Read. *Algebraic and Discrete Mathematical Methods for Modern Biology*, by Robeva. Ch 6: Reduction of Boolean models.

Exercises.

1. The following is a model of the tryptophanase (*tna*) operon in *E. coli*:

$$\begin{array}{ll} f_A = M \wedge \overline{\gamma} & f_W = \omega_e \wedge B \\ f_B = M & f_{W_m} = (\omega_{em} \wedge B) \vee \omega_e \vee W \\ f_C = \overline{\gamma} & f_{\omega_e} = \omega_e \\ f_M = C \wedge \overline{P} & f_{\omega_{em}} = \omega_{em} \\ f_P = \overline{W} \wedge \overline{W_m} & f_\gamma = \gamma \end{array}$$

   The parameters are encoded by "frozen" variables: γ is glucose, ω_e is high levels of extracellular tryptophan, and ω_{em} represents (at least) medium levels.

   (a) Write down a system of nonlinear equations whose solutions are the fixed points.

   (b) Solve this system computationally by using Macaulay2 to compute a Gröbner basis of a particular ideal, and then solve the resulting simpler system by hand.

   (c) Use Cyclone to find the attractors. Are there attractors that are not fixed points?

   (d) Use BoolNet in RStudio to plot the state space. First, run the commands

```
> install.packages("BoolNet")
> library(BoolNet)
```

   Then, create a file "`tna-operon.txt`" with the model, and run the following commands:

```
> tnaModel <- loadNetwork("tna-operon.txt")
> tnaAttractors <- getAttractors(tnaModel)
> plotStateGraph(tnaAttractors)
```

   You have to set the working directory to where the file is located. There are sample BoolNet files on course webpage. Each must end in a single newline.

   (e) Use BoolNet to find the attractors under an asynchronous update, and summarize your findings. This can be done with the command:

```
> getAttractors(tnaModel,type="asynchronous")
```

   How does this compare to the synchronous state space?

   (f) Does this model exhibits bistability? Justify your answer.

2. More to be added...