

A logical approach to identify Boolean networks modeling cell differentiation

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Inference of Boolean networks compatible with biological data

Qualitative method

Boolean network (BN) with n genes :

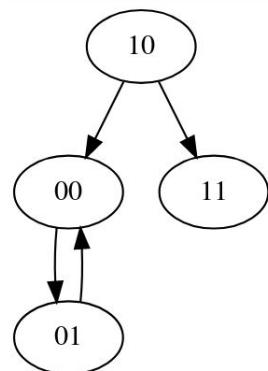
$F = (f_1, \dots, f_n)$, $\forall i \in \{1, \dots, n\}$, $f_i : \mathbb{B}^n \rightarrow \mathbb{B}$ ($\mathbb{B} = \{0, 1\}$),
with f_i the target value of the i^{th} gene

Boolean network dynamic : transition graph

Example :

$$f_A = A \wedge B$$

$$f_B = A \vee \neg B$$



Nodes : **states** (active/inactive status of all the genes)

Edges : **asynchronous updates** (one gene is updated)

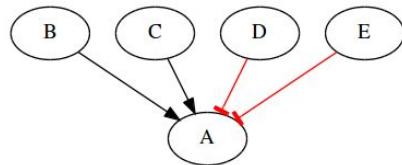
What are the genes interactions that allow the differentiation?

A priori knowledge

Complex biological interactions :

- Non contextualized network
- Genes cooperation needed for the influence?

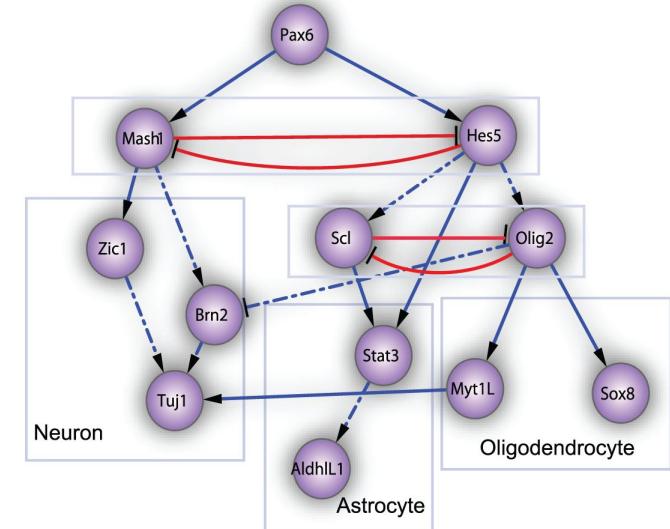
Example for A activation : $B \vee \neg D \vee (C \wedge \neg E)$



But 168 possibilities
for this node !

Which are the relevant relationships involved in a biological process?

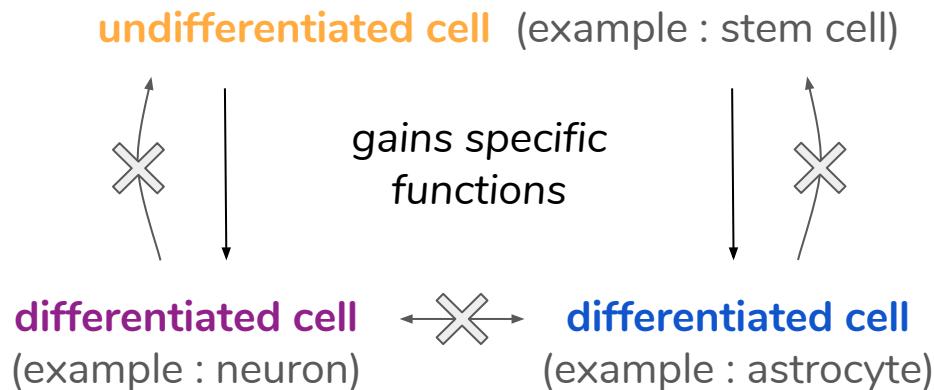
Influence graph from databases and expert knowledge :
Prior Knowledge Network (PKN)



