

Automatic Synthesis of Boolean Networks from Biological Knowledge and Data

Athénaïs Vaginay, Taha Boukhobza, Malika Smaïl-Tabbone

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Automatic Synthesis of Boolean Networks from Biological Knowledge and Data. International Conference on Optimization and Learning, Jun 2021,
online.

Boolean Network (BN)

set of n **Boolean functions** (one per component)

$$\{f_i : \mathbb{B}^n \rightarrow \mathbb{B}, \forall i \in V\}$$

V : set of n **components** (= genes, proteins...)

$\mathbb{B} = \{0/\text{inactive}, 1/\text{active}\}$

configuration: a vector of \mathbb{B}^n

Boolean Network — an example

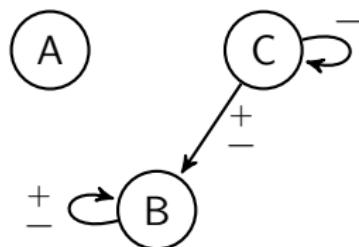
$$\mathcal{B} = \begin{cases} f_A := 0 \\ f_B := (B \wedge \neg C) \vee (\neg B \wedge C) \\ f_C := \neg C \end{cases}$$

Boolean functions in minimal disjunctive normal form (minDNF)

Boolean Network — an example, its structure

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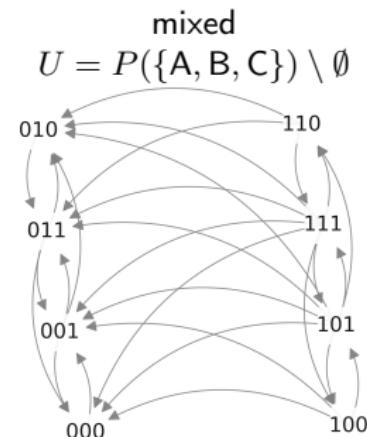
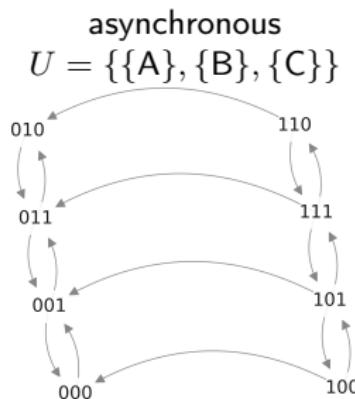
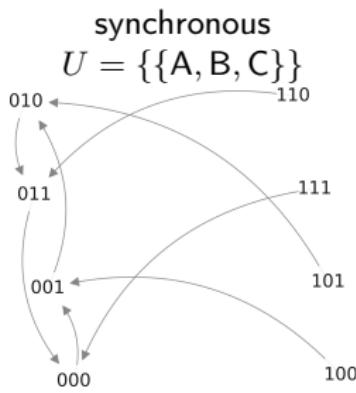
interaction graph:



Boolean Network — an example, its dynamics

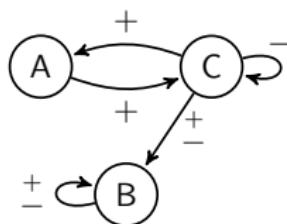
$$\mathcal{B} = \begin{cases} f_A := 0 \\ f_B := (B \wedge \neg C) \vee (\neg B \wedge C) \\ f_C := \neg C \end{cases}$$

state transition graph under an update scheme U :



Structural Knowledge and Dynamical Data

structural knowledge: Prior Knowledge Network (PKN)
= putative interactions between the components

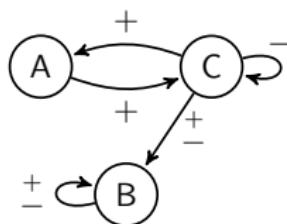


dynamical data: Time Series (TS) = concentrations of the components over time, sequence of configurations

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	...

Structural Knowledge and Dynamical Data

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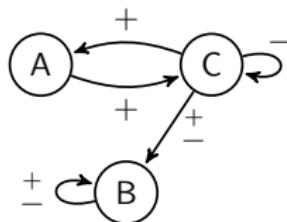


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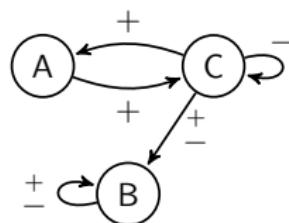


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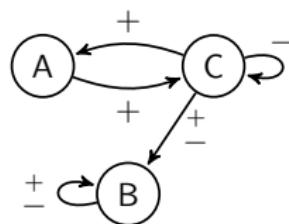


dynamical data: Time Series (TS) = concentrations of the components over **time**, sequence of configurations

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	...
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Structural Knowledge and Dynamical Data

structural knowledge: Prior Knowledge Network (PKN)
= putative interactions between the components



dynamical data: Time Series (TS) = concentrations of the components over time, **sequence of configurations**

t	010				→ 011			→ 100			→ 001			...
	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	...

Our Wishes VS Existing Approaches

- ▶ use a signed PKN + TS
- ▶ synthesise *all* the compatible BNs (with all the equivalent minDNFs)
- ▶ no assumption on the class of functions and on the underlying update scheme of the seq. of config.

Our Wishes VS Existing Approaches

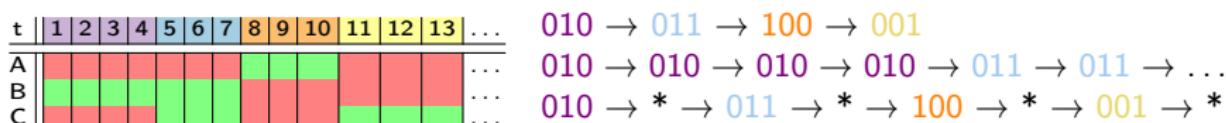
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	signed PKN	all minDNF, all class	assumption on TS & config. seq.
REVEAL	✗	✗	✓ each timestep = sync. transition
Best-Fit	✗	✗	✓ each timestep = sync. transition
caspo-TS	✓	✓ monotonous	async. reachability

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Our own approach: ASKeD-BN

For each component: use ASP to generate all the possible transition functions (in minDNF) compatible with a given PKN and TS. Then: use python to produce all the possible BNs.

Why ASP? Because...

- ▶ several tools are now developed with ASP in systems biology
- ▶ we can focus only on modeling the problem and not on the way to get the solutions
- ▶ we were told it is very fast and efficient, fun to learn, ...
(and at the end we happy of this choice! :))))

ASKeD-BN— modeling a candidate DNF

ASP picks a subset of conjunctions among all the possible ones (given)

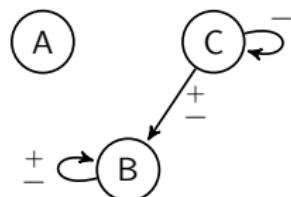
```
1{ conjTakenID(0..maxNbPossibleConj) }.
conjTaken(I, N, V) :- conj(I, _, _); conjTakenID(I).
```

```
% GIVEN : conj(ID, Component, Sign)
conj(0, a, 0). conj(0, b, 0). conj(0, c, 0).
conj(1, a, 1). conj(1, b, -1). conj(1, c, 0). % A ∧ ¬B
conj(2, a, -1). conj(1, b, 0). conj(1, c, -1). % ¬A ∧ ¬C
conj(3, a, -1). conj(3, b, -1). conj(3, c, -1). % ¬A ∧ ¬B ∧ ¬C
conj(4, a, 1). conj(4, b, 1). conj(4, c, 1). % A ∧ B ∧ C
...
```

Example: taken = {1, 2} \rightarrow candidate = $(A \wedge \neg B) \vee (\neg A \wedge \neg C)$

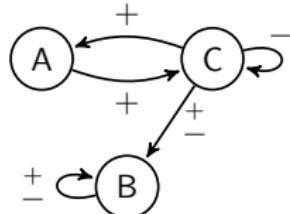
ASKeD-BN— structural constraints

interaction graph



\subseteq

PKN



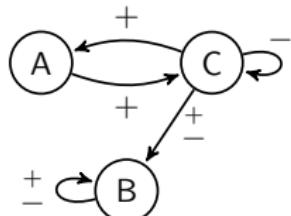
"it is false to select a conjunction that uses a literal that is not allowed by the PKN"

```
ig(ParentID, x, V) :- conjTaken(ConjID, ParentID, V); V!=0.  
:- ig(ParentID, x, V) ; not pkn(ParentID, x, V).
```

ASKeD-BN— dynamical constraints

- (1) Use configurations sequence with the parsimonious update schema possible + the PKN to build partial truth tables

$010 \xrightarrow{\{C\}} 011 \xrightarrow{\{A,B,C\}} 100 \xrightarrow{\{A,C\}} 001$



	putative input	output
for A:	C	
0	0	0
1	1	1
for B:	B, C	
0	00	
1	01	
2	10	
3	11	0
for C:	A, C	
0	00	
1	01	0
2	10	1
3	11	

ASKeD-BN— dynamical constraints

(2) discard candidates that doesn't match the truth table

examples of eliminated candidates
for A:

$$\begin{array}{l} 0 \\ \neg C \end{array}$$

for B:

$$\begin{array}{l} 1 \\ B \vee C \\ B \wedge C \\ (A \wedge B) \vee (\neg A \wedge \neg B) \end{array}$$

for C:

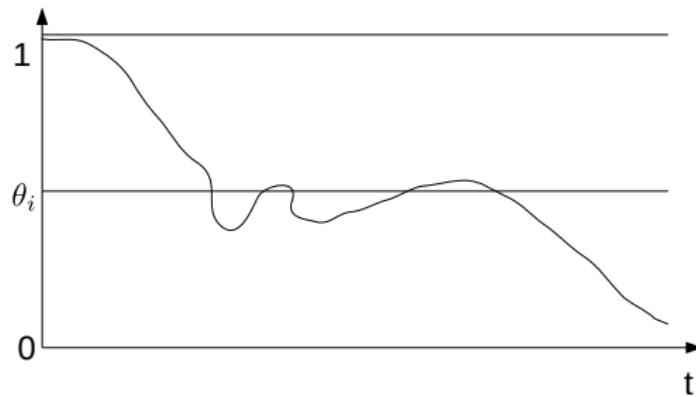
$$\begin{array}{l} 0 \\ 1 \\ C \end{array}$$

	putative input	output
for A:	C	
0	0	0
1	1	1
for B:	B, C	
0	00	
1	01	
2	10	
3	11	0
for C:	A, C	
0	00	
1	01	0
2	10	1
3	11	

ASKeD-BN— dynamical constraints

(3) Optional: minimize the error (to avoid UNSAT)

#minimize{E@2 : error(E)}. % highest priority



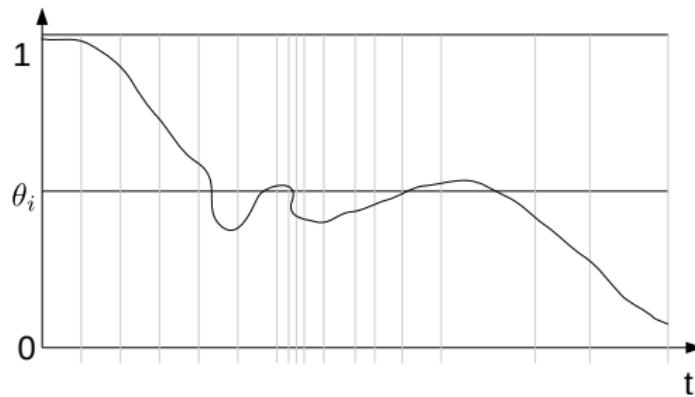
i_t : continuous value of i at time t

θ_i : binarisation threshold for i

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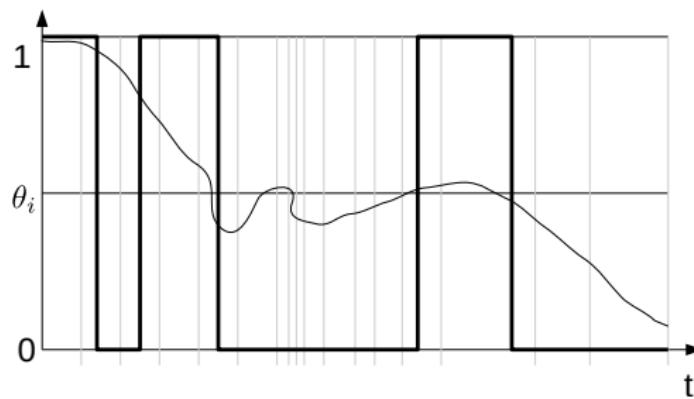
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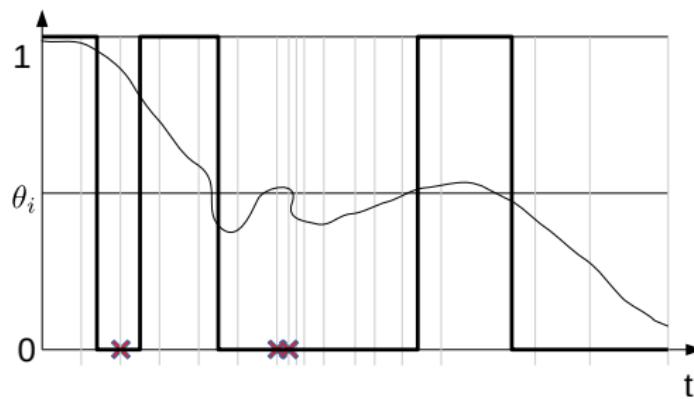
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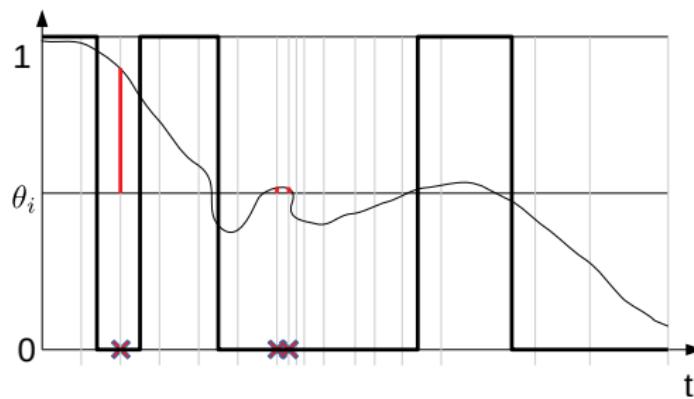
T : # time steps

\mathcal{U} : set of unexplained time steps

ASKeD-BN— dynamical constraints

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i_t : continuous value of i at time t

θ_i : binarisation threshold for i

T : # time steps

\mathcal{U} : set of unexplained time steps

minimise the Mean Absolute Error
(ideally 0)

$$\text{MAE}_{f_i} = \frac{\sum_{t \in \mathcal{U}_{f_i}} |\theta_i - i_t|}{T}$$

ASKeD-BN— minimality constraint

Find the smallest minDNF(s) among the minDNFs compatible with the (partial) truth table

	putative input	output	possible guess				
			minDNF	$\neg A \wedge B$	$\neg A$	B	$\neg A \vee B$
		size	2	1	1	2	
0	00		0	1	0	1	
1	01	0	0	0	0	0	
2	10	1	1	1	1	1	
3	11		0	0	1	1	

```
sizeconj(C, S):-conjTakenID(C);S=#sum{|V|,N:conj(C, N, V)} .  
sizeDNF(S):- S=#sum{N,C: sizeconj(C, N), conjTakenID(C)} .  
% N elements in conjunction C  
#minimize{S@1 : sizeDNF(S)}. % lower priority
```

ASKeD-BN— Evaluation and Results

Main goal: transforming existing ODE-like biological models to Boolean networks.

2 papers so far.

Nice results on our criteria, on this (**very specific**) application case
→ better than REVEAL, Best-Fit and caspo-TS

- ▶ $\text{IG} \subseteq \text{PKN}$ (by construction)
- ▶ the mixed STG BNs recovers a good proportion of the transitions of the sequence.
- ▶ small number of BNs synthesised (thanks to mincard minDNF)

Remaining Things to Investigate

- ▶ overfitting to the given seq. of configurations? (drawback of mincard minDNF)
- ▶ choice binarisation procedure and error measure
- ▶ long solving time & a lot of memory ($> 30\text{h}$, $> 700 \text{ Go RAM}$)
→ is there a better encoding possible? better clingo options?

ASP for a system biologist: ✓

Thanks for your attention.

Enjoy the workshop and conference, and come try the
“Bergamotes de Nancy” I brought (available starting tomorrow)



athenais.vaginay@loria.fr
(looking for “write a PhD thesis” and “find a post-doc” advice :)))

$$\mathcal{R} = \begin{cases} r_{\text{on}} = e_{\text{on}} & : S + E \rightarrow C \\ r_{\text{off}} = e_{\text{off}} & : C \rightarrow S + E \\ r_{\text{cat}} = e_{\text{cat}} & : C \rightarrow E + 2 \times P \end{cases}$$

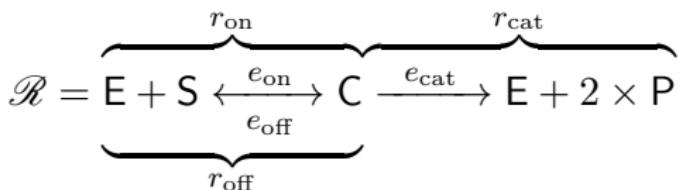
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$$\mathcal{R} = \begin{cases} r_{\text{on}} = e_{\text{on}} & : \textcolor{blue}{S} + \textcolor{blue}{E} \rightarrow \textcolor{black}{C} \\ r_{\text{off}} = e_{\text{off}} & : \textcolor{blue}{C} \rightarrow \textcolor{black}{S} + \textcolor{black}{E} \\ r_{\text{cat}} = e_{\text{cat}} & : \textcolor{blue}{C} \rightarrow \textcolor{black}{E} + 2 \times \textcolor{black}{P} \end{cases}$$

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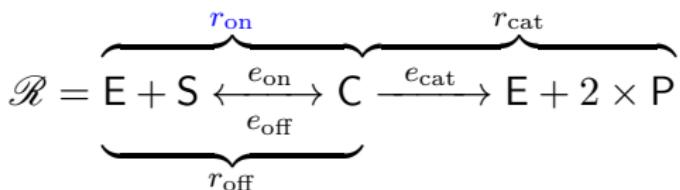
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Chemical Reactions Network



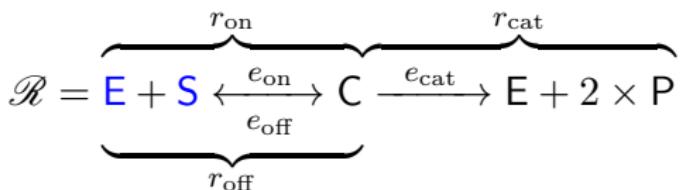
A reaction transforms some reactants to products at a given speed

Chemical Reactions Network



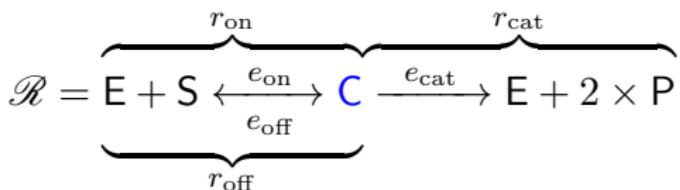
A **reaction** transforms some reactants to products at a given speed

Chemical Reactions Network



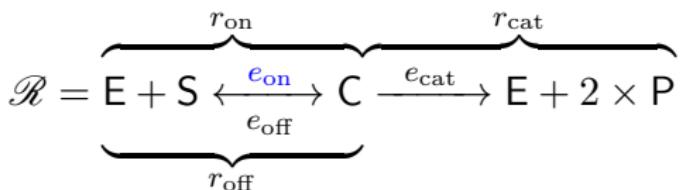
A reaction transforms some **reactants** to products at a given speed

Chemical Reactions Network



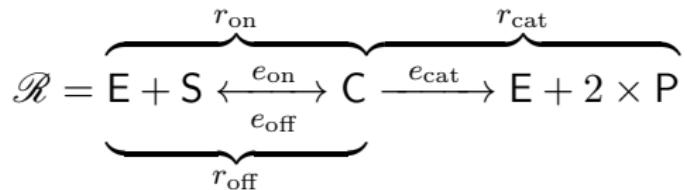
A reaction transforms some reactants to **products** at a given speed

Chemical Reactions Network

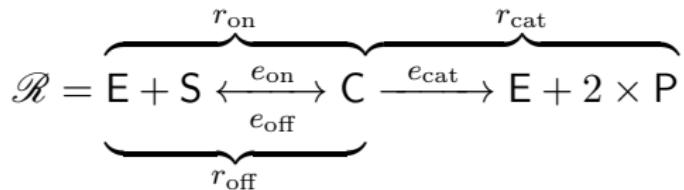


A reaction transforms some reactants to products at a given speed

Chemical Reaction Network — ODEs

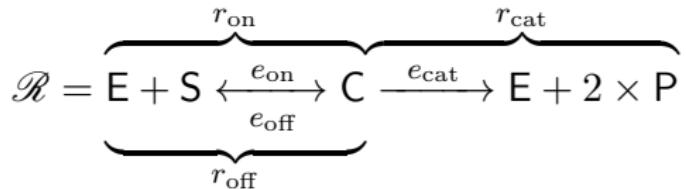


Chemical Reaction Network — ODEs



$$\forall i \in V : \frac{di}{dt} = \sum_{r \in \mathcal{R}} e_r \times \delta_r(i)$$

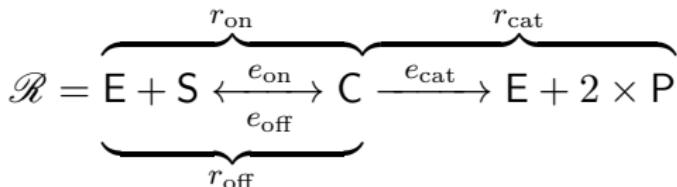
Chemical Reaction Network — ODEs



$$\forall i \in V : \frac{di}{dt} = \sum_{r \in \mathcal{R}} e_r \times \delta_r(i)$$

$$\frac{d[C]}{dt} = \underbrace{e_{\text{on}} \times 1}_{r_{\text{on}}} + \underbrace{e_{\text{off}} \times -1}_{r_{\text{off}}} + \underbrace{e_{\text{cat}} \times -1}_{r_{\text{cat}}}$$

Reaction Network — Structure and Dynamics



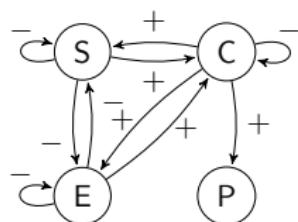
Structure:

1. If Y is a reactant and X disappears
then $Y \xrightarrow{-} X$
2. If Y is a reactant and X appears
then $Y \xrightarrow{+} X$

Dynamics:

numerical simulation of the ODEs
+ binarisation

[Fages et al. 2008]



	putative input	output	candidate functions							
for B:	B, C									
	0	00	0	1	0	1	0	1	0	1
	1	01	0	0	1	1	0	0	1	1
	2	10	0	0	0	0	1	1	1	1
	3	11	0	0	0	0	0	0	0	0
for C:	A, C		rota	rota	rota	rota	rota	rota	rota	rota
	0	00								
	1	01								
	2	10	0	0	0	0	0	0	0	0
	3	11	1	1	1	1	1	1	1	1
			with guess							
			0	1	0	1	0	1	0	1
			0	0	0	0	0	0	0	0
			1	1	1	1	1	1	1	1
			0	0	1	1	0	1	1	1
			$\neg A \wedge B$							

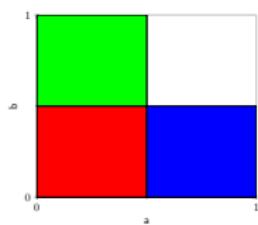
ASKeD-BN— minimality constraints

→ For finding the minDNF(s) given a truth table

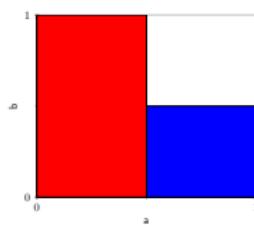
	putative input	output
0	00	1
1	01	1
2	10	1
3	11	0

Several candidate DNFs, but only one minimal

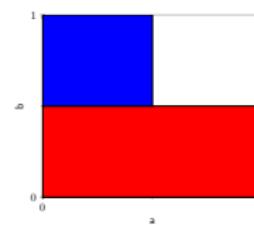
$$\neg A \wedge \neg B$$
$$V(A \wedge \neg B)$$
$$V(\neg A \wedge B)$$



$$\neg A$$
$$V(A \wedge \neg B)$$



$$\neg B$$
$$V(\neg A \wedge B)$$



$$\neg A \vee \neg B$$

