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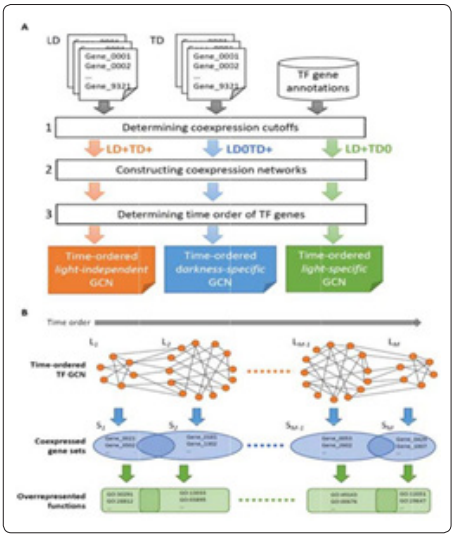
A comparative transcriptomics method with applications

Transcriptomes obtained from the same tissue under different conditions can provide massive data for identifying genes differentially expressed between conditions. Moreover, transcriptomes from time-series experiments provide dynamic information to profile gene expressions over time. Such Three-Dimensional (3D) (gene expression, condition and time) data are very useful for studying dynamic gene regulatory networks and biological processes (note that conditions can be replaced by species or strains and time-series can be replaced by tissues or sources). However, three issues, i.e., heterogeneity of samples, unequal numbers of time points and uneven time period lengths between studies, made it difficult to analyze the data. The first issue affects the determination of gene expression differences between conditions. The second and third issue requires transformation of the original time-series transcriptomes for cross-condition comparisons. Although methods have been developed for analyzing 3D data, there is still no method to deal with all of these issues. In this study, we developed a comparative Gene Co-expression Network (GCN) method to analyze 3D data. To illustrate our method, we applied it to two sets of time-series transcriptomes of maize embryonic leaf development under the normal Light/Dark (LD) cycle and under Total Darkness (TD). As a C4 plant, maize leaves exhibit the Kranz anatomy, which is crucial for C4 photosynthesis. Since Kranz anatomy develops under both LD and TD, we applied our method to compare the two types of transcriptomes to obtain a time-ordered light independent GCN. This GCN should include all regulators of Kranz anatomy development. Indeed, from this GCN we inferred and experimentally validated a number of upstream regulators of a key Kranz anatomy regulator, SHR (SHOOTROOT). In addition, we also obtained a light-specific GCN and a darkness-specific GCN. From these three GCNs, we inferred light-independent, light-preferred and darkness-preferred genes. Moreover, from the darkness-specific GCN, we could also explain why embryonic leaf cells first divide faster but then more slowly under TD than under LD. As will be explained, our method can be applied to other types of data.



Flowchart of the comparative transcriptomics method. (A) Three steps of constructing the time-ordered TF gene co-expression networks (GCNs). (B) The levels in a time-ordered GCN represent the up-regulation time order of TF genes, their co-expressed genes and overrepresented functions.

Biography

Chun-Ping Yu has received his PhD degree in Physics from National Central University, Taiwan. He is currently working as a Postdoctoral Fellow at Biodiversity Research Center, Academia Sinica, Taiwan. His research interests include gene regulation, evolutionary genetics and systems biology. His current work focuses on developing NGS functional genomics applications for a large-scale determination of transcription factor binding sites using bioinformatics techniques, machine learning and artificial intelligence methods.

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