

Gene Regulatory Networks: Lessons from plants.

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By studying the genome wide effect of nitrate regulated transcription factors in the model plant (*Arabidopsis thaliana*) [technique named TARGET¹], we yielded several insights into i) gene regulatory network complexity in Arabidopsis, ii) transcription factor dynamics², iii) potential connections between nutrient-related signaling cross-talks³.

Since we now have some cues about the Arabidopsis gene regulatory network topology, we used this knowledge to build the algorithm named FRANK (Fast Randomizing Algorithm for Network Knowledge). FRANK generates *in silico*, very large GRNs having the known characteristics of Arabidopsis transcriptional network (and very likely to other eukaryotic genomes) and simulates gene expression (experiments) at a genome-wide scale. In our endeavor to develop stable GRNs (“stable” means: gene expression should be constant or in oscillation) we have defined basic mathematical rules that find echo in network biology that will be presented⁴.

A reverse engineering approach, using machine learning algorithms also yielded several interesting results concerning our capacity to learn large GRNs by combining transcriptomic datasets as well as prior-knowledge on networks (Chip-seq, DAP-seq, Yeast 1 hybrid)⁴.

- . 1 Bargmann *et al. Mol Plant* (2013) **6**, 978
- . 2 Para *et al. PNAS* (2014) **111**, 10371
- . 3 Medici *et al. Nature Commun*(2015) **6**, 6274
- . 4 Carre *et al. NPJ Systems Biol and App.* (2017) **3**, 17