We will train our static network using time series phosphoproteomic perturbation training data to produce a Boolean network (BN) compatible with the network. This can be done with either a heuristic approach through software such as CellNoptR [ 23079107] and Optimusqual [27716031], or via answer set programming (ASP) as applied in Caspo-ts **[**30372442]. The former method trains the static network with a genetic stochastic optimization algorithm to best describe the existing data. Optimusqual requires an additional input of essential nodes that are either related to important biological processes or are potential readout nodes. It is unique in that it combines information on both network dynamics and equilibrium properties to generate an asynchronous BN. However, these heuristic approaches do not guarantee the global optimum BN because they do not search the complete solution space as ASP does [<https://arxiv.org/pdf/1210.0690.pdf>]. Taking that into consideration, we will use Caspo-ts to train our static network as it uses ASP to exhaustively enumerate candidate BNs including our essential nodes. In this method, BNs not resulting in an over-approximation of the reachability between the Boolean states from the training data are removed from the set of candidates, and optimization is done using a root means square error objective function to select the candidate BNs with minimal distance between the actual time series and the over-approximated time series. After, a model checking step is carried out on the remaining candidate BNs produced by ASP using computational tree logic to identify true positive BNs that exactly reproduce the binarized time series data.

23079107: <https://bmcsystbiol.biomedcentral.com/articles/10.1186/1752-0509-6-133>

27716031: <https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-016-1287-z>

30372442: <https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1006538>