

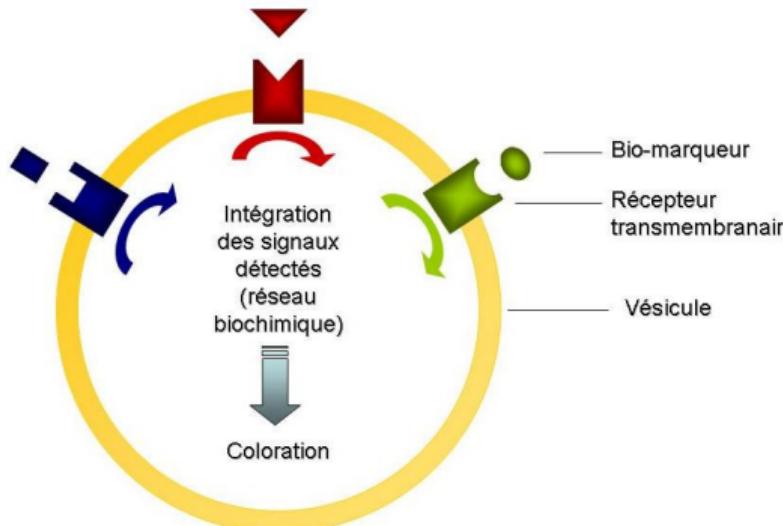
Silicell Maker CAD tool for biochemical networks

Patrick Amar

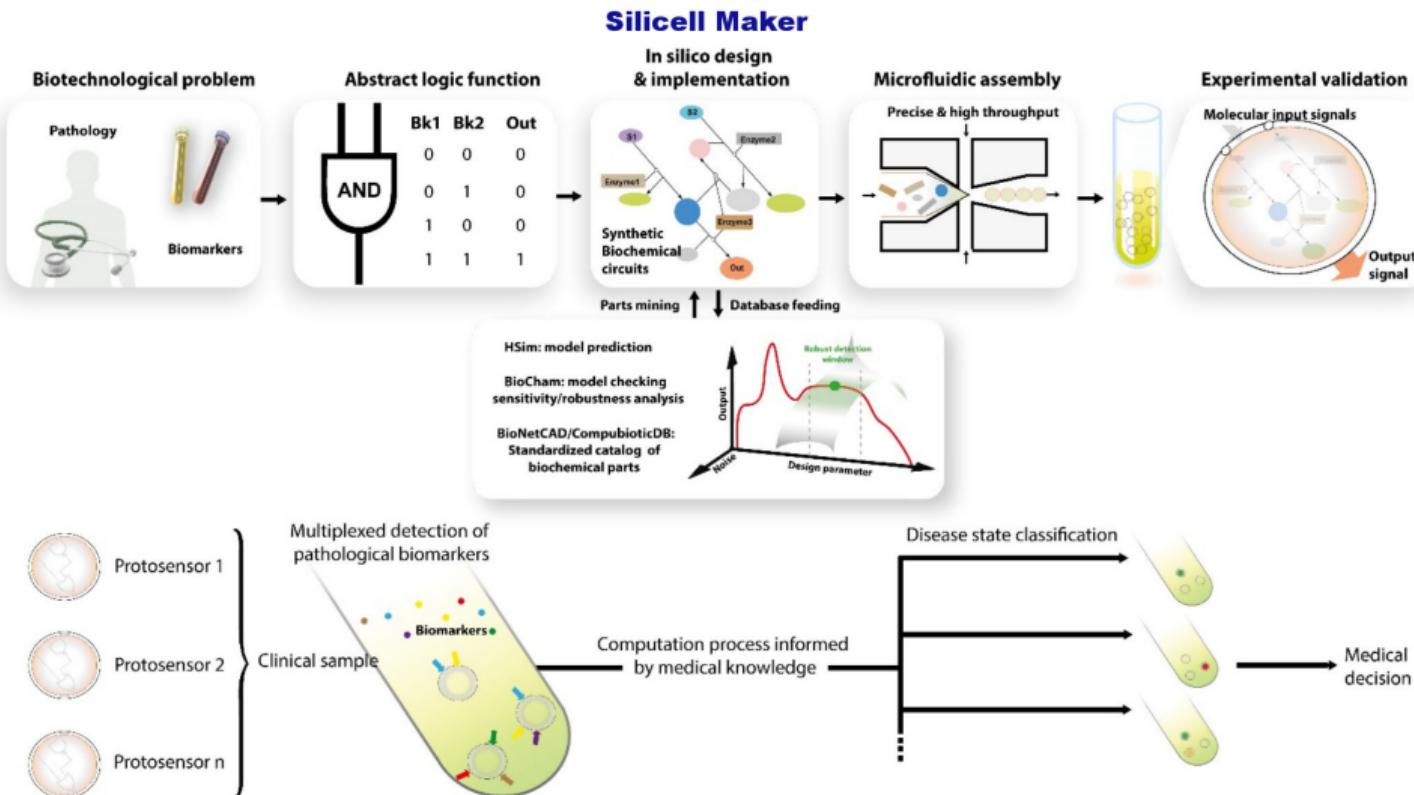
April 12th 2022

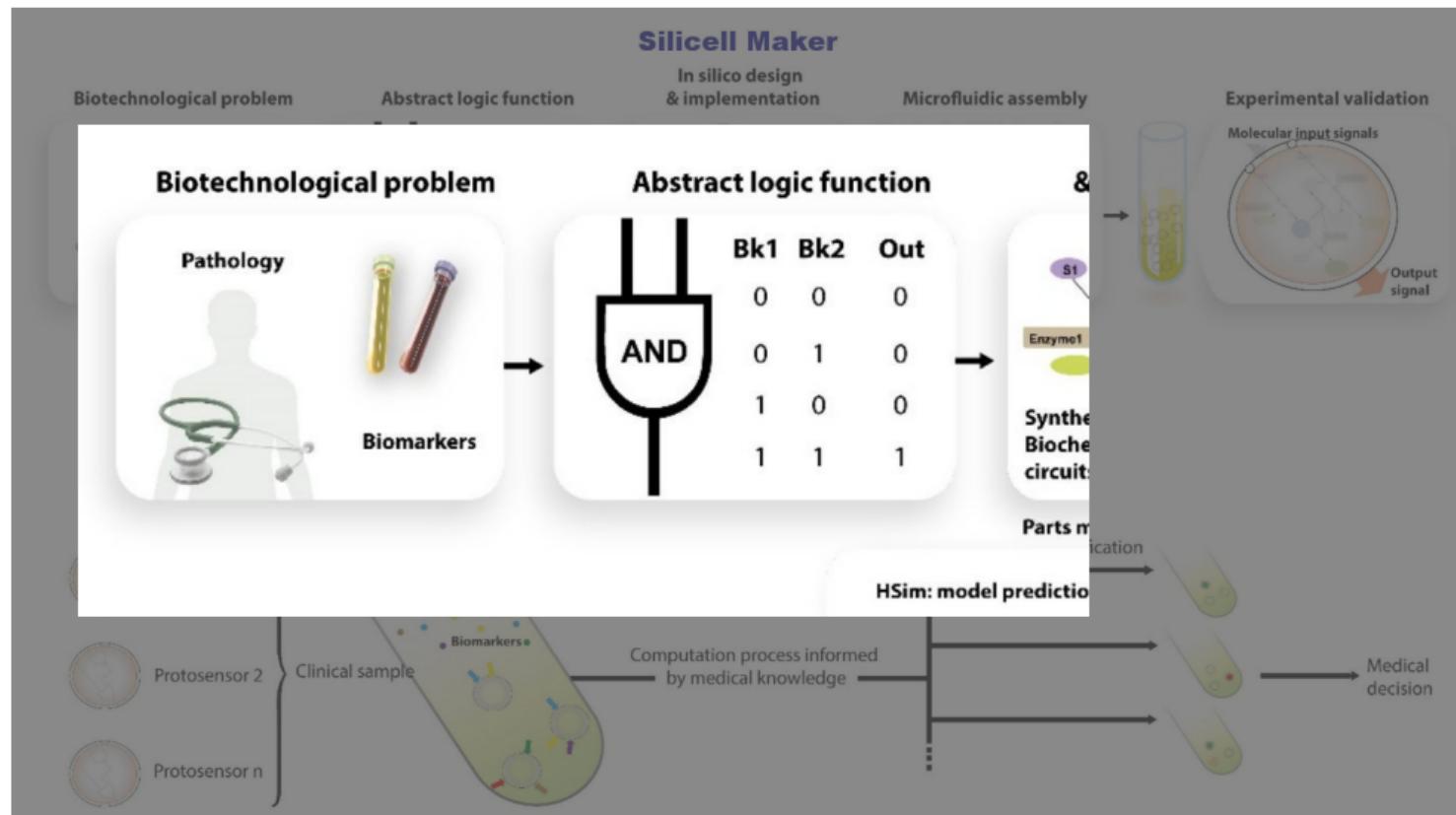
Séminaire INRIA - Lifeware

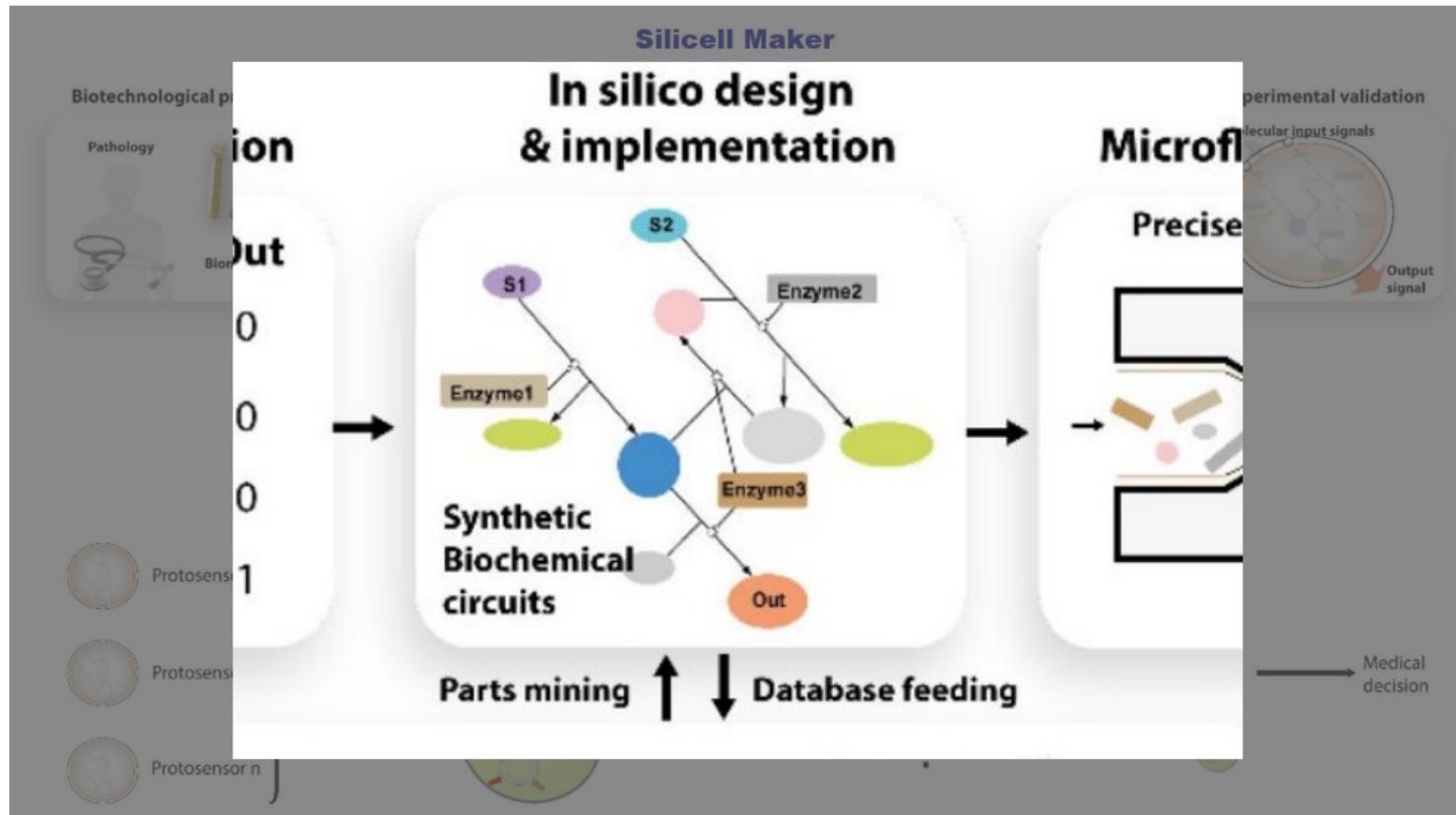
Artificial biochemical nano-system for medical diagnosis

