

Step 2. Pseudo-perturbation generation

Cell	Inputs + intermediates					Readouts			Class
	A	B	C	D	E	F	G	H	
1	1	1	0	1	0	0.8	0.4	0.6	A
2	1	0	1	0	0	0.2	0.5	0.3	A
3	1	1	0	1	1	0.8	0.3	0.9	A
4	1	1	1	0	1	0.6	0.1	0.2	B
5	1	0	0	1	1	0.7	0.8	0.5	B
6	0	0	1	0	1	0.7	0.2	0.3	B

Logic program
in ASP
($k=3$)

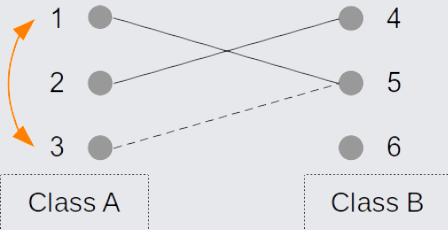
Cell	A	C	D	F	G	H	Class
1	1	0	1	0.8	0.4	0.6	A
2	1	1	0	0.2	0.5	0.3	A

Cell	A	C	D	F	G	H	Class
5	1	0	1	0.7	0.8	0.5	B
4	1	1	0	0.6	0.1	0.2	B

- 3 selected genes: A, C, D ($k=3$)
- Matching cells: (1,5), (2,4) ← pseudo-perturbations
- Different guaranteed pseudo-perturbation vector
- Optimal number of matching cells: 2

Step 2. Maximizing the readout difference

Redundancy



N. of matching cells: 2 (max)

Solution 1 : (1,5), (2,4)

Solution 2 : (3,5), (2,4)

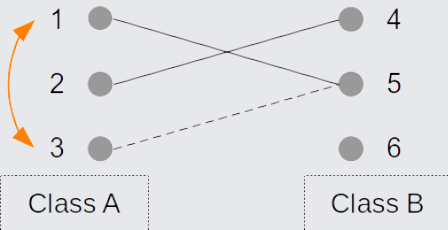
Cell representativity:

Class A : 3 out of 3 (100%)

Class B : 2 out of 3 (66%)

Step 2. Maximizing the readout difference

Redundancy



N. of matching cells: 2 (max)

Solution 1 : (1,5), (2,4)

Solution 2 : (3,5), (2,4)

Cell representativity:

Class A : 3 out of 3 (100%)

Class B : 2 out of 3 (66%)

Readout difference maximization

$$\text{diff}(1,5) = |0.8-0.7| + |0.4-0.8| + |0.6-0.5| = 0.6$$

Cell	A	C	D	F	G	H	Class
1	1	0	1	0.8	0.4	0.6	A

$$\text{diff}(3,5) = |0.8-0.7| + |0.3-0.8| + |0.9-0.5| = 0.9$$

Cell	A	C	D	F	G	H	Class
3	1	0	1	0.8	0.3	0.9	A

Cell	A	C	D	F	G	H	Class
5	1	0	1	0.7	0.8	0.5	B

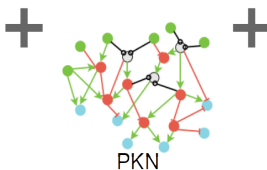
Step 3. BNs inference using Caspo [Guziolowski *et al.*, *Bioinformatics*, 2013]

Cell	A	C	D	F	G	H	Class
3	1	0	1	0.8	0.3	0.9	A
2	1	1	0	0.2	0.5	0.3	A

Experimental design for Class A

Cell	A	C	D	F	G	H	Class
5	1	0	1	0.7	0.8	0.5	B
4	1	1	0	0.6	0.1	0.2	B

Experimental design for Class B



Learning Boolean
Networks (Caspo)

