	57	54	53	51	49	45	37	33	28	22	19	14	12	9	5	2	0
C	0	27	36	42	60	75	54	44	38	48	60	72	88	90	100	100	100	100	100	100

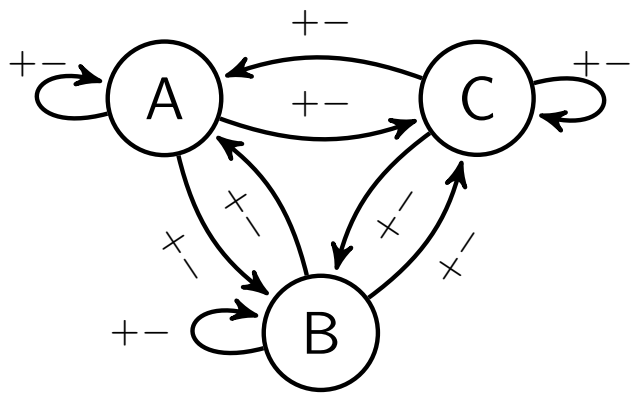
$\mathscr{U}$ set of unexplained timesteps

Mean Absolute Error $\mathrm{MAE}_{\mathsf{X}} = \frac{\sum_{t' \in \mathscr{U}} |\theta_{\mathsf{X}} - x_{t'}|}{T}$

	$b_{t+1} = b_t \wedge \neg \mathsf{c}_t$	✓	$b_{t+1} = (b_t \wedge \neg c_t) \vee (\neg b_t \wedge c_t)$	
$\mathscr{U}$	$\emptyset$		$\emptyset$	
MAE	0	✓	0	✓
# influences	2	✓	4	

How does the PKN help reducing the search space?

Without information



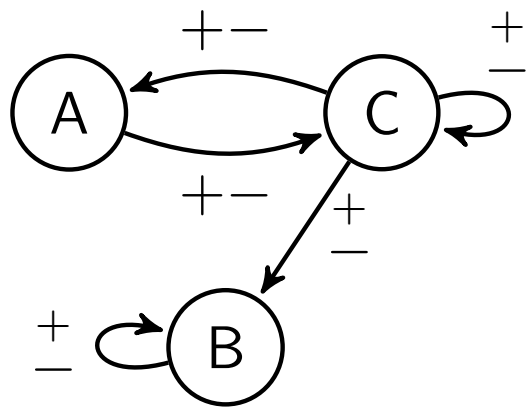
$2^{2^3} = 256$ candidates for each components

$\rightarrow 256 \times 256 \times 256 = 16777216$ candidate BNs

How does the PKN help reducing the search space?

With PKN

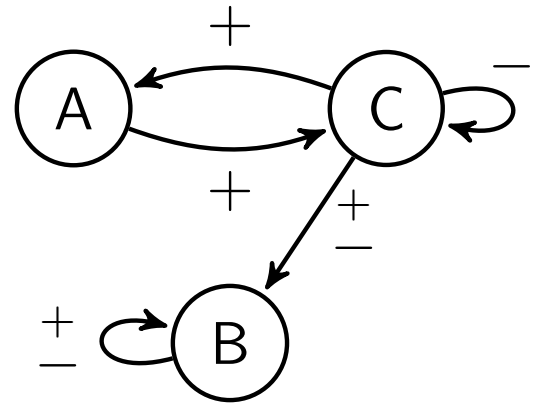
directions only
(`REVEAL` & `Best-Fit`)



A	B	C
4	16	16

$\rightarrow 4 \times 16 \times 16 = 1024$
candidate BNs

direction + signs
(`caspo-TS` & `ASKeD-BN`)



	A	B	C
all	3	16	6
monotonous	3	14	6

$\rightarrow 3 \times 16 \times 6 = 288$
candidate BNs
including 252 locally
partial-monotonous.