Luis Guