Dynamic System Modeling of Gene Expression in Plant-Fungi Symbiosis

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***Short Abstract* —Fungal-plant association elicits nutrient exchange between the organisms. Dynamic system model is applied on regulated genes during arbuscular mycorrhizae *Glomus versiforme-Medicago trunculata* root symbiosis [1]. Dynamic gene expression data derived from various days post-inoculation (dpi) were clustered into genes regulated in media containing and without phosphate. With the available data, we create a first-order linear discrete dynamic model [2] using data-driven method to fit the data. The result of the modeling constitutes active interactions in the gene network of the plant root during this period. The reconstructed network will be compared against established gene interactions in literature. [3, 4, 5]**

***Keywords* —*Glomus versiforme*, *Medicago trunculata*, dynamic system model, fungi-plant symbiosis, gene network**

I. Introduction

PLANTS associate with many organisms to enhance their growth. Fungal-plant symbiotic association starts by the localized colonization of the fungi to the plant root. Over time, the fungi invade the host's tissue through formation of hyphae and later, arbuscules. These associations enable the fungi to obtain photosynthetic carbon sources from the plant. In return, the plant acquires poorly-obtainable compounds from the soil such as phosphate and nitrogenous chemicals needed for metabolism and defense. Liu et al [1] explores the temporal changes in plant gene expression during the different stages of *Glomus versiforme* (fungi)-*Medicago trunculata* (plant) association, which presents genes regulated after 8 (initial formation of fungal arbuscules), 15 and 22 (full maturation of the arbuscules) and, 31 and 36 (arbuscule senescence) dpi [1 and references therein].

We propose to utilize (1) as the dynamic system model to describe the complexity of the interactions of the genes involved in the different time points of fungal interaction.

$$\frac{\vec{g}[t]-\vec{g}[t-1]}{h} = A\vec{g}[t-1] \quad (1)$$

where, $\vec{g}[t]$ represents the amount of all genes expression at time *t*. *A* is the system matrix, represents the relationship between genes in the regulatory network.

After using data-driven method to solve the system matrix *A*, we can create a graph which represents the gene regulatory network in plant root during arbuscular mycorrhizae *Glomus versiforme-Medicago trunculata* root symbiosis [1].

Analysis of the results will include two components. In the computational modeling part, we show how well our model fit the gene expression data using the *p*-value (*F*-test) under the hypothesis test of the first-order linear discrete dynamic model against the non-interactive model. In the biological interpretation part, the obtained network can be compared against existing metabolic [4,5] and signal transduction pathways [3]. Moreover, novel unknown regulated genes and cross-talk between pathways may be elucidated.

II. Methods

The gene expression data [1], at each time point, include two reads for each gene representing two replicates. The temporal gene expression data should be linked together between different time points to show the dynamics. This link may be created by either using the mean, maximum or minimum reads at each time point which creates one dynamic change for each gene.

We use the linear regression to get a close form solution by minimizing Eq. (2) to get the $\vec{a}_i$ which is the *i*-th row in *A*:

$$F(\vec{a}_i) = \sum_{t=1}^{T}((g_i[t]-g_i[t-1])/h - \vec{a}_i^T \cdot \vec{g}_i[t-1])^2 \quad (2)$$

Solving the former equation to get one solution of $\vec{a}_i$ omits the biological meaning. Because this solution means all genes are the parents of gene *i*. To find the best solution for biological meaning, we search all combinations under the assumption of one to two parents for each gene *i*, according to the sample size.

Final result will be represented as described in the previous section.

[1] Liu J et al. (2003). Transcript Profiling Coupled with Spatial Expression Analyses Reveals Genes Involved in Distinct Developmental Stages of an Arbuscular Mycorrhizal Symbiosis. *Plant Cell* **15**, 2106-2123.

[2] Song, M., Liu, Z. 2007. A linear discrete dynamic system model for temporal gene interaction and regulatory network influence in response to bioethanol conversion inhibitor HMF for ethanologenic yeast. Lecture Notes in Bioinformatics. 4532:77-95.

[3] Pollard TD, Earnshaw WC. (2004). *Cell Biology*. Saunders (Elsevier), Philadelphia, Pennsylvania.

[4] Voet, D, Voet JG. (2004). *Biochemistry*. 3rd ed. John Wiley & Sons, Inc., New Jersey.

[5] Michal G. *ed* (1993). Biochemical Pathways. 3rd ed. Boehringer Mannheim GmbH – Biochemica, Germany

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