

STEADY STATE ANALYSIS OF BOOLEAN MOLECULAR NETWORK MODELS VIA MODEL REDUCTION AND COMPUTATIONAL ALGEBRA.

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EXAMPLE

Here we show an example of how our algorithm works. We use the Th-cell differentiation model from [1]:

$$\begin{aligned}
 x_1 &= GATA3 & , & f_1 = (x_1 \vee x_{21}) \wedge \neg x_{22}; \\
 x_2 &= IFN - \beta & , & f_2 = 0; \\
 x_3 &= IFN - \beta R & , & f_3 = x_2; \\
 x_4 &= IFN - \gamma & , & f_4 = (x_{14} \vee x_{16} \vee x_{20} \vee x_{22}) \wedge \neg x_{19}; \\
 x_5 &= IFN - \gamma R & , & f_5 = x_4; \\
 x_6 &= IL - 10 & , & f_6 = x_1; \\
 x_7 &= IL - 10R & , & f_7 = x_6; \\
 x_8 &= IL - 12 & , & f_8 = 0; \\
 x_9 &= IL - 12R & , & f_9 = x_8 \wedge \neg x_{21}; \\
 x_{10} &= IL - 18 & , & f_{10} = 0; \\
 x_{11} &= IL - 18R & , & f_{11} = x_{10} \wedge \neg x_{21}; \\
 x_{12} &= IL - 4 & , & f_{12} = x_1 \wedge \neg x_{18}; \\
 x_{13} &= IL - 4R & , & f_{13} = x_{12} \wedge \neg x_{17}; \\
 x_{14} &= IRAK & , & f_{14} = x_{11}; \\
 x_{15} &= JAK1 & , & f_{15} = x_5 \wedge \neg x_{17}; \\
 x_{16} &= NFAT & , & f_{16} = x_{23}; \\
 x_{17} &= SOCS1 & , & f_{17} = x_{18} \vee x_{22}; \\
 x_{18} &= STAT1 & , & f_{18} = x_3 \vee x_{15}; \\
 x_{19} &= STAT3 & , & f_{19} = x_7; \\
 x_{20} &= STAT4 & , & f_{20} = x_9 \wedge \neg x_1; \\
 x_{21} &= STAT6 & , & f_{21} = x_{13}; \\
 x_{22} &= T - bet & , & f_{22} = (x_{18} \vee x_{22}) \wedge \neg x_1; \\
 x_{23} &= TCR & , & f_{23} = 0.
 \end{aligned}$$

The wiring diagram is shown in Figure 1. The AND-NOT representation¹ of this Boolean network is shown in Figure 2 and the reduced AND-NOT network is shown in Figure 3.

The polynomial representation of the reduced AND-NOT network is

$$\begin{aligned}
 f_1 &= x_1 x_{22} + x_1, \\
 f_{22} &= x_1 x_{22} + x_{22}.
 \end{aligned}$$

To compute the steady states we need to solve

$$\begin{aligned}
 x_1 &= x_1 x_{22} + x_1, \\
 x_{22} &= x_1 x_{22} + x_{22},
 \end{aligned}$$

¹The AND-NOT representation is not unique and this particular representation was selected by hand for an easier comparison between the original Boolean network and its AND-NOT representation.

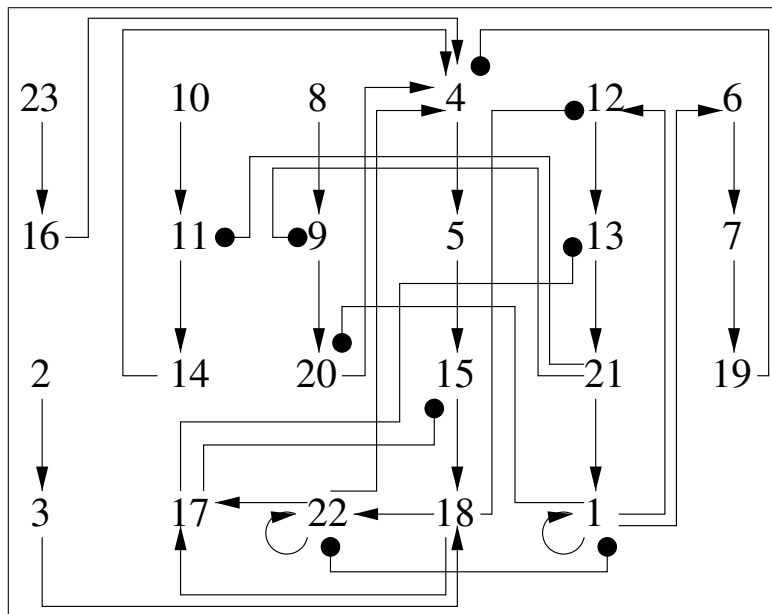


FIGURE 1. Wiring diagram of original Boolean network.

