Read:

- Chapter 6 of Robeva: *Steady state analysis of Boolean models: a dimension reduction approach.* By D. Murrugarra and A. Veliz-Cuba, pages 121–139.
- Chapter 3.1–3.4 of Robeva/Hodge: *Inferring the topology of gene regulatory networks: an algebraic approach to reverse engineering.* By B. Stigler and E. Dimitrova, pages 75–88.

1. Consider the following Boolean network model of the *lac* operon:

$x_1 =$ *lac* mRNA (M)	$f_1 = x_4 \wedge \overline{x_5}$
$x_2 =$ *lac* permease (P)	$f_2 = x_1$
$x_3 = \beta$-galactosidase (B)	$f_3 = x_1$
$x_4 =$ catabolite activator protein (C)	$f_4 = \overline{x_{11}}$
$x_5 =$ repressor protein (R)	$f_5 = \overline{x_6} \wedge \overline{x_7}$
$x_6 =$ high allolactose (A)	$f_6 = x_3 \wedge x_8$
$x_7 =$ allolactose (A_ℓ)	$f_7 = x_6 \vee x_8 \vee x_9$
$x_8 =$ high intracellular lactose (L)	$f_8 = x_2 \wedge x_{10} \wedge \overline{x_{11}}$
$x_9 =$ intracellular lactose (L_ℓ)	$f_9 = (x_8 \vee x_{10}) \wedge \overline{x_{11}}$
$x_{10} =$ extracellular lactose (L_e)	$f_{10} = x_{10}$
$x_{11} =$ extracellular glucose (G_e)	$f_{11} = x_{11}$

   (a) Reduce this Boolean network starting from the last variable. It is strongly recommended that you use Macaulay2 in Sage.

   (b) Draw the wiring diagram of the reduced network. Find its fixed points and use these to determine the fixed points of the original network.

   (c) Repeat Part (a) but using a completely different variable order.

2. Find two finite dynamical systems $f = (f_1, f_2, f_3)$ over $\mathbb{Z}_2$ that fit the following data:

$$(1,1,0) \xrightarrow{f} (0,0,1) \xrightarrow{f} (0,0,1)\,.$$

   You may express your answer using Boolean algebra or as polynomials in $\mathbb{Z}_2[x_1, x_2, x_3]$.

3. Consider the following *time series* in a 3-node polynomial dynamical system over $\mathbb{Z}_3$:

$$\begin{tikzcd}
\mathbf{s}_1 = (1,1,1) \arrow[d] \\
\mathbf{s}_2 = (2,0,1) = \mathbf{t}_1 \arrow[d] \\
\mathbf{s}_3 = (2,0,0) = \mathbf{t}_2 \arrow[d] \\
\mathbf{s}_4 = (0,2,2) = \mathbf{t}_3 \arrow[d] \\
(0,2,2) = \mathbf{t}_4
\end{tikzcd}$$

For reference, here are the input vectors $\mathbf{s}_i$ and output vectors $\mathbf{t}_i$:

$$\begin{aligned}
\mathbf{s}_1 &= (s_{11}, s_{12}, s_{13}) = (1,1,1)\,, & \mathbf{t}_1 &= (t_{11}, t_{12}, t_{13}) = (2,0,1)\,,\\
\mathbf{s}_2 &= (s_{21}, s_{22}, s_{23}) = (2,0,1)\,, & \mathbf{t}_2 &= (t_{21}, t_{22}, t_{23}) = (2,0,0)\,,\\
\mathbf{s}_3 &= (s_{31}, s_{32}, s_{33}) = (2,0,0)\,, & \mathbf{t}_3 &= (t_{31}, t_{32}, t_{33}) = (0,2,2)\,,\\
\mathbf{s}_4 &= (s_{41}, s_{42}, s_{43}) = (0,2,2)\,, & \mathbf{t}_4 &= (t_{41}, t_{42}, t_{43}) = (0,2,2)\,.
\end{aligned}$$

(a) For each $j = 1, 2, 3, 4$, write down the ideal $I(\mathbf{s}_j)$ of polynomials that vanishes on the data point $\mathbf{s}_j$.

(b) Use Macaulay2 in Sage to compute the ideal I that vanishes on all of the data points. The following commands will be useful:

```
%default_mode macaulay2
R = ZZ/3[x1,x2,x3,MonomialOrder=>Lex];
I = intersect{I1, I2, I3, I4};
```

Turn in a print-out of your Sage worksheet.

(c) Find polynomials f_1, f_2, f_3 in $\mathbb{Z}_3[x_1, x_2, x_3]$ that fit the data. That is, $f_j(\mathbf{s}_i) = \mathbf{t}_i$ for each i and j. Use this to write down the *model space* of the time series.