Learning Gene Regulatory Networks in Plants: Predicting the future of Agriculture.

*Synopsis/abstract.*

The ultimate goal of Systems Biology is to generate models that can predict how a system will react to untested conditions or genetic perturbations. This area of research is particularly relevant to plants where such predictive models can be useful for interventions in agriculture, and to engineer plants that are response to environmental change.

Due to their sessile mode of life, plants are subject to drastic variations in their environment that lead to rapid adaptation of molecular behaviors of gene regulatory networks. A critical question is understanding the cascade of gene responses that underlie a plant’s adaptation to environmental perturbations. In the present review we : i) describe experimental approaches to understand such dynamic and causal gene relationships in plants using time-series (kinetic) and other data, ii) review the analytical approaches used to infer causality in the Gene Regulatory Network from these types of genomic data, iii) suggest best practices in experimental design and analytical approaches for future efforts of this kind, Iv) review methods for high through put validation of GRNs in plants. [We had agreed before to focus on time series. That’s why I’ve replaced “or” by “and”. Otherwise it’s too broad. I like iv, but it could be a huge endeavour]

This article focuses on inference of causality in genomics, but its techniques apply to any setting (whether in plants or other species) in which elements may singly or collectively affect others. The article consists of four parts:

1. A review of efforts to use time-series (which is especially useful to derive causal networks) and other data to infer regulatory edges in gene networks (in plants and other species), showing the kinds of predictive networks that can be obtained. (GAB)

2. A description and a categorization of the analytical methods that are currently used to infer causal networks. (DENNIS)

3. An in-silico exploration of methods for causal network using the data from the DREAM framework (<http://www.the-dream-project.org/>)- for validation. This will address questions of practical interest, notably how to plan experiments to gain the maximum insight from each experiment (e.g. number of replicates vs number of time-pont experiments). (DENNIS/JESSE)

4. Experimental Methods for high through put validation of networks in plants (GAB- TARGET and others?)

**OUTCOME:** The outcome will be to help design experiments and analytical workflows that will lead to the construction of causal networks for plants.

**REFS COMPLIED BY GAB**

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3.         Pokhilko A, Fernandez AP, Edwards KD, Southern MM, Halliday KJ, Millar AJ: **The clock gene circuit in Arabidopsis includes a repressilator with additional feedback loops.** *Mol Syst Biol* 2012, **8:**574.

4.         Salazar JD, Saithong T, Brown PE, Foreman J, Locke JC, Halliday KJ, Carre IA, Rand DA, Millar AJ: **Prediction of photoperiodic regulators from quantitative gene circuit models.** *Cell* 2009, **139:**1170-1179.

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