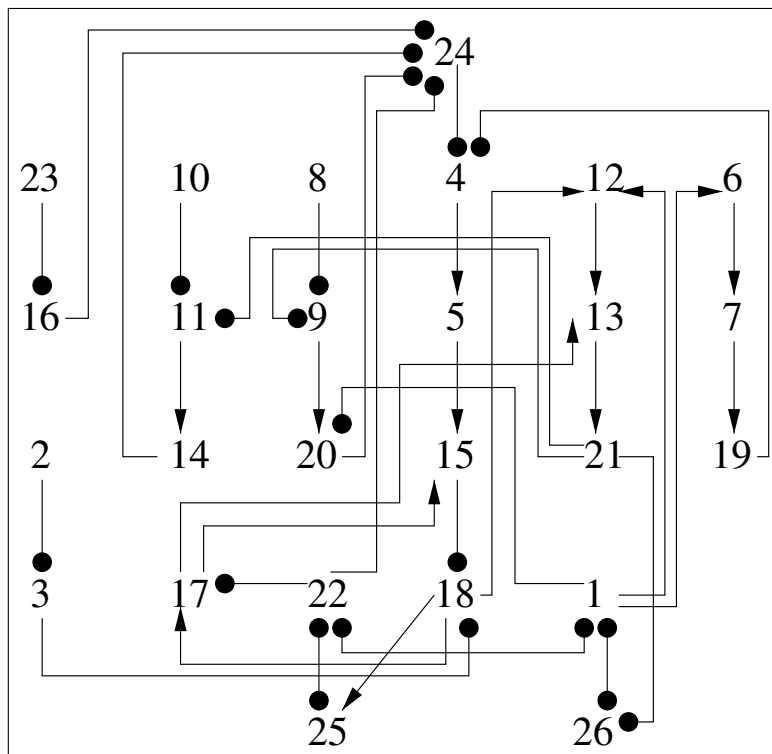


FIGURE 2. Wiring diagram of the AND-NOT network representation.

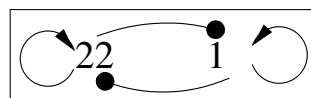


FIGURE 3. Wiring diagram of the reduced AND-NOT network.

that is,

$$0 = x_1 x_{22},$$

which is clearly satisfied for $(x_1, x_{22}) = (0, 0), (0, 1), (1, 0)$. Now that we have the steady states of the reduced network, we can use backwards substitution to obtain the steady states of the larger AND-NOT network and then project on the variables of the original Boolean network; we obtain $x = 000000000000000000000000, 000110000000000001000010, 10000110000110000010100$ (parenthesis were omitted). The first steady state corresponds to the “naive” Th-cell and the other two steady states correspond to the so-called Th-1 and Th-2 cells in charge of proinflammatory and anti-inflammatory responses in the immune system, respectively [1].

To use our code, the Boolean network has to be written in the form

```
(x1 | x21 ) & !x22
0
x2
(x14 | x16 | x20 | x22 ) & !x19
x4
x1
x6
0
x8 & !x21
0
x10 & !x21
x1 & !x18
x12 & !x17
x11
x5 & !x17
x23
x18 | x22
x3 | x15
x7
x9 & !x1
x13
(x18 | x22 ) & !x1
0
```

and one can simply run

```
./BNReduction.sh input_file
```

where `input_file` is the file shown above (all steps and “piping” are done automatically). The steady states will be printed in a file named `input_file.fp`:

```
user@computer:~$ ./BNReduction.sh input_file; cat input_file.fp
00000000000000000000000000000000
00011000000000000001000010
10000110000110000010100
```

COMMENTS ABOUT PERFORMANCE OF REDUCTION AND POLYNOMIAL ALGEBRA

In the manuscript we combined two main methods: (AND-NOT) network reduction and computational algebra [2, 3, 4, 5]. Also, in order to use the reduction of AND-NOT networks, we had to use the intermediate step of transforming a Boolean network into an AND-NOT network [6].

The reduction method by itself does not provide any means for computing steady states, it only guarantees that the reduced AND-NOT network has fewer variables. The reduction algorithm has to ensure that the number of steady states is preserved, so in many cases even the reduced AND-NOT network is too large to analyze by exhaustive search. For example, for Kauffman networks with $k = 3$ and $n = 100$, about 40% of the reduced AND-NOT networks had more than 50 variables. Using polynomial algebra allows to fill the gap and complete steady state computation (Table 2 in manuscript).

The polynomial algebra approach does provide a way to compute steady states, but it has trouble handling a large number of variables. For example, even with 500 variables and Kauffman networks with $k = 2$, the timings were 80s on average; for larger networks the timings are worse. However, by using the reduction method as a preprocessing step, the polynomial algebra approach can handle thousands of variables (Table 1 in manuscript).

REFERENCES

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