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METHODOLOGY

Comparing time series transcriptome data between plants using a network module finding algorithm

Jiyoung Lee[1,3], Lenwood S. Heath[2], Ruth Grene[3] and Song Li[1,3*]

Abstract

Background: Comparative transcriptome analysis is the comparison of expression patterns between homologous genes in different species. Since most molecular mechanistic studies in plants have been performed in model species, including Arabidopsis and rice, comparative transcriptome analysis is particularly important for functional annotation of genes in diverse plant species. Many biological processes, such as embryo development, are highly conserved between different plant species. The challenge is to establish one-to-one mapping of the developmental stages between two species.

Results: In this manuscript, we solve this problem by converting the gene expression patterns into co-expression networks and then apply network module finding algorithms to the cross-species co-expression network. We describe how such analyses are carried out using bash scripts for preliminary data processing followed by using the R programming language for module finding with a simulated annealing method. We also provide instructions on how to visualize the resulting co-expression networks across species.

Conclusions: We provide a comprehensive pipeline from installing software and downloading raw transcriptome data to predicting homologous genes and finding orthologous co-expression networks. From the example provided, we demonstrate the application of our method to reveal functional conservation and divergence of genes in two plant species.

Keywords: Comparative transcriptome analysis, Network, Sequence homology, Arabidopsis, Soybean, Embryo development

Background

Expression analysis is commonly used to understand the tissue or stress specificity of genes in large gene families [1–5]. The goal of comparative transcriptome analysis is to identify conserved co-expressed genes in two or more species [3, 6, 7]. The traditional definition of orthologous genes is based solely on sequence homology [8–11] and syntenic relationships [2, 12–14] and not at all on gene expression patterns. In contrast, comparative transcriptome analysis combines a comparison of gene sequences with a comparison of expression patterns between homologous genes in different species. Homologous genes have been reported to be expressed at different developmental stages, in different tissue types, or under different stress conditions [3, 15–17]. This documented divergence of expression patterns provides crucial evidence for the existence of functional divergence of homologous genes across species [18, 19]. Therefore, comparative transcriptome analysis is an important tool for distinguishing those genes that have retained functional conservation from those that have undergone functional divergence. Comparative transcriptome analysis is particularly important for plant research, since most molecular mechanistic studies in plants have been performed in model species, primarily *Arabidopsis thaliana* [20]. The consequence of this narrow focus is that

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