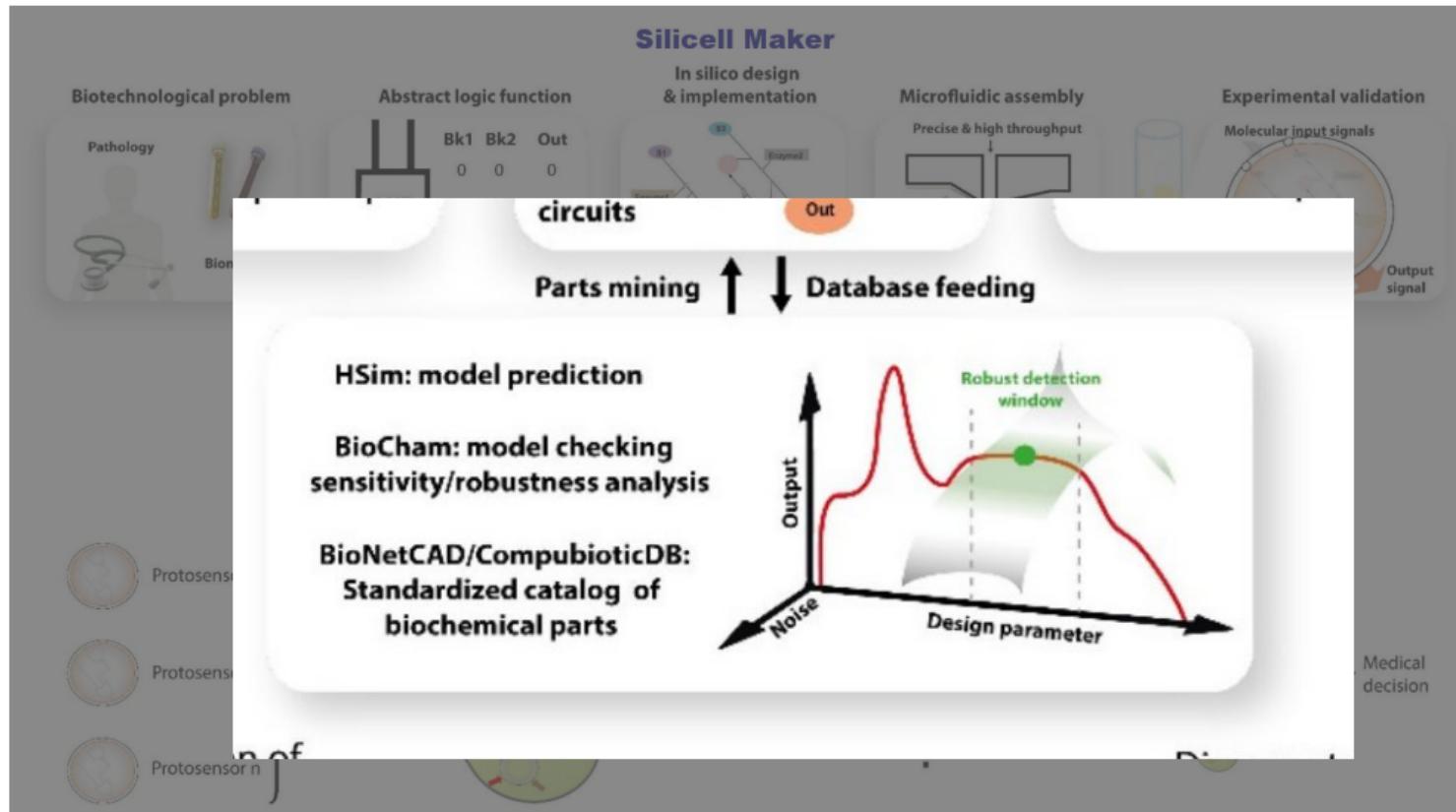


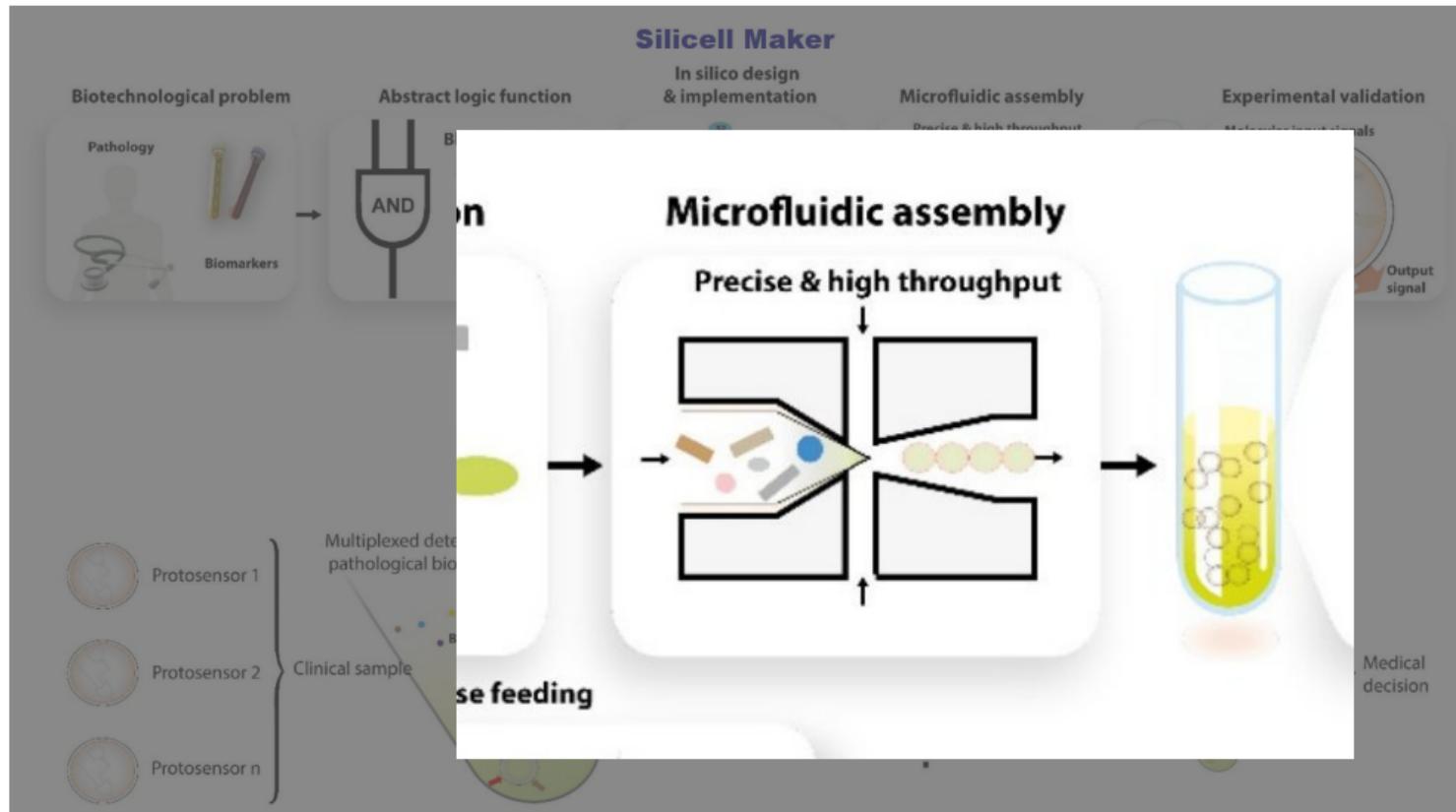
- ▶ **stable and robust system** ->
no bacterial host,
no genetic system
- ▶ lipidic vesicle +
trans-membrane receptors
- ▶ enzymatic network artificially
designed
- ▶ results easy to get
(ex.: color change)

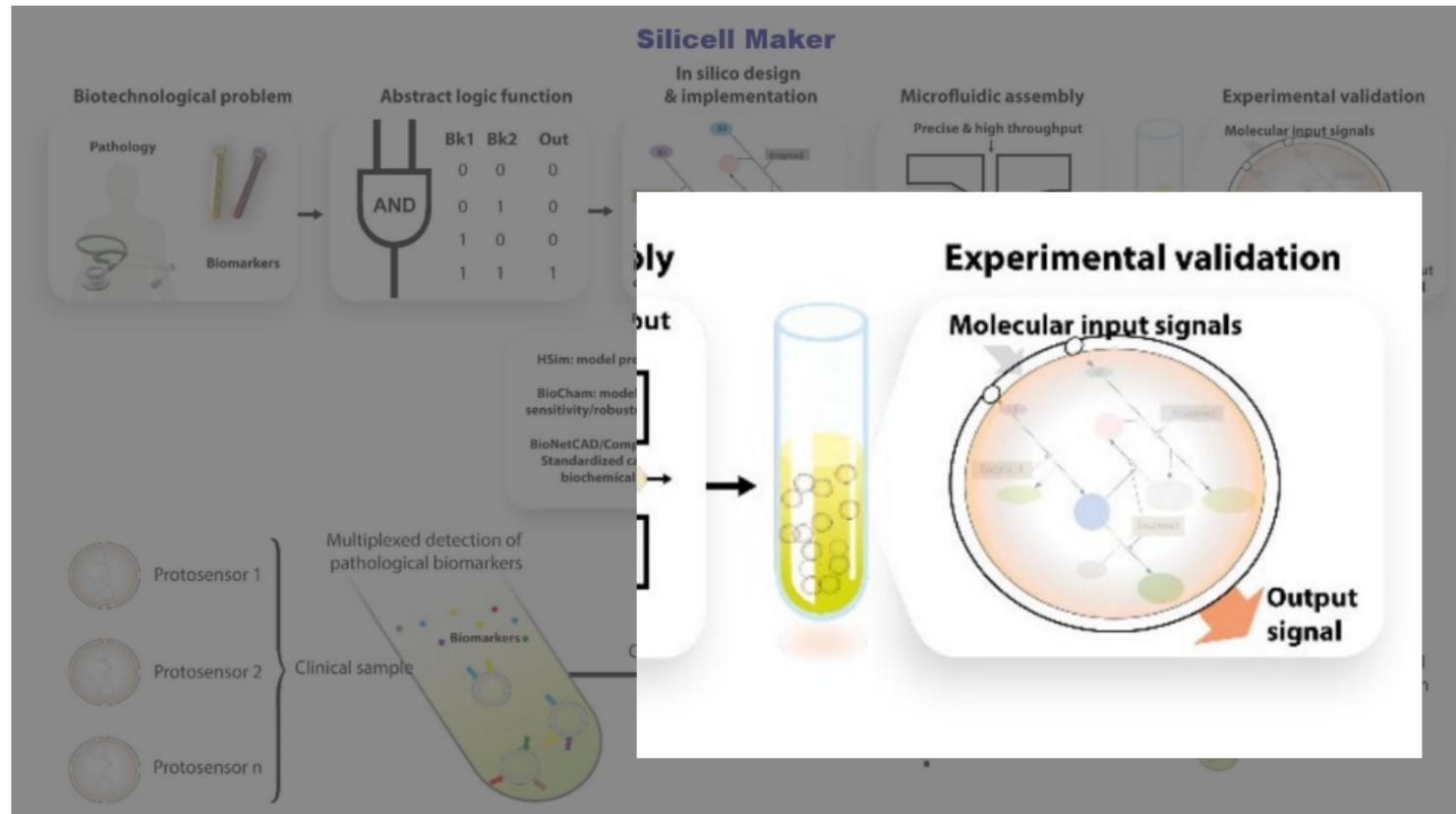


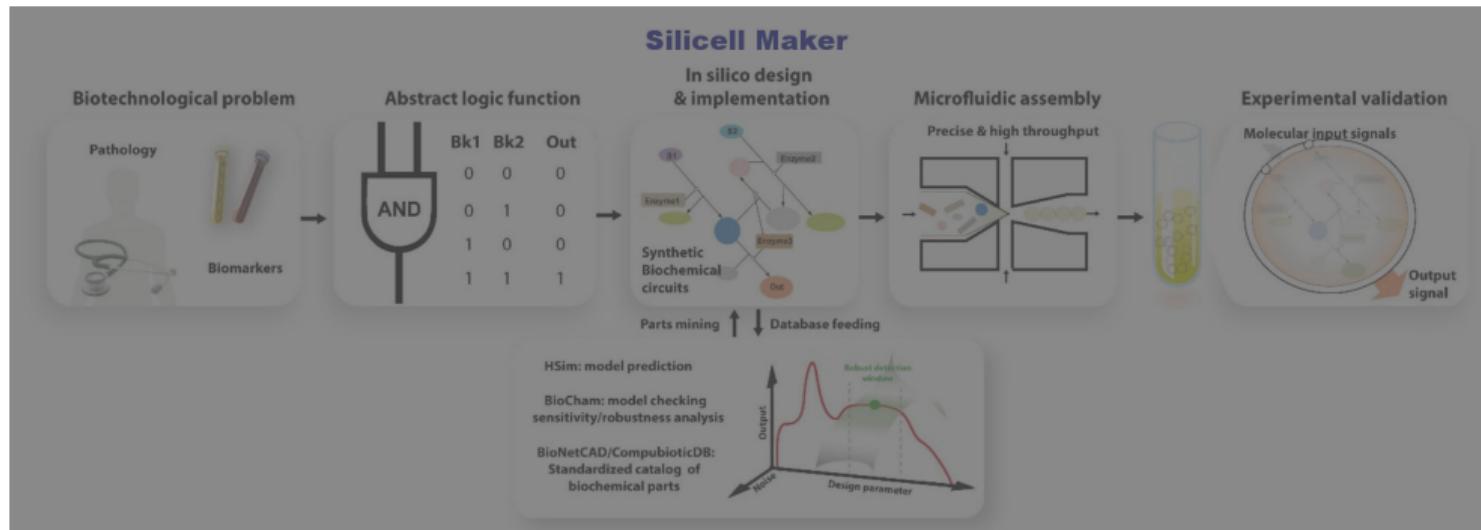


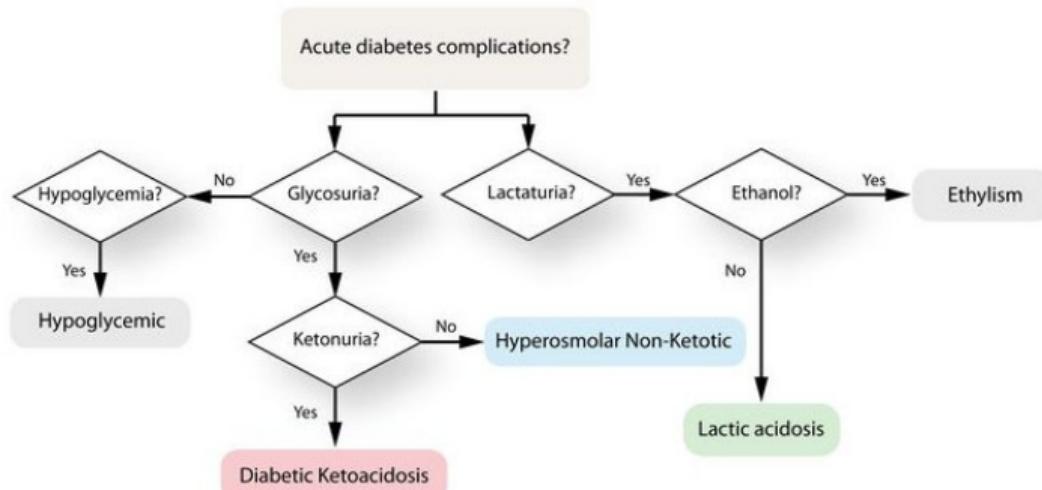








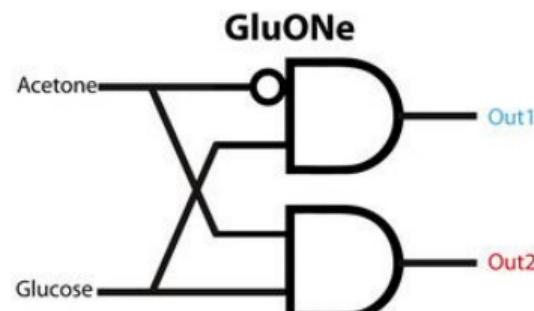




Hyperosmolar non-ketotic: output 1

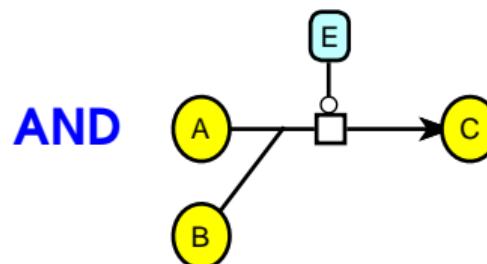
Diabetic Ketoacidosis: output 2

note: the two outputs are never true at the same time

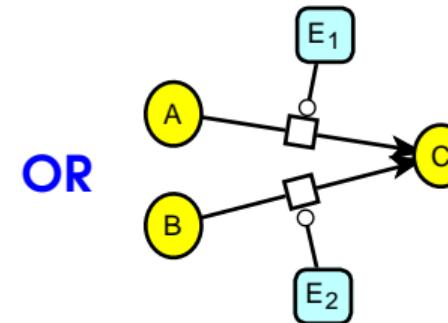


Boolean computing with enzymatic reactions

false: $[s] < \text{threshold}_l$, true: $[s] > \text{threshold}_h$



$$E: A + B \rightarrow C$$



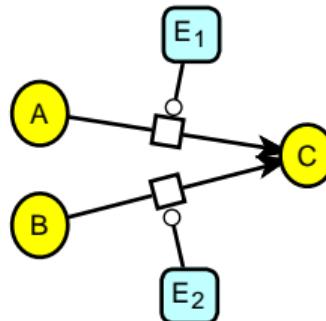
$$E_1: A \rightarrow C$$

$$E_2: B \rightarrow C$$

- ▶ simple and robust
- ▶ constraints and limitations
 - ▶ composability and reusability
 - ▶ enzyme kinetics

Threshold value does matter!

false: $[s] < Th$, true: $[s] \geq Th$

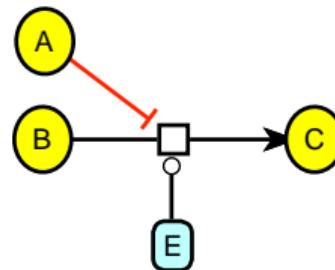


A	B	C	Th = 10	Th = 20
0	0	0	False	False
0	15	15	True	False
15	0	15	True	False
15	15	30	True	True

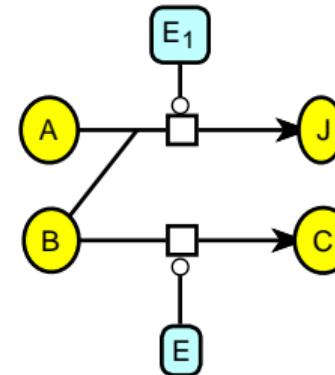
OR ???

Inverters

$$C = B \wedge \neg A$$



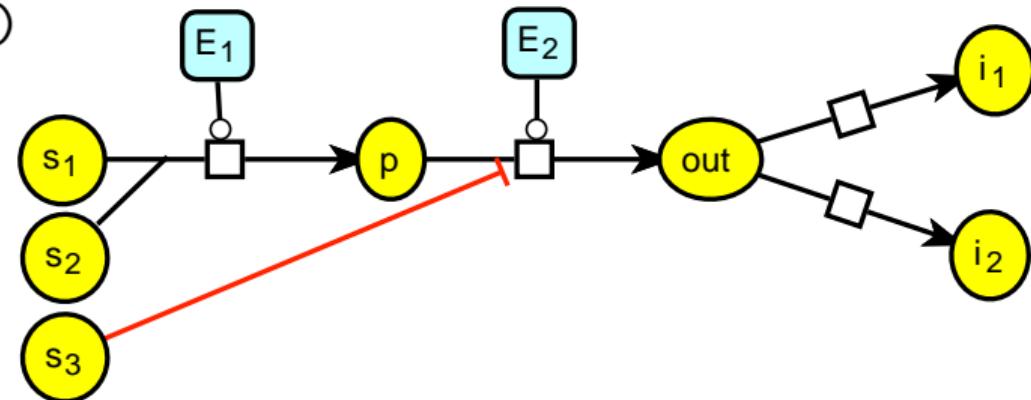
Inhibition



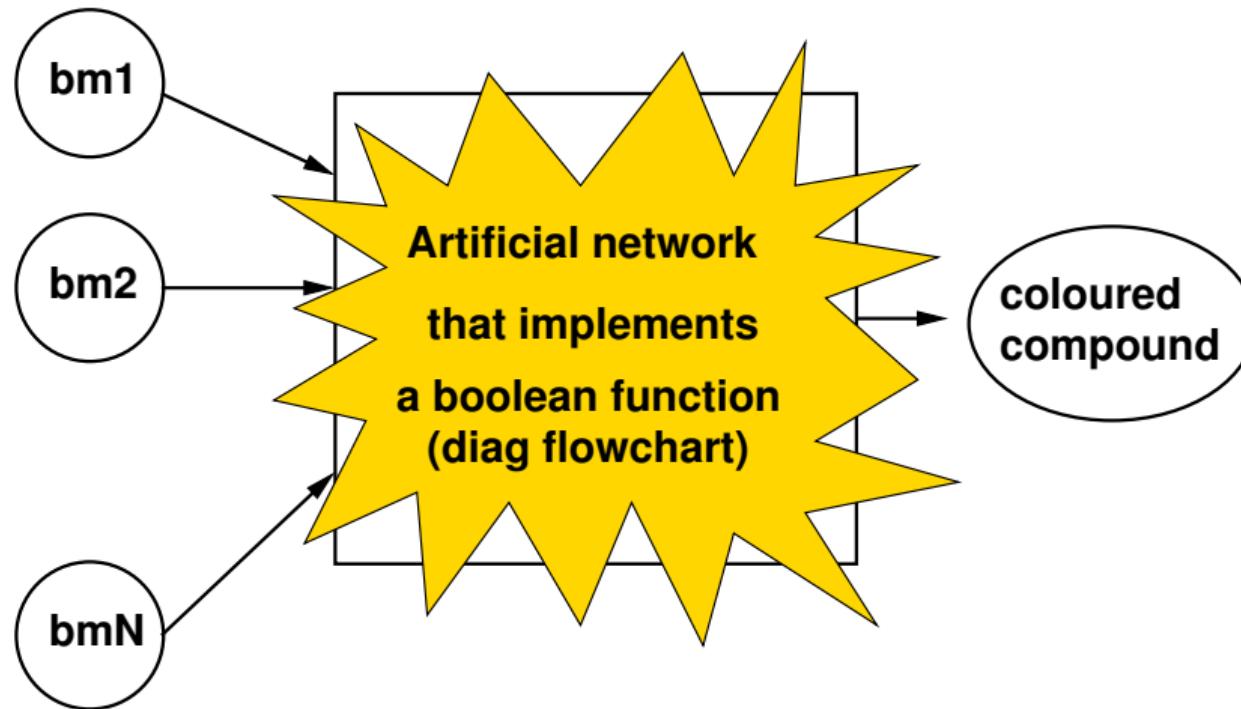
Concurrency

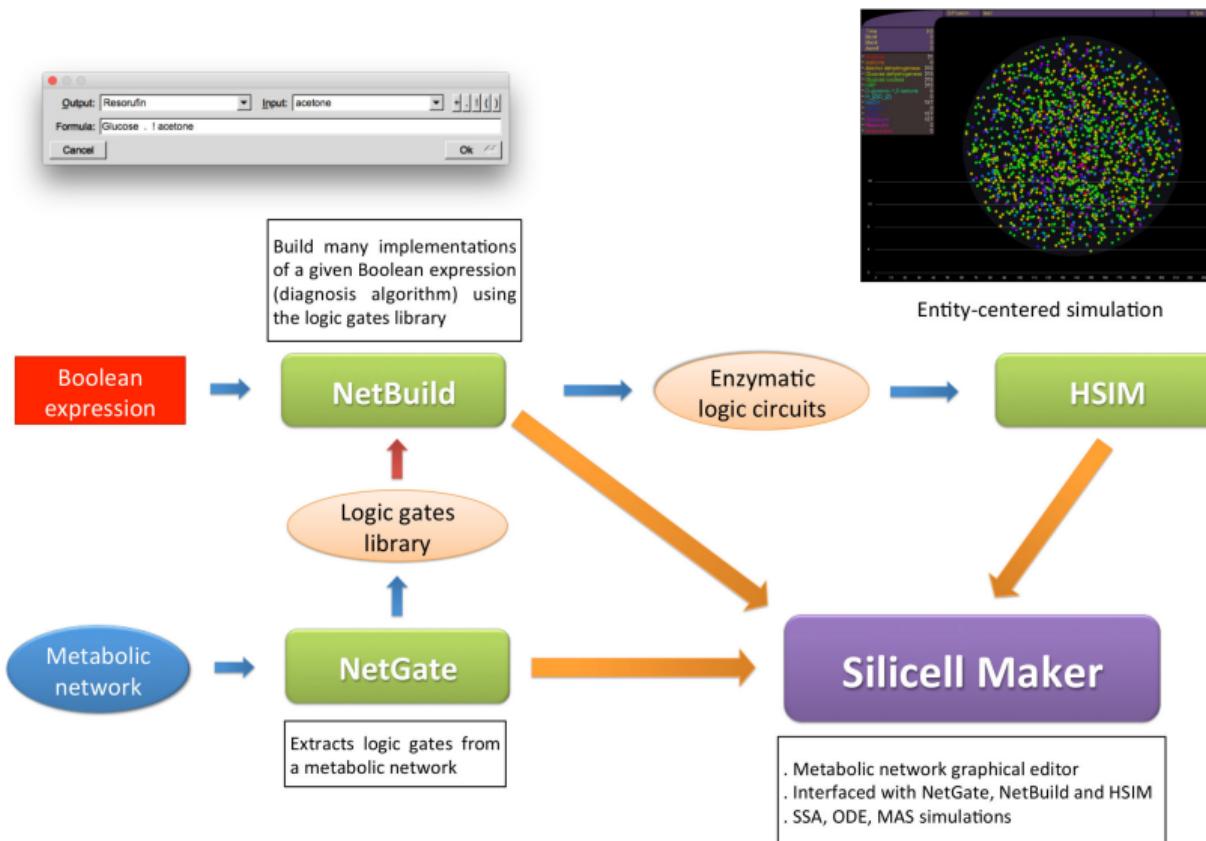
- ▶ highly dependent on the enzymes kinetics
- ▶ and on the thresholds values...

- ▶ connection wires: metabolites
 - ▶ need to find the **adequate** enzymes set...
 - ▶ everything is in the same compartment => beware the **short circuits!**
 - ▶ need a large **variety** of each type of logic gate
- ▶ **Synchronisation** constraints (mainly with inverters)
- ▶ Signal **fading** (fan out)

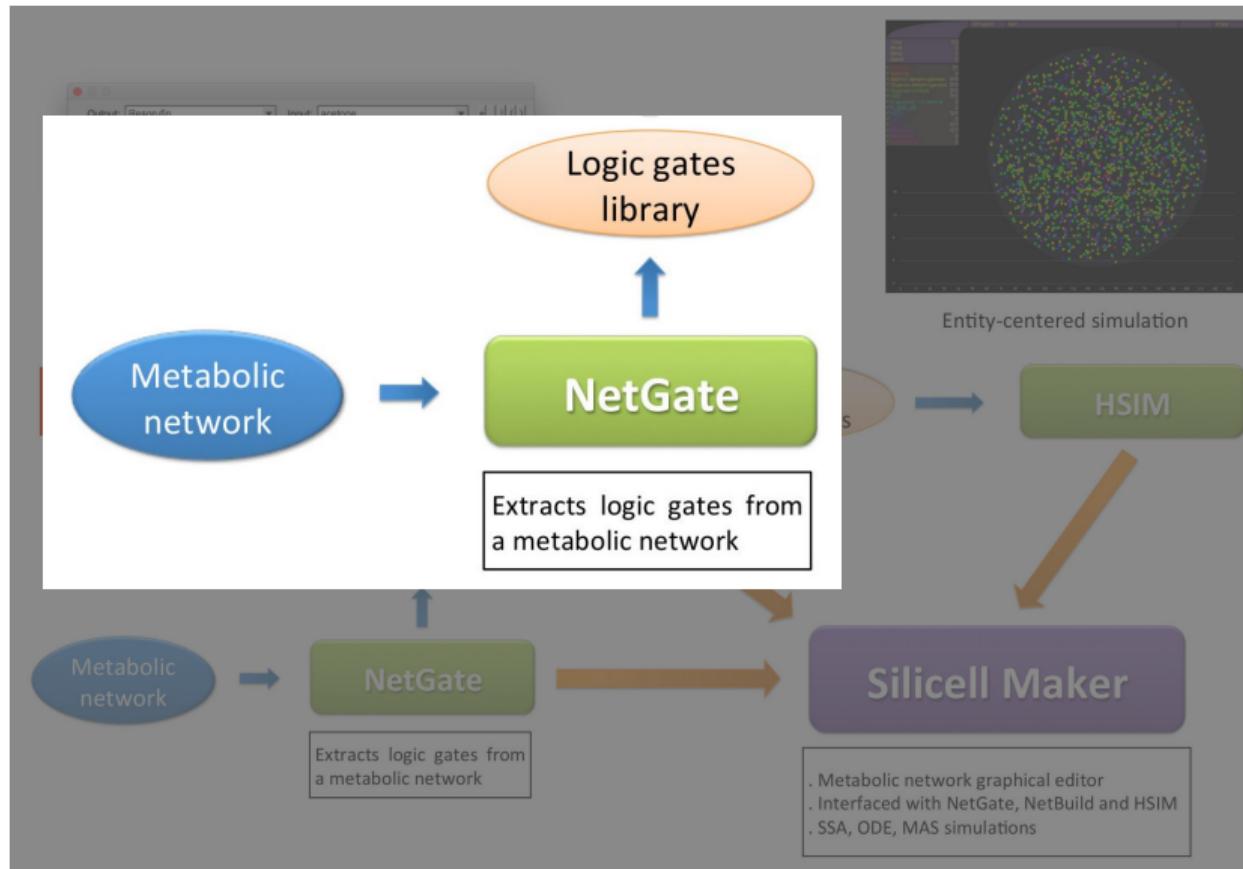


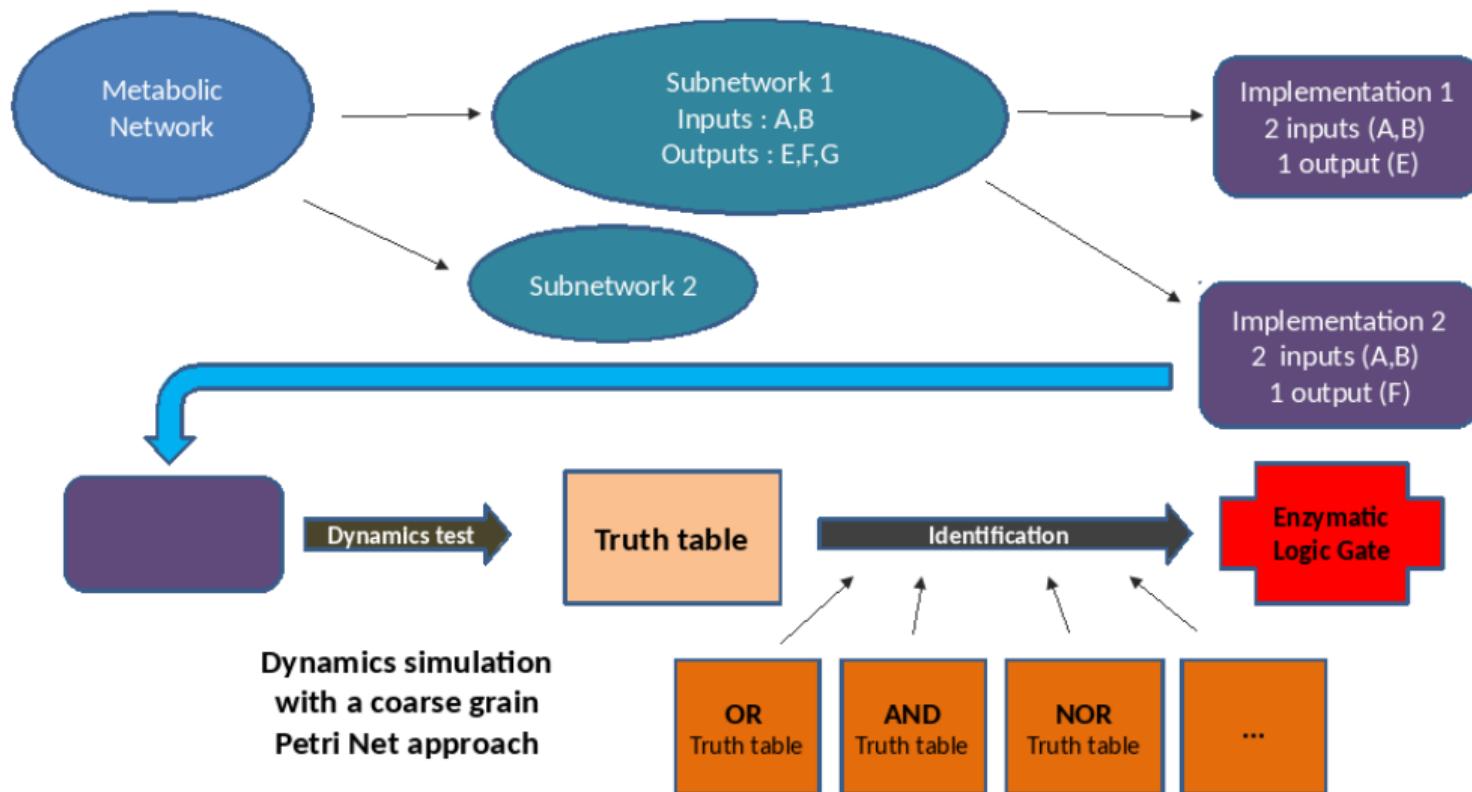
$$out = (s_1 \wedge s_2) \wedge \neg s_3$$

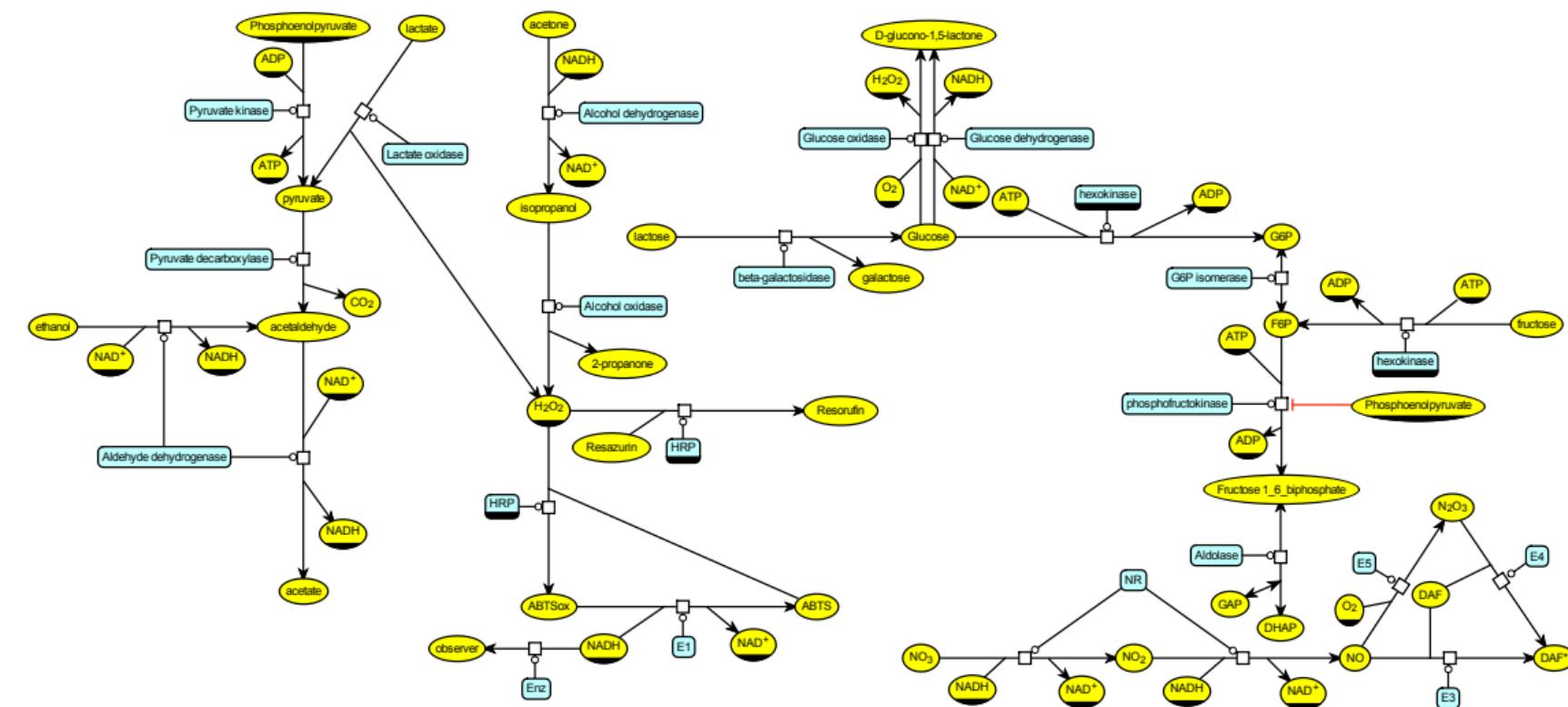




Step 1: build the library

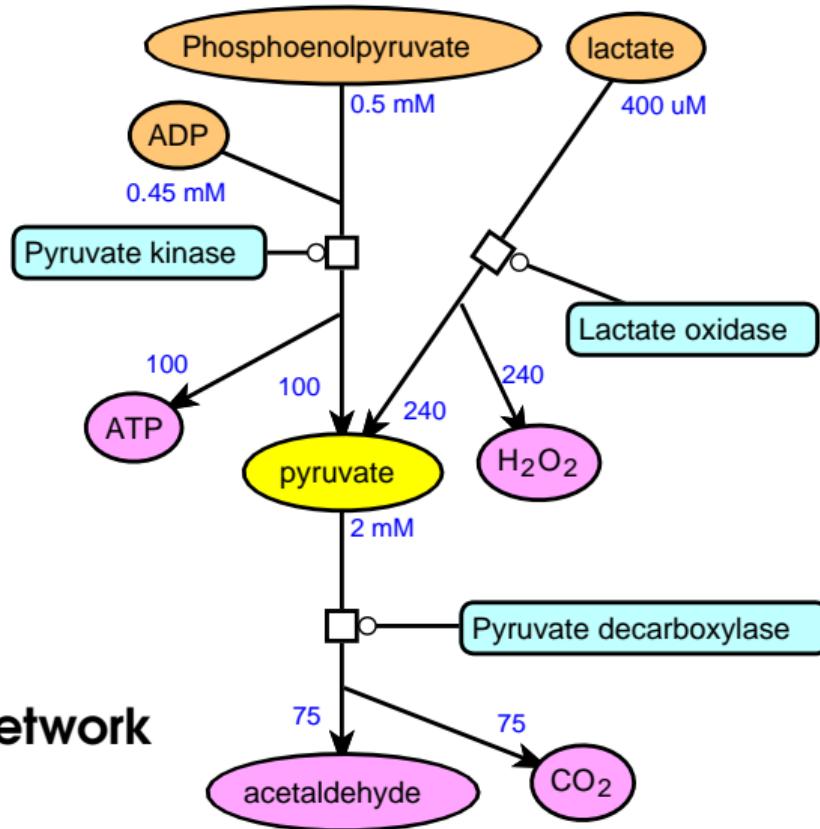




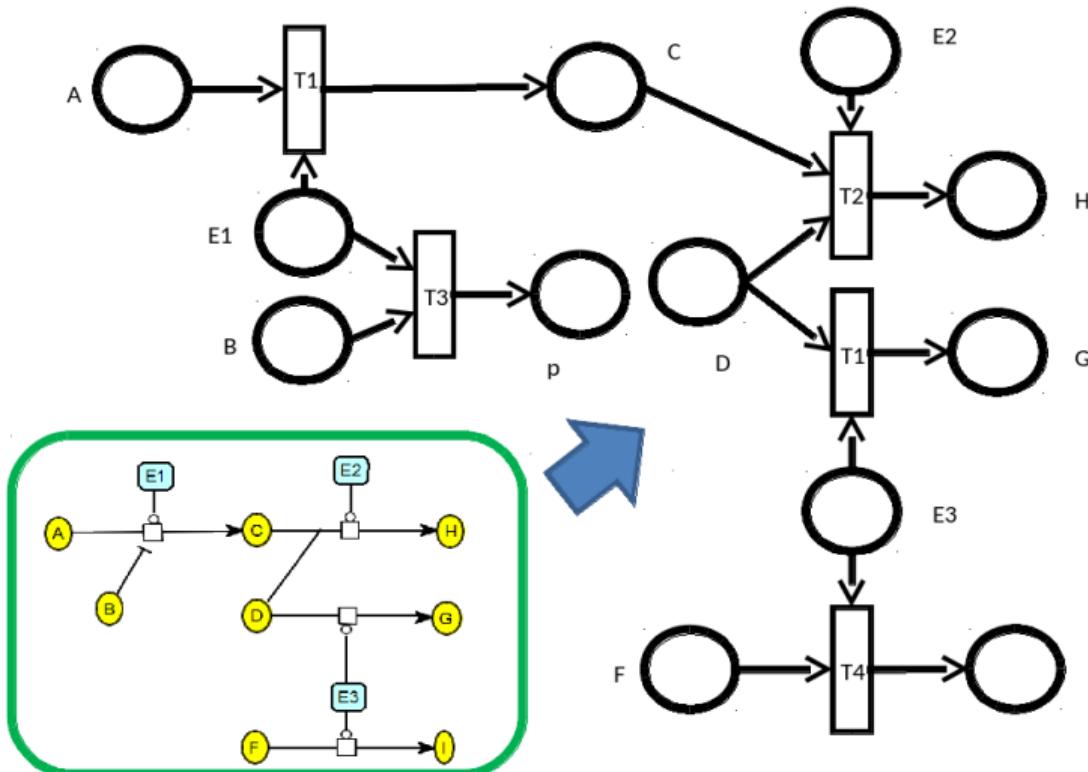


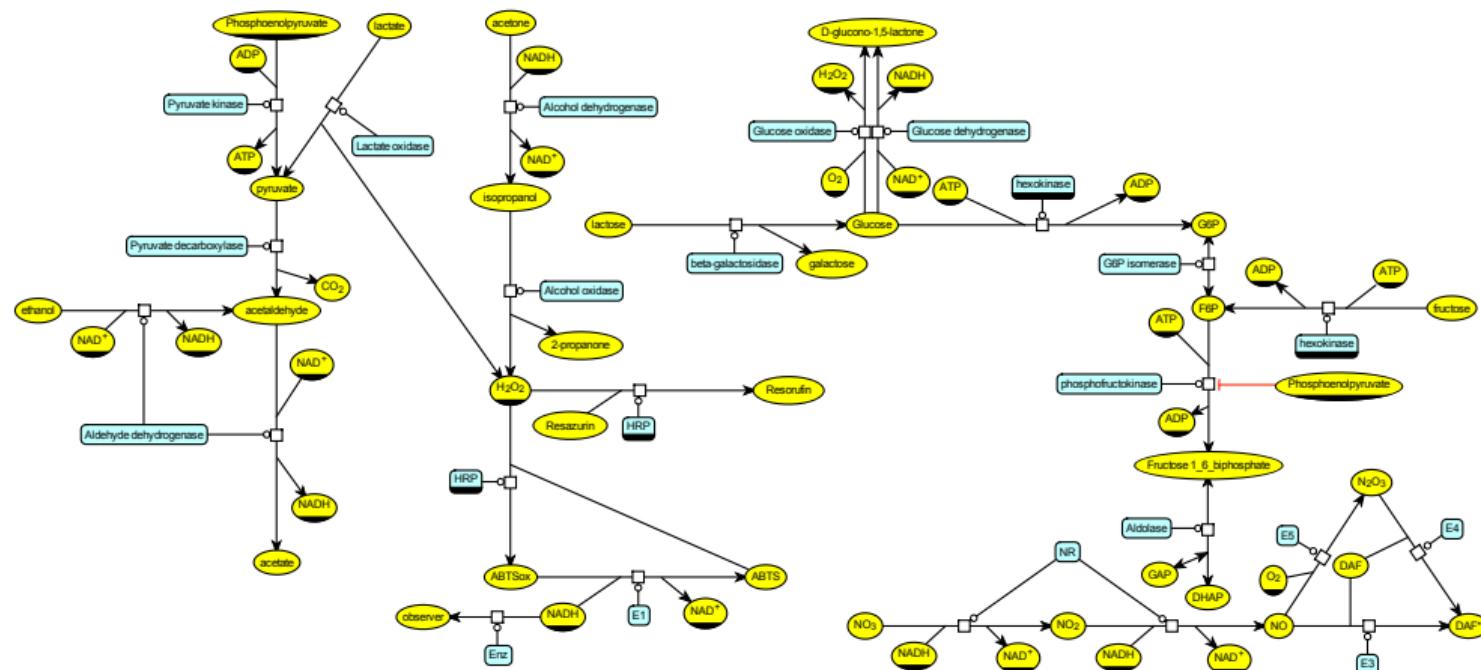
Inputs: orange
outputs: purple
in-out: yellow

3-reactions subnetwork



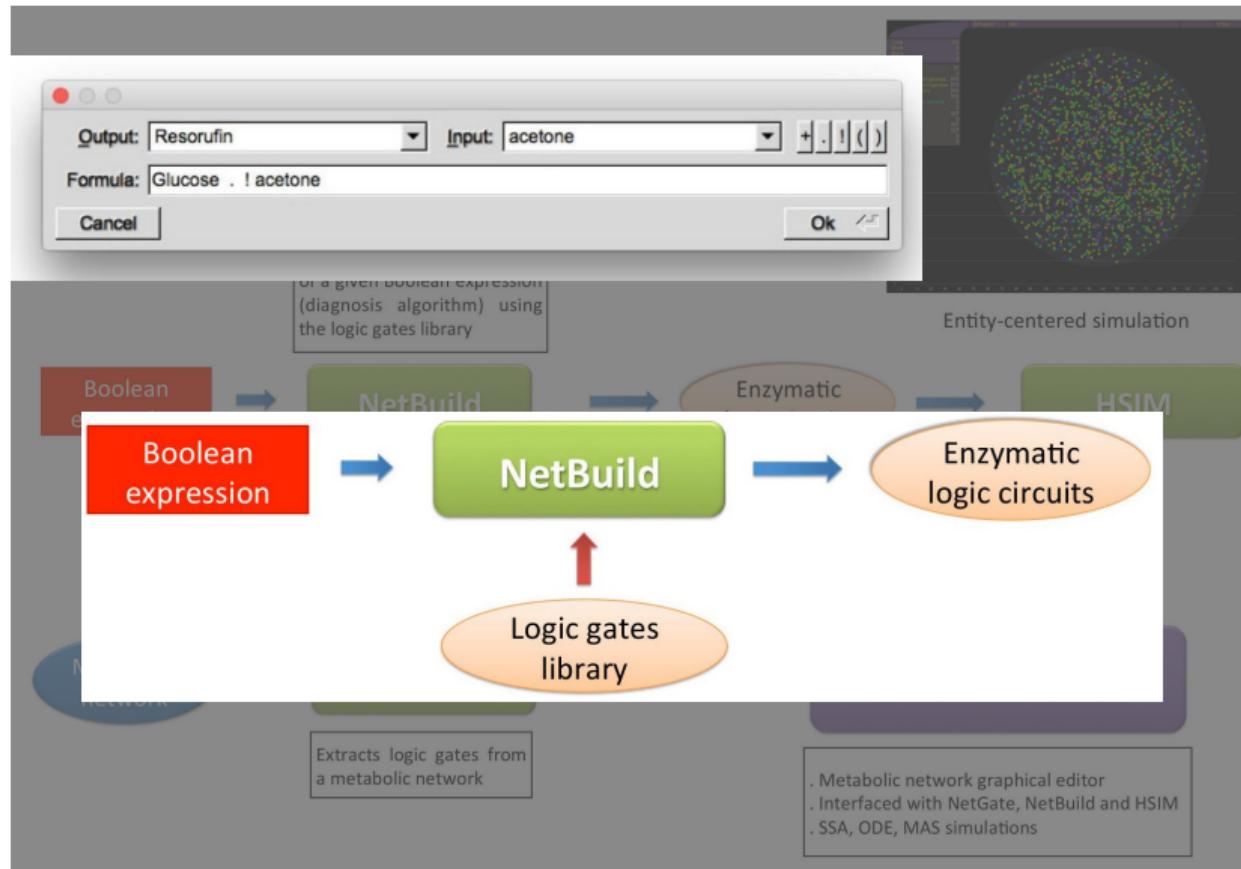
Coarse grain simulation to infer the dynamics

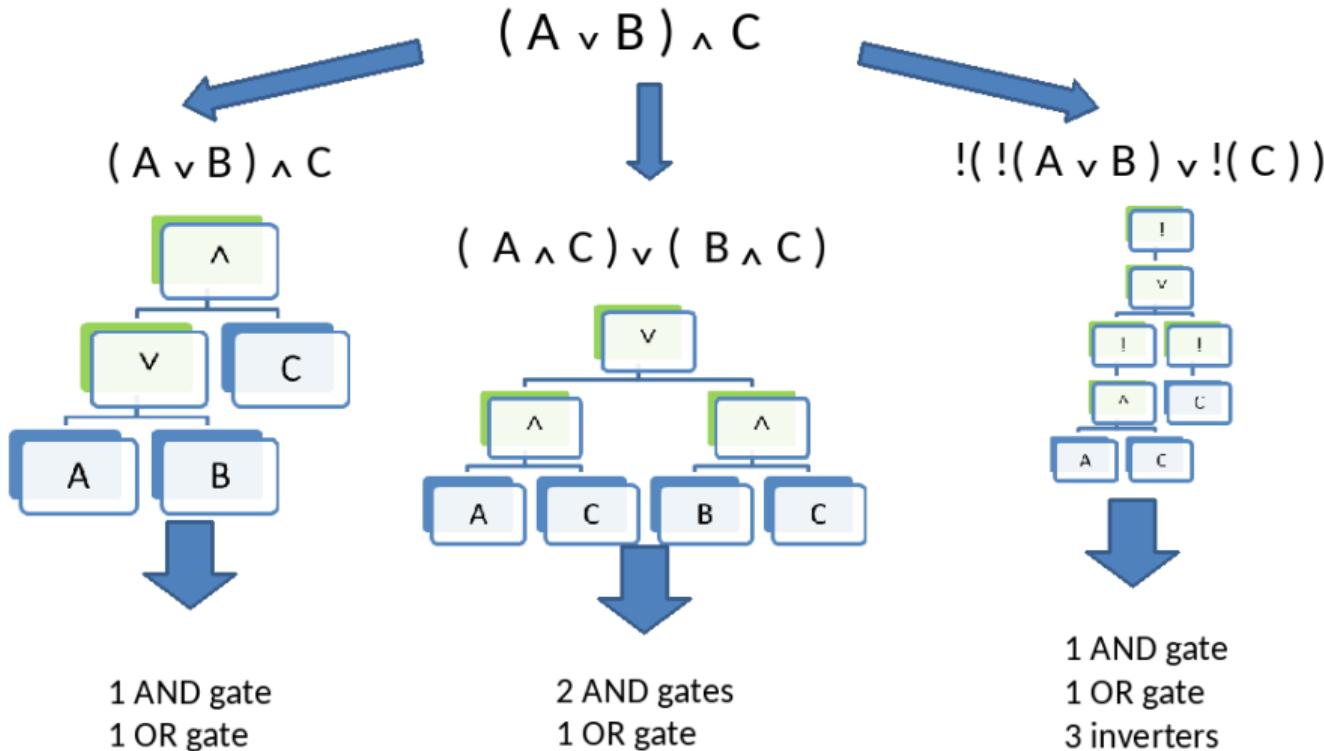


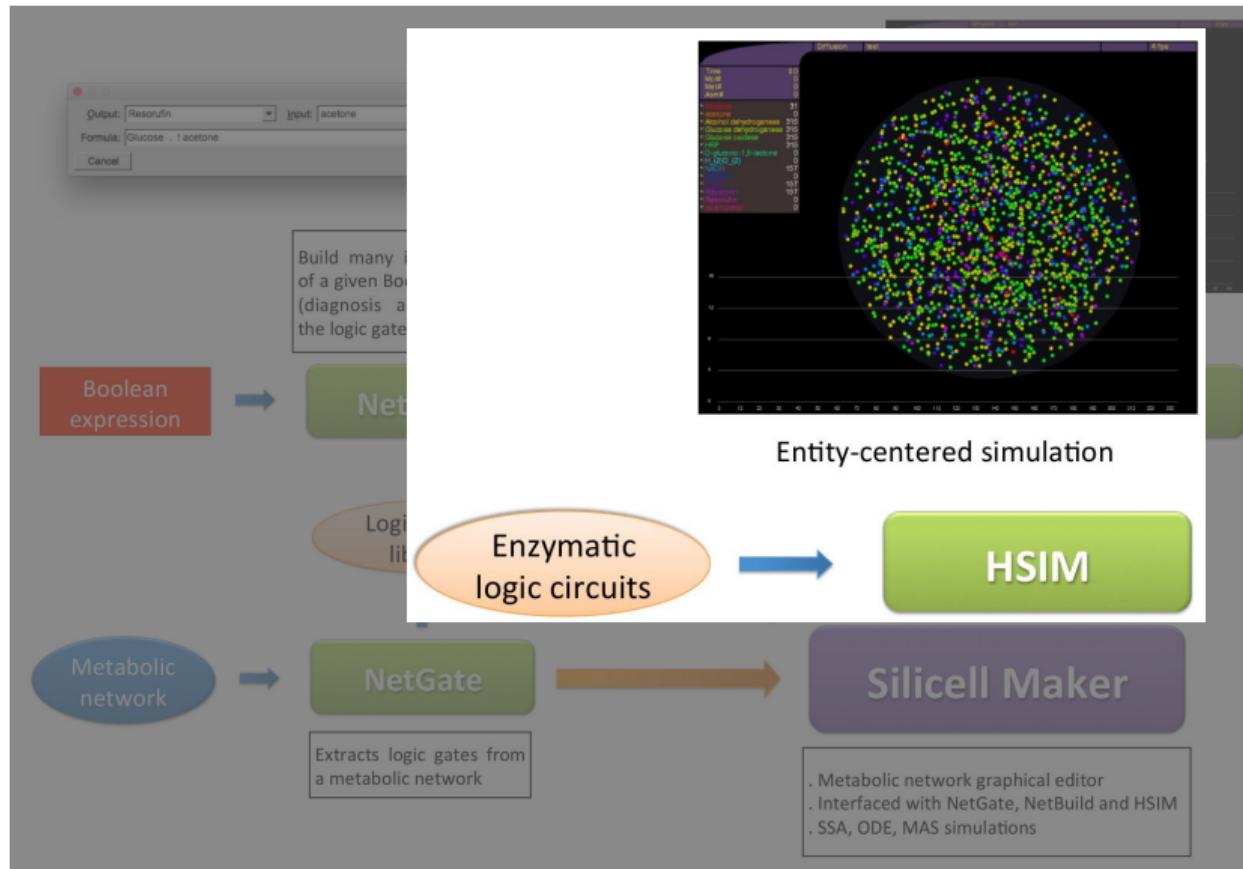


206 AND, 98 OR, 7 NAND, 16 NOT-OR,
29 Inverters, 194 YES, 203 NOT-AND

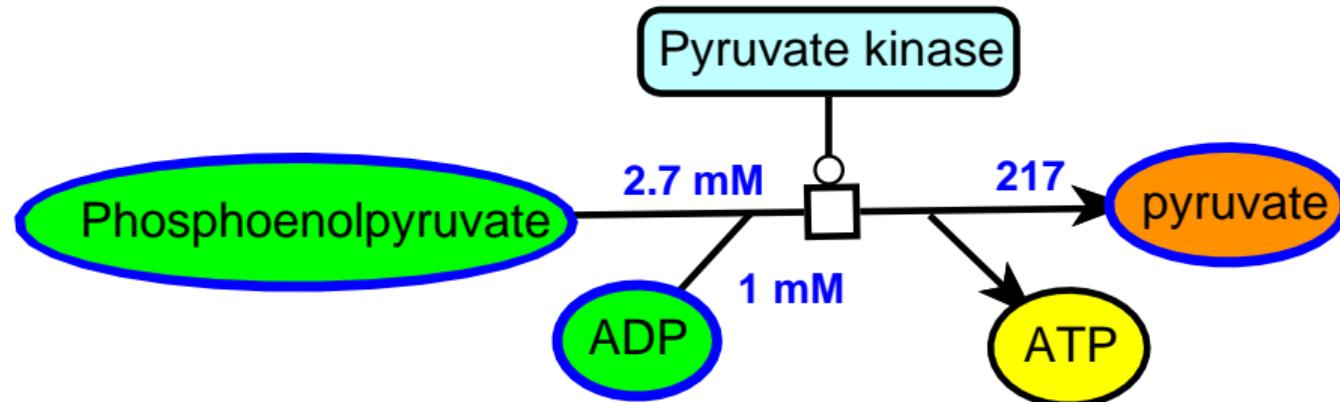
Reactions: 20
Gates: 753



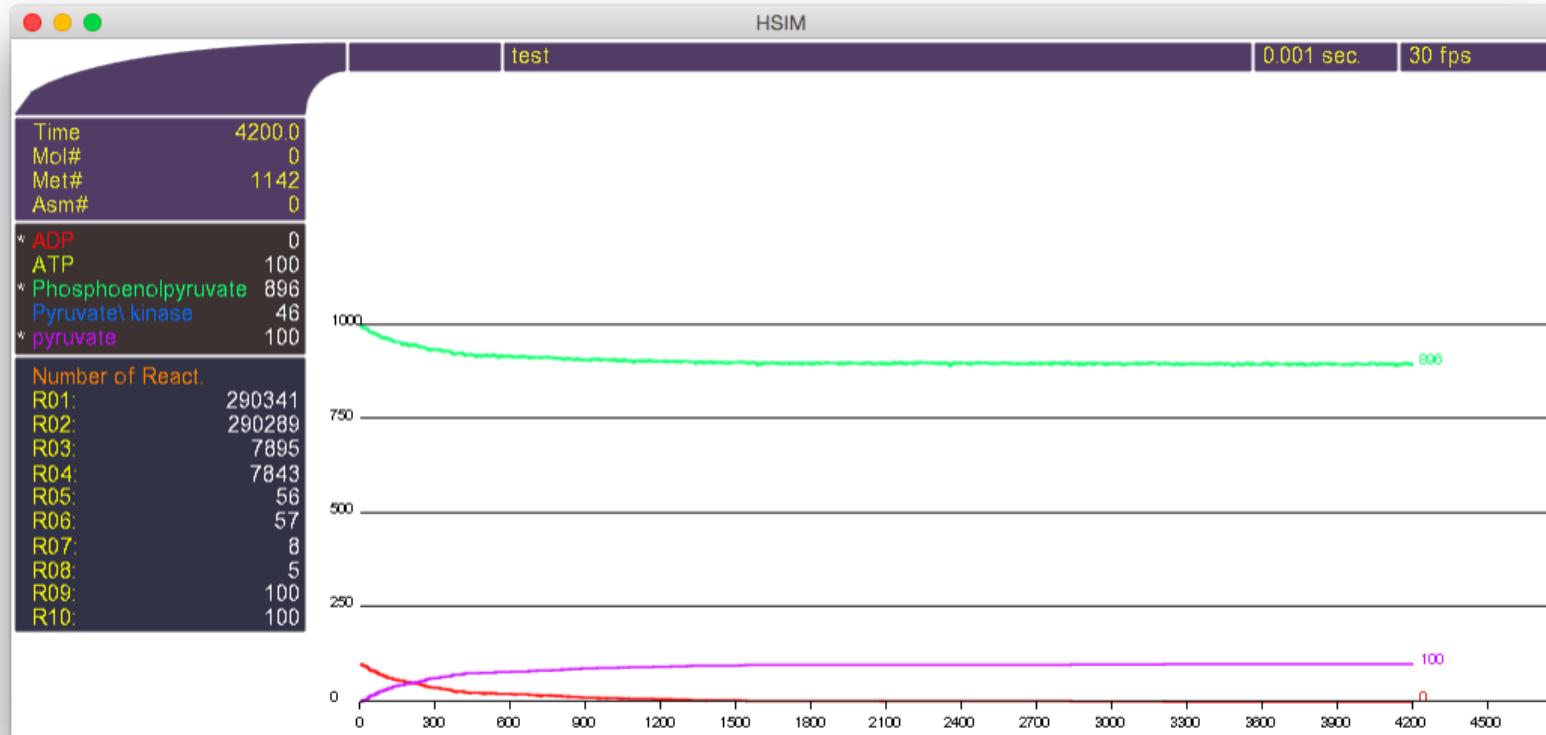


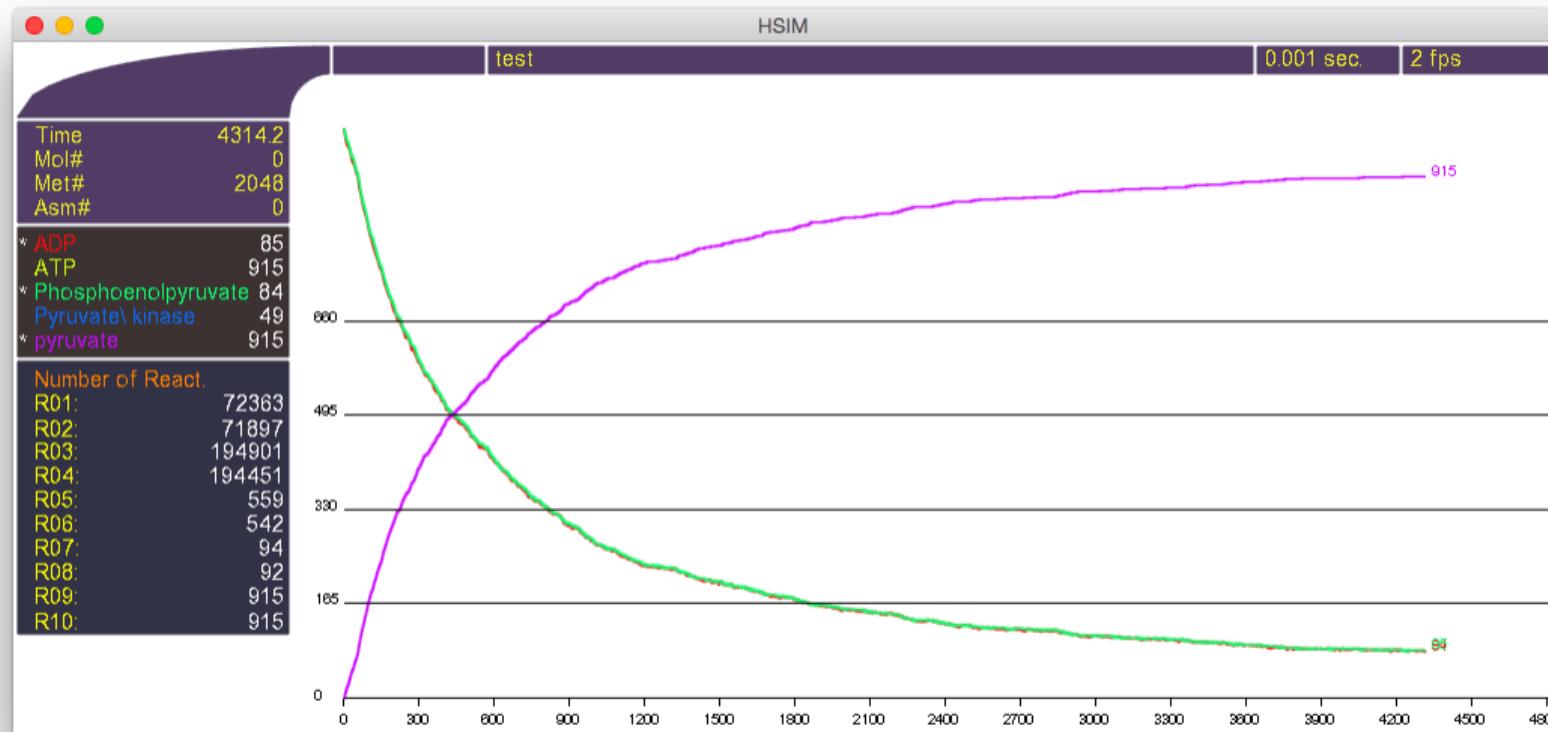


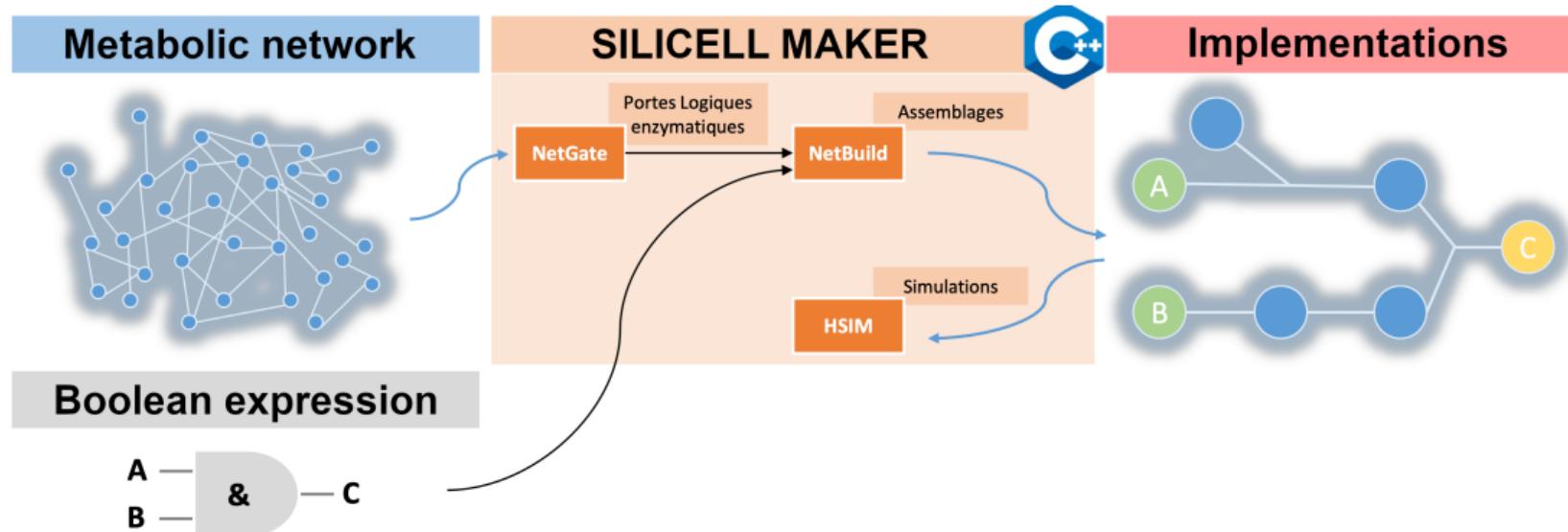
Boolean formula: **pyruvate = PEP \wedge ADP**

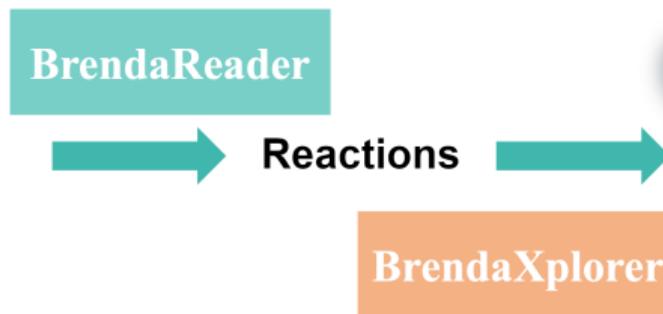


PK	+	PEP	\rightarrow	Ea1	[0.0221019]*;
Ea1			\rightarrow	PK + PEP	[0.00217]*;
<hr/>					
PK	+	ADP	\rightarrow	Eb1	[0.059675]*;
Eb1			\rightarrow	PK + ADP	[0.00217]*;
<hr/>					
Ea1	+	ADP	\rightarrow	CF1	[0.059675]*;
Eb1	+	PEP	\rightarrow	CF1	[0.0221019]*;
<hr/>					
CF1			\rightarrow	Ea1 + ADP	[0.00217]*;
CF1			\rightarrow	Eb1 + PEP	[0.00217]*;
CF1			\rightarrow	CFb1 + pyruvate	[0.0217]*;
<hr/>					
CFb1			\rightarrow	PK + ATP	[1];

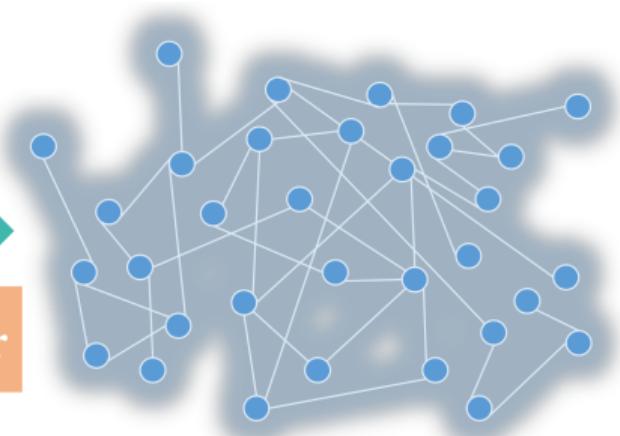






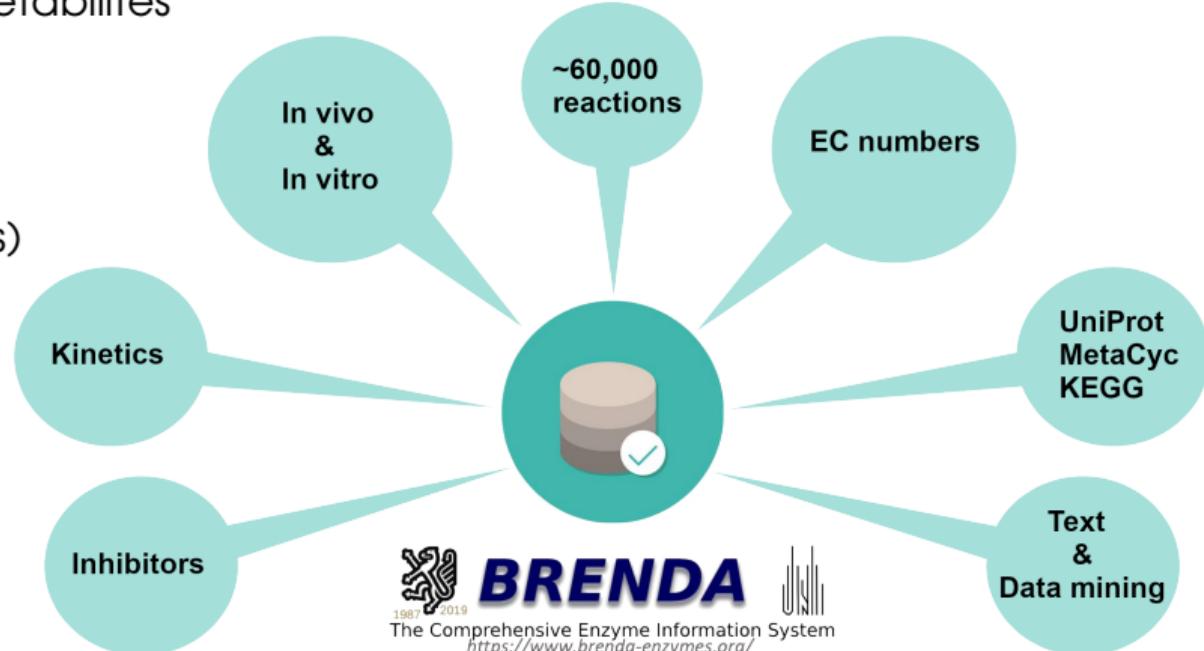


Reactions data base

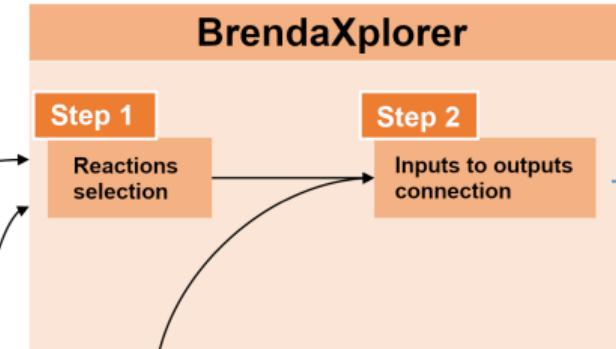


Netgate input network

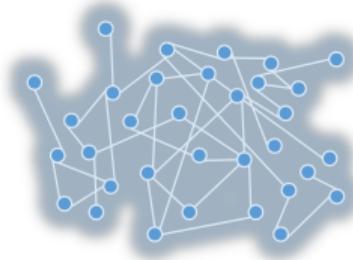
- ▶ ≈ 60,000 input metabolites
- ▶ ≈ 50,000 output metabolites
- ▶ ≈ 6500 enzymes
- ▶ 304848 reactions
- ▶ ≈ 5 organisms
(≈ 60,000 reactions)



Reactions list (BRENDA)