[1] Qiu X, Ding S, Shi T. From Understanding the Development Landscape of the Canonical Fate-Switch Pair to Constructing a Dynamic Landscape for Two-Step Neural Differentiation. PLOS ONE 7(12):e49271, 2012

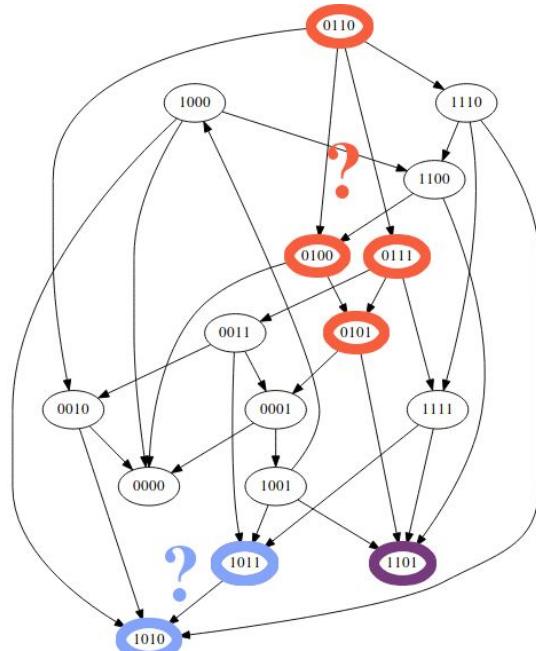
Inference of Boolean networks compatible with differentiation data

Differentiation process



Inference of Boolean networks compatible with differentiation data

Differentiation process



Transition graph of a 4 genes BN

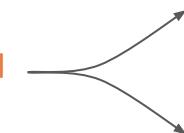
Experimental measurements :

- Time series through a differentiation process
- Measurements for only a few genes

Example :

T0 : undifferentiated cell

- gene1 inactive
- gene2 active



T1>T0 : differentiated cell type 1

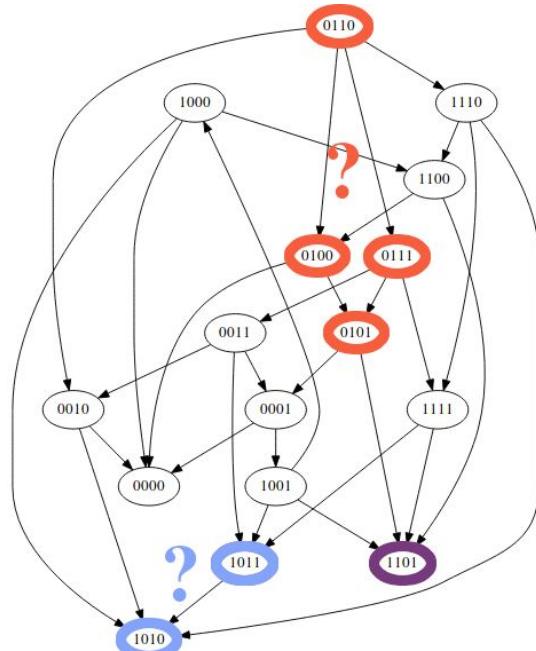
- gene1 active
- gene2 active

T1>T0 : differentiated cell type 2

- gene1 active
- gene2 inactive

Inference of Boolean networks compatible with differentiation data

Differentiation process



Transition graph of a 4 genes BN

Differentiation data interpretation (hypotheses) :

- **Reachability** : state T_{i+1} reachable from T_i
- **Specialization** : differently differentiated states have no common descendant
- **Stability** : stable differentiated states are in attractors
- **Representativeness** : proportion of states compatible with the observations

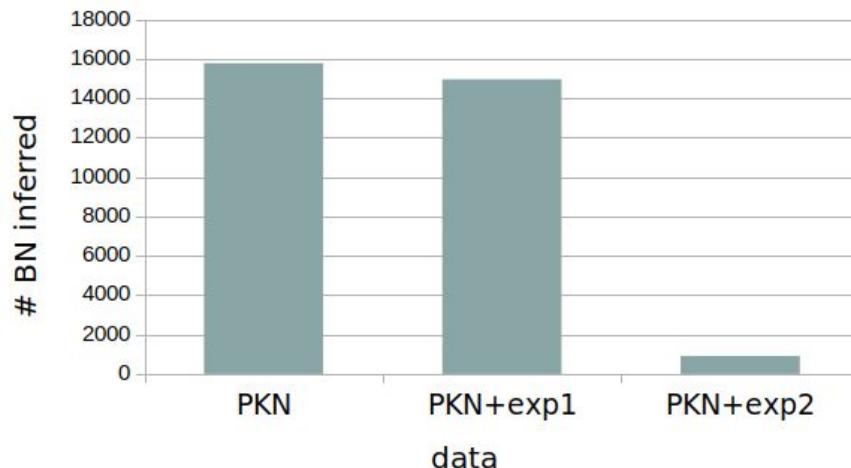
How infer Boolean network that respect these properties ?

Inference of Boolean networks compatible with differentiation data

BN exhaustive inference

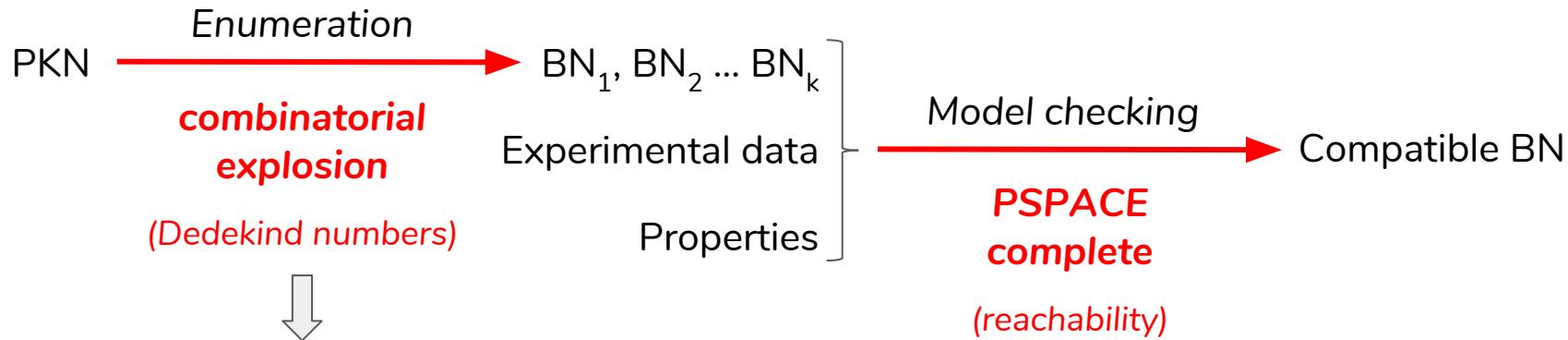
Exhaustiveness importance :

- **study the inferred BN variability**
(graph influence topology & nodes importance)
- **quantify the data informativeness :**
(data relevance to infer BN)



