Learning global network structures with any certainty is impossible from association data alone. However, by utilising a large number of separate microarray experiments inference of local sub-structures is possible and useful. This research aims to infer transcriptomic networks for *Arabidopsis thaliana*, specifically to predict how some poorly-characterised genes are regulated by the clock and other signals, rather than modelling the clock components themselves.

Interventions have proved highly useful in inferring gene regulatory networks, since generally data from a few microarray experiments are used. With well informed choice of interventions, similar networks may be distinguished, allowing inference of the underlying causal model. This work investigates how well we can learn a network of genes regulated by the clock from all available *Arabidopsis thaliana* gene expression data, using a Bayesian network structure learning algorithm which iteratively grows the network, adding the most likely gene to the model at each stage.