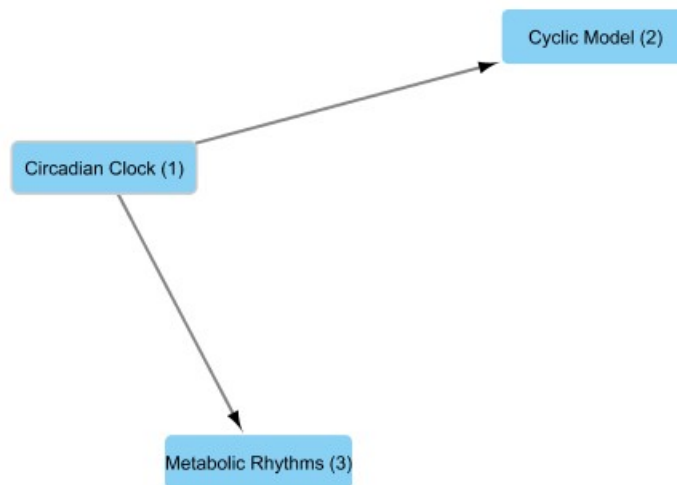


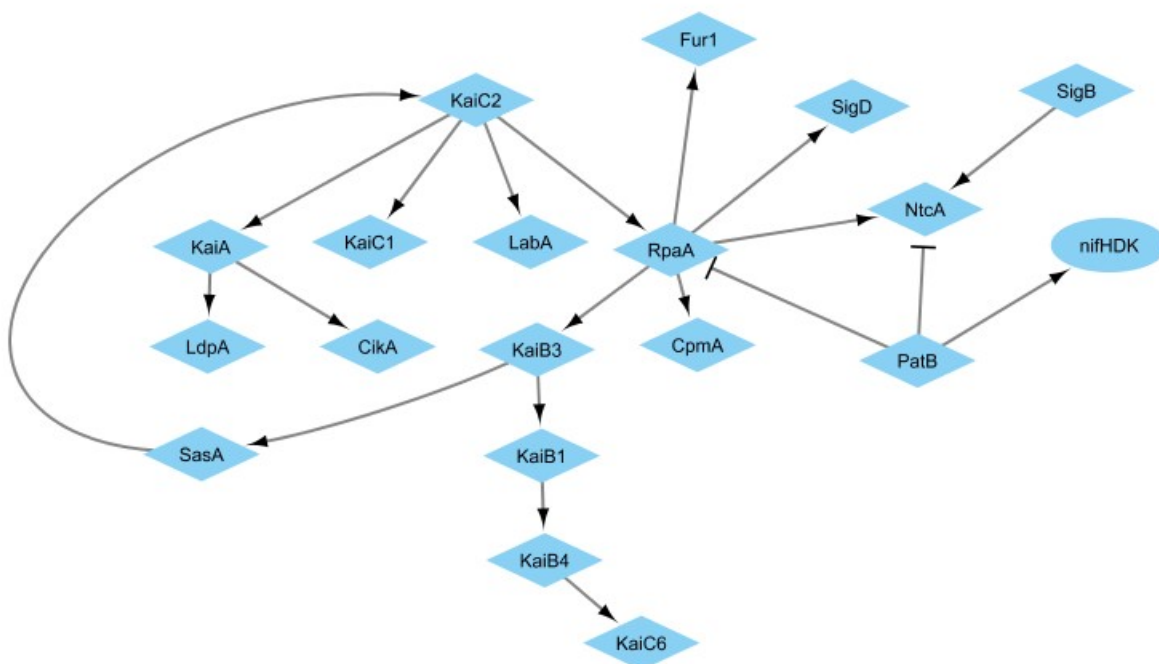
Summary

1. Identified multiple transcription factor(tf), target gene(tg) mappings from various literature sources.
2. Created a cytoscape model depicting the identified tf-tg interactions.
3. Most of the papers lack a single mapping between a specific tf and it's tg. They are mainly working with clusters of tfs or tgs. I have avoided including such interactions in the above model.
4. The inference networks in the literature sources are developed mainly from microarray experimental data using co-expression based methods.

The cytoscape model



The above figure shows the model visualization grouped into 3 different literature sources. By clicking on these sources, the model expands and shows the entire network as shown below:



Here, the diamond boxes are the individual genes and the oval box is an operon. The directed arrow represents positive interaction between the tf-tg pair. The T-arrow shows negative interactions between the same.

Path Forward

1. Go through more literature sources to find further interactions.
2. Can include tf cluster-tg cluster interactions.
3. Can combine various micro-array data from the literature sources and develop a Gene Regulatory Network based on newer techniques like GRENITS [1](https://bioconductor.org/packages/release/bioc/html/GRENITS.html), GENIE3 [2](https://bioconductor.org/packages/release/bioc/html/GENIE3.html) or maybe a combination of various methods [3](https://www.frontiersin.org/articles/10.3389/fpls.2018.01770/full#B21).

1. <https://bioconductor.org/packages/release/bioc/html/GRENITS.html>
2. <https://bioconductor.org/packages/release/bioc/html/GENIE3.html>
3. <https://www.frontiersin.org/articles/10.3389/fpls.2018.01770/full#B21>