Inference of Boolean networks compatible with differentiation data

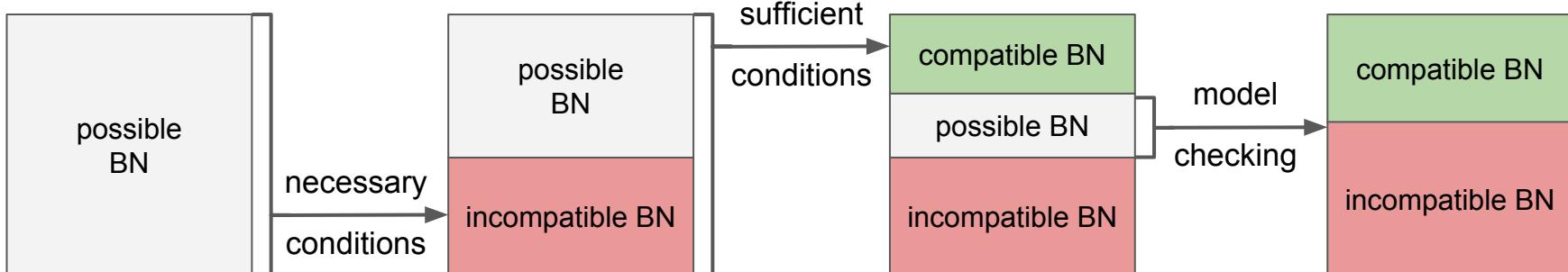
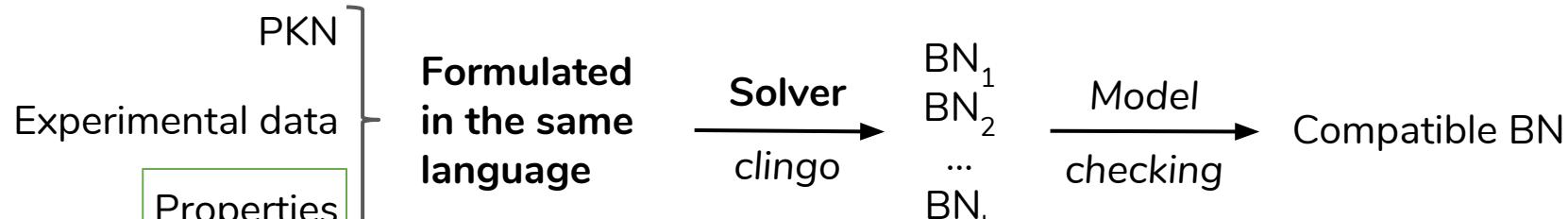
BN exhaustive inference



indegree	# monotonous Boolean functions per node
0	2
2	6
4	168
6	7 828 354
8	56 130 437 228 687 557 907 788

Inference of Boolean networks compatible with differentiation data

BN exhaustive inference



Inference of Boolean networks compatible with differentiation data

BN exhaustive inference

2) Logical approach : Answer-Set Programming (ASP)

Necessary condition on **reachability** (Casspots^[2])

Caspots extension :

→ necessary and sufficient condition on a stability hypothesis : **fixed point**

```
eval(E,clause,N,C,-1) :- clause(N,C,L,-V) ; fp(E,L,V) ; not clamped(E,N,_).  
eval(E,clause,N,C,1) :- fp(E,L,V) : clause(N,C,L,V) ; clause(N,C,_,_) ; fp(E,_,_) ; not clamped(E,N,_).  
  
eval(E,N,V) :- clamped(E,N,V).  
eval(E,N,V) :- constant(N) ; fp(E,N,V) ; not clamped(E,N,_).  
eval(E,N,1) :- eval(E,clause,N,C,1) ; clause(N,C,_,_) ; not clamped(E,N,_).  
eval(E,N,-1) :- eval(E,clause,N,C,-1) : clause(N,C,_,_) ; fp(E,_,_) ; node(N) ; not constant(N) ; not clamped(E,N,_).  
  
:- node(N) ; fp(E,N,V) ; eval(E,N,-V).  
:- constant(N) ; fp(E1,N,V) ; fp(E2,N,-V) ; not clamped(E1,N,V) ; not clamped(E2,N,-V).  
  
fp(E,N,V) :- guessed(E,T,N,V) ; is_fixpoint(E,T).
```

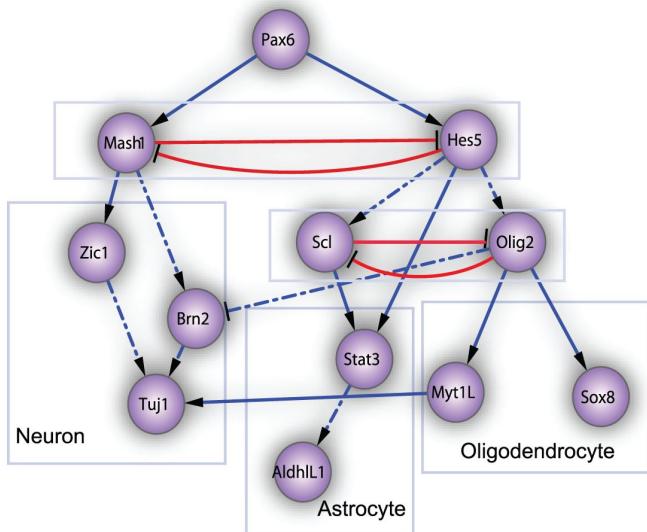
ASP file for fixed point

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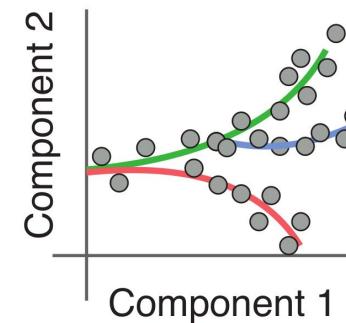
Small application on :

