Internship project: Dimension reduction and Boolean networks
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Boolean networks are a popular modeling framework in computational biology to capture the dynamics of molecular networks, such as gene regulatory networks. For example, one can encode an expression of a set of genes by assigning a Boolean variable (true or false) to each gene to indicate whether it is expressed or not. The dynamics (how the state at time $n+1$ depends on the state at time $n$) is defined by Boolean functions (such as AND, OR, XOR, etc.).

One of the major computational problems about analyzing Boolean networks is to find their attractors (the sets of states to which the dynamics will eventually converge). Although, the state space is finite, it may be huge (100 genes yield $2^{100}$ combination, no way to brute-force them all!). Therefore, it is natural to try to reduce the size of the model before finding the attractors. Such an approach has been taken, for example, in [2] by applying some transformations to the Boolean functions defining the network.

The goal of the internship is to adapt and apply a recent model reduction algorithm CLUE [1] based on linear algebra to reducing Boolean networks and finding their attractors. This algorithm performs a reduction for models defined by differential equation but the same approach can be applied to Boolean networks. The goal of the internship would be to adapt CLUE to Boolean networks, test the resulting algorithm on examples from the computational biology literature, and (if time permits) apply the reduction to make the search for attractors more efficient.

Prerequisites: knowledge of Python and linear algebra.

References
