We will train our static network using 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 **[**23853063]. 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 to train our static network as it uses ASP to exhaustively enumerate candidate BNs. This software compresses the static network to simplify its structure and generates a set of candidate BNs that are compatible with the static network. Normalized experimental observations are compared to Boolean predictions by calculating MSE. Networks are then optimized first to minimize MSE and second to minimize size [23853063], [28065903].

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>

23853063: <https://academic.oup.com/bioinformatics/article-lookup/doi/10.1093/bioinformatics/btt393>

28065903: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5351548/pdf/btw738.pdf>