- PKN : CNS development^[1]



2) Logical approach : Answer-Set Programming (ASP)

- Data : 4 possible fates (3 specializations + 1 steady state)
→ 4 fixed points

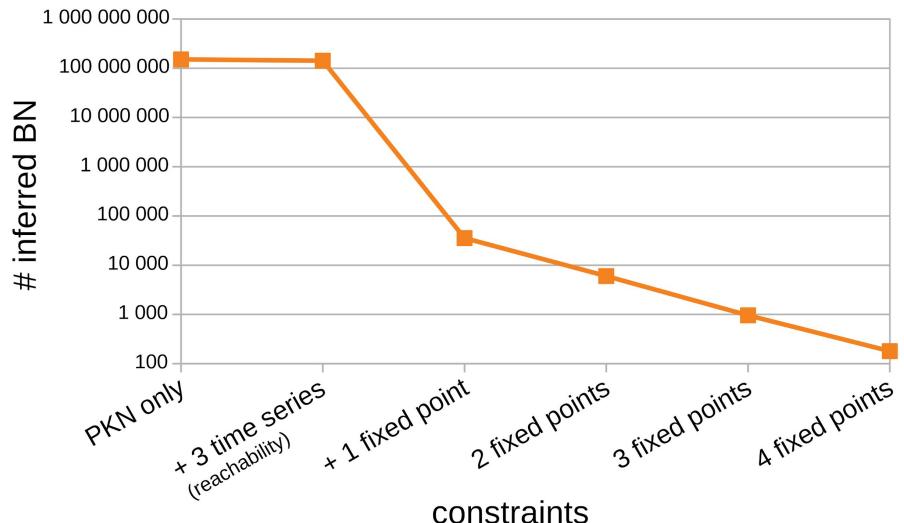


Inference of Boolean networks compatible with differentiation data

BN exhaustive inference

2) Logical approach :
Answer-Set Programming (ASP)

Constraints impact : reachability & fixed point



Conclusion & Perspectives

Exhaustive model inference for differentiation data

- thanks to **constraints** fitting the experimental conditions (fixed points already implemented)
- allows **data informativeness quantification**

Coming work :

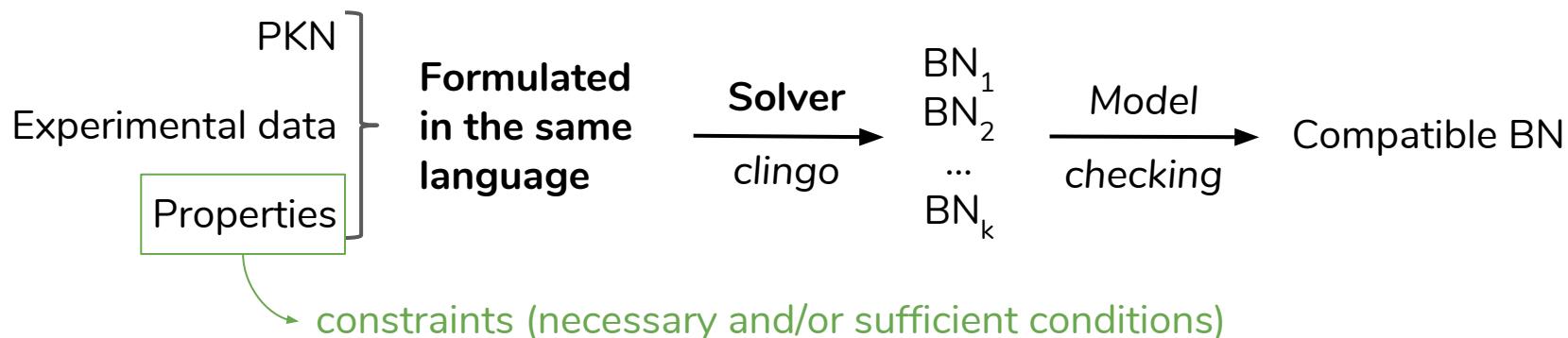
- Implementation of **negative reachability conditions**
- Generalization of the method to **mutation data** (perturbed differentiation data) and **quantitative** mutation data (fates proportion w.r.t. mutation)
- **Predict mutations combinations** that trigger fates

Inference of Boolean networks compatible with differentiation data

BN exhaustive inference

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Answer-Set Programming (ASP)

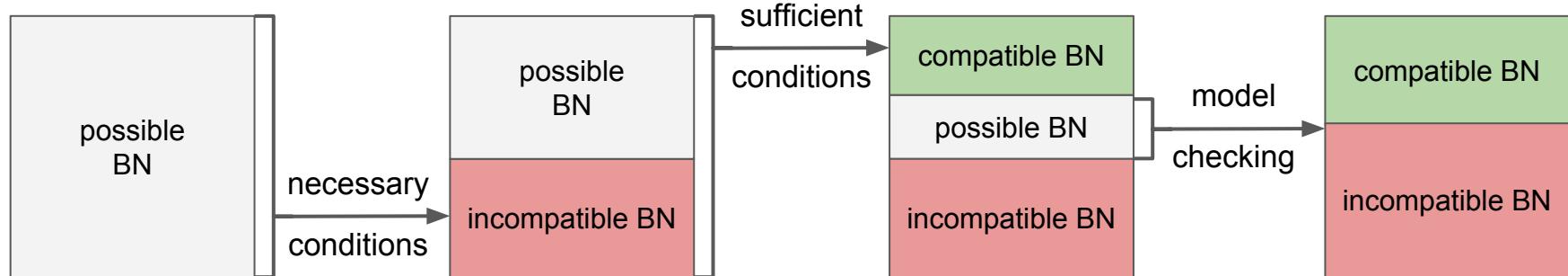


Inference of Boolean networks compatible with differentiation data

BN exhaustive inference

2) Logical approach : Answer-Set Programming (ASP)

constraints (necessary and/or sufficient conditions)



- necessary condition on **reachability** (Caspots^[2])
- necessary and sufficient condition on a stability hypothesis : **fixed point**

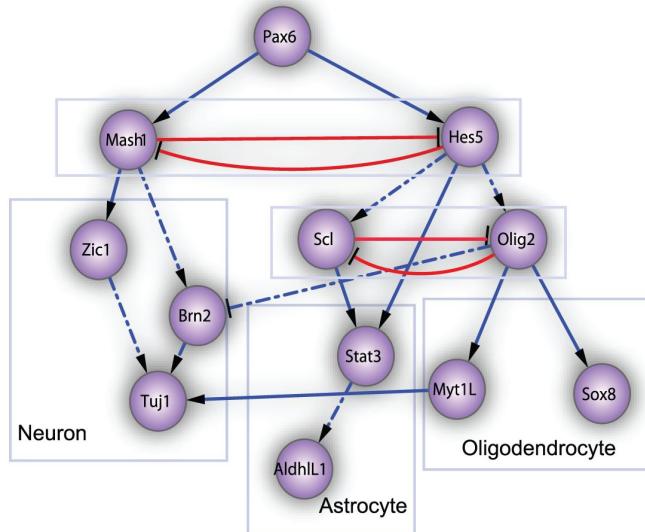
[2] Max Ostrowski, Loïc Paulevé, Torsten Schaub, Anne Siegel, Carito Guziolowski. Boolean Network Identification from Perturbation Time Series Data combining Dynamics Abstraction and Logic Programming. BioSystems, Elsevier, 2016

Inference of Boolean networks compatible with differentiation data

BN exhaustive inference

Small application on :

- PKN : CNS development^[2]
- Data : 4 fates



2) Logical approach : Answer-Set Programming (ASP)

Constraints impact : reachability & fixed point