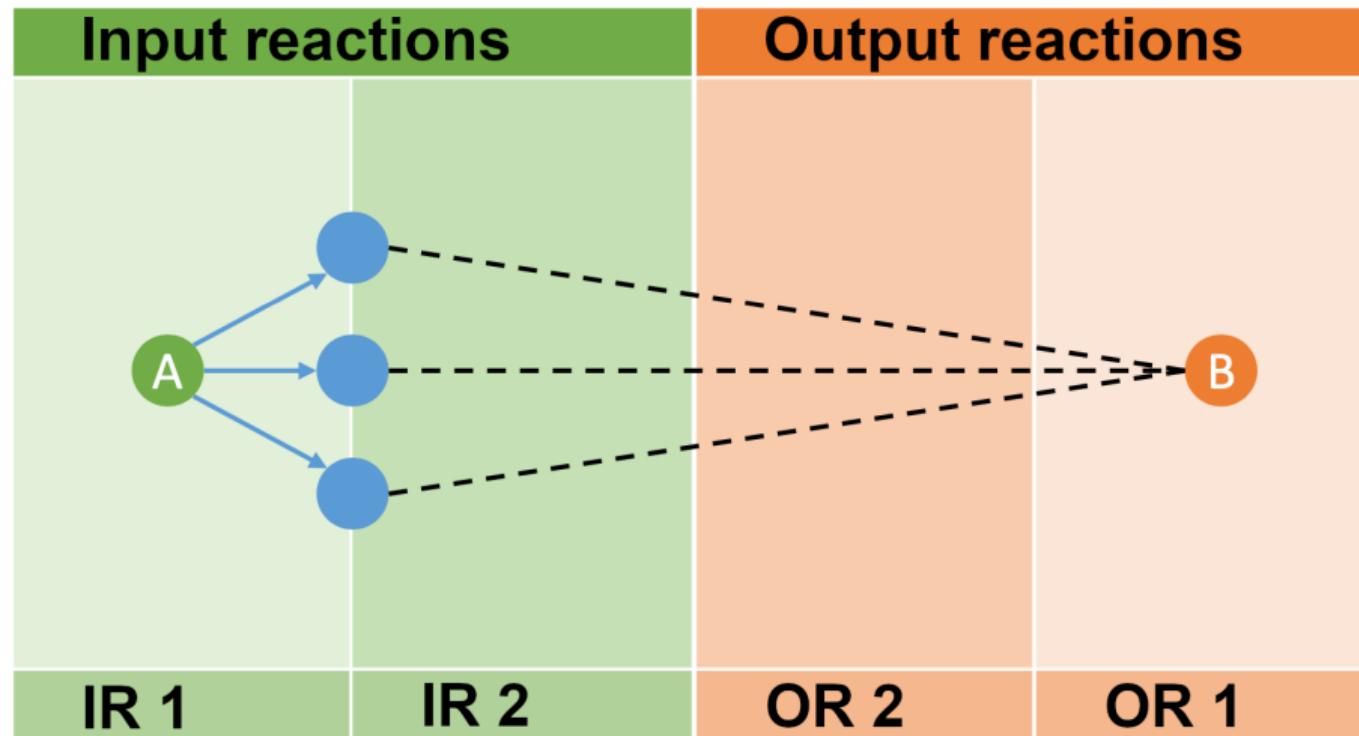
Metabolic network

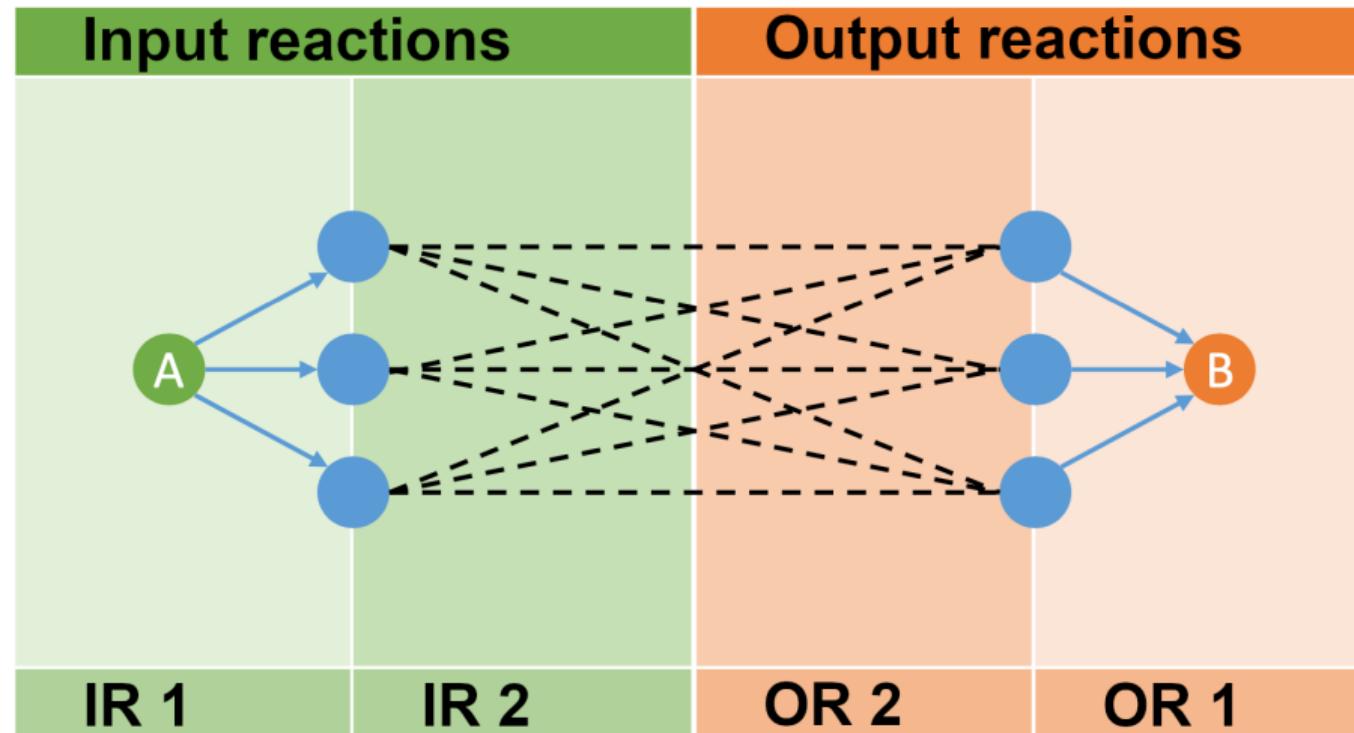


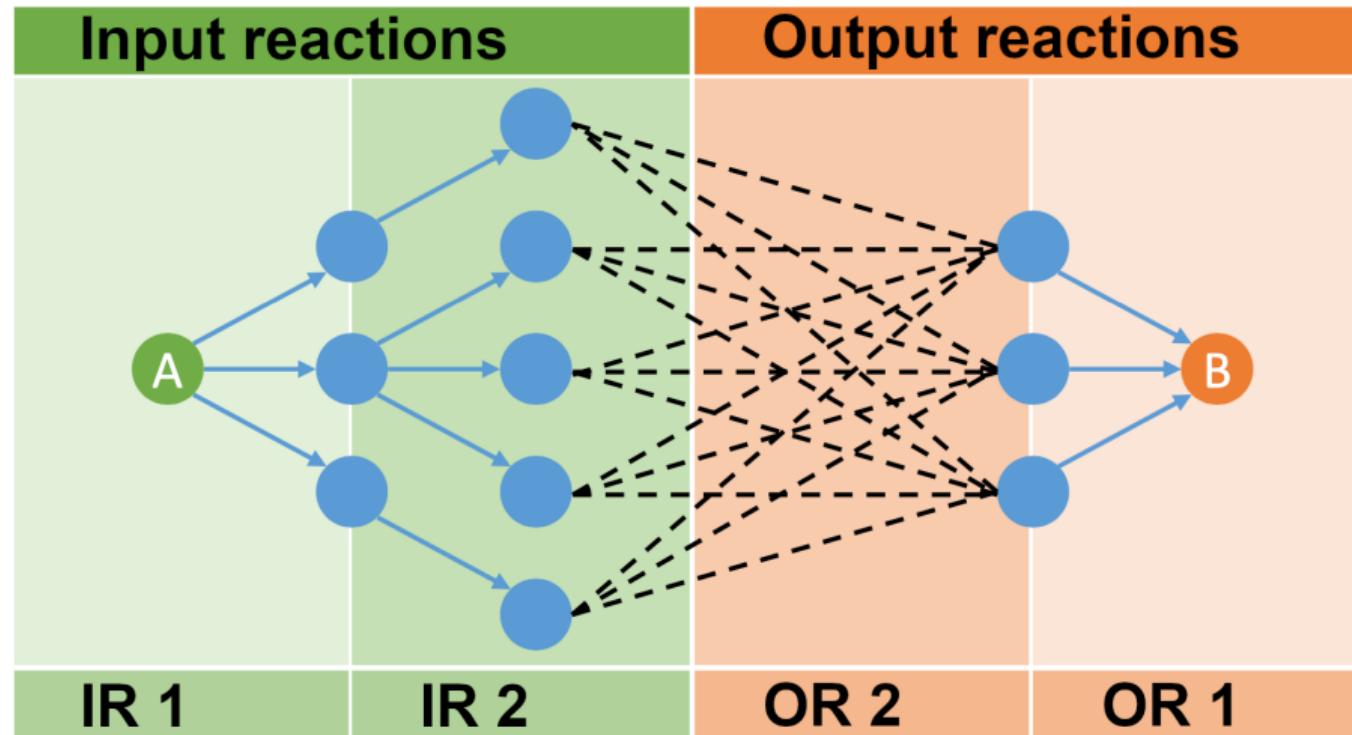
Parameters

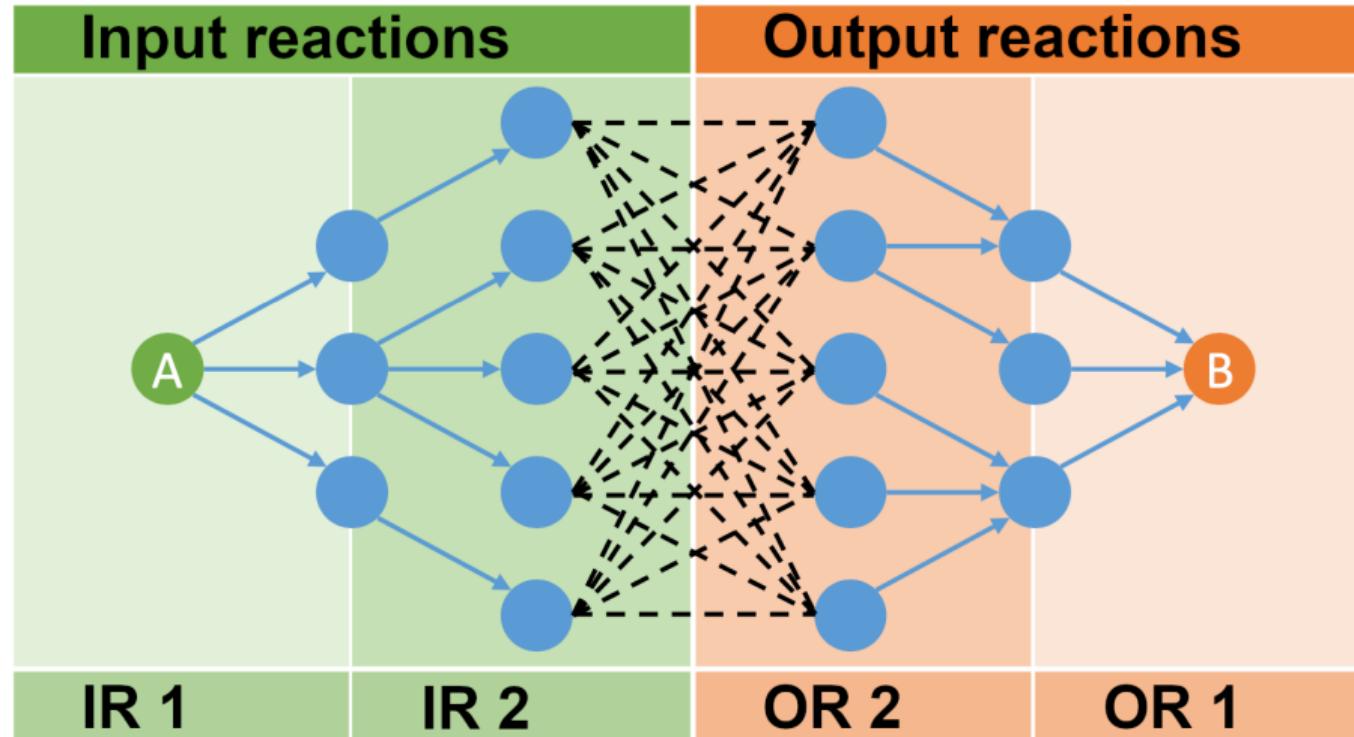
Inputs
Outputs

Max path length



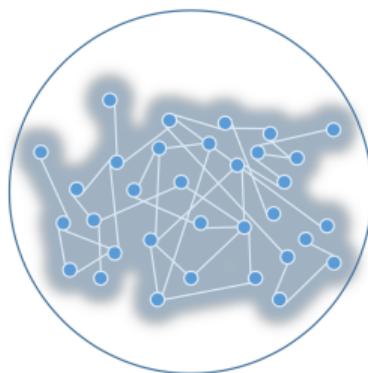






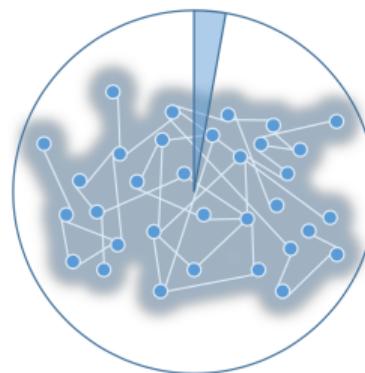
- ▶ 500 input-output couples randomly chosen
- ▶ success: inputs connected to outputs by at least one path

Path length 1



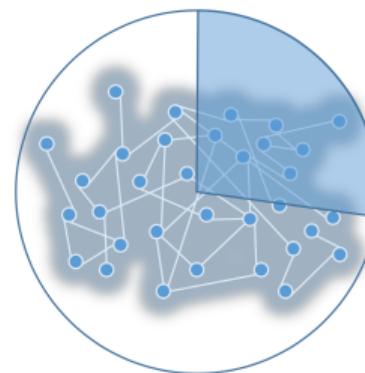
0%

Path length 2



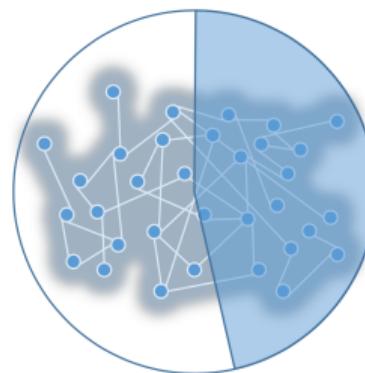
2.6%

Path length 3



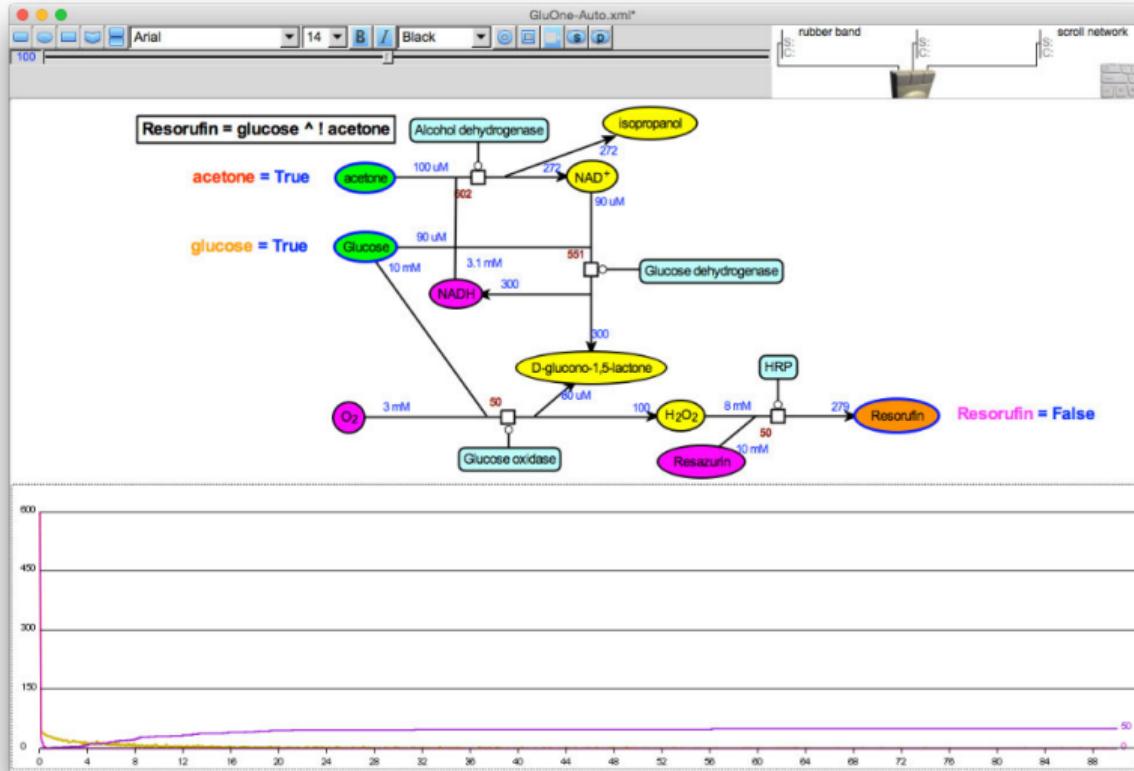
27.6%

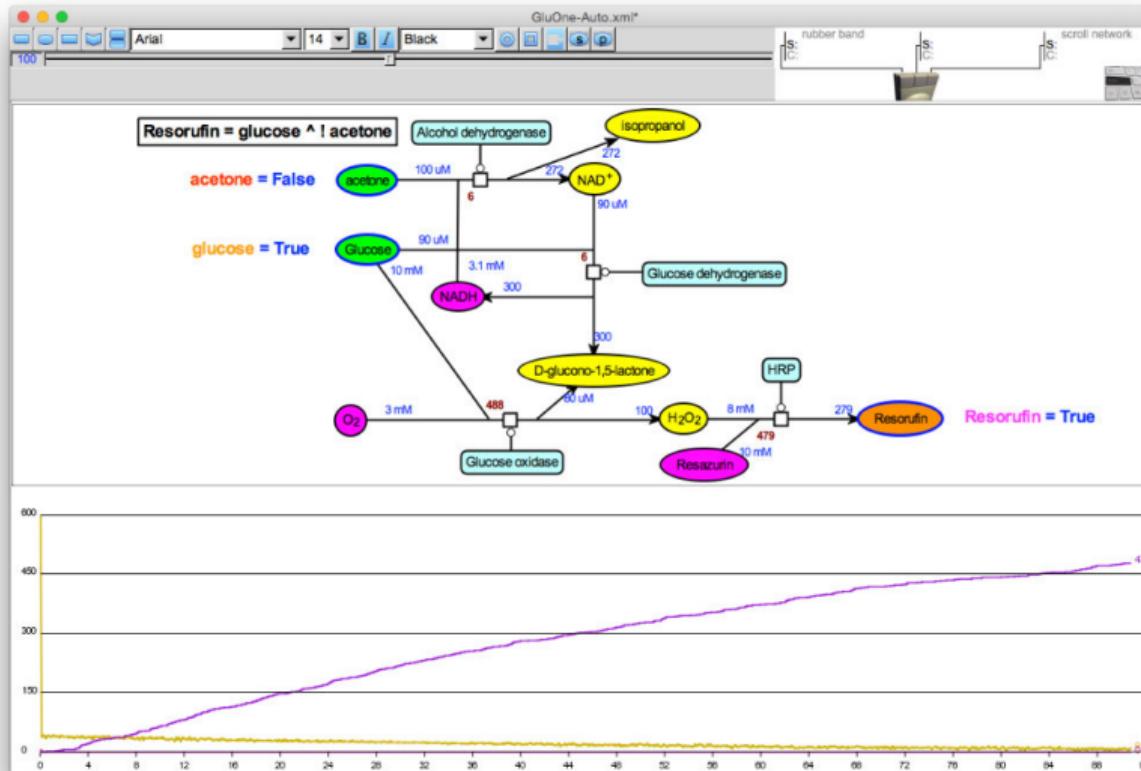
Path length 4



47%

Merci de votre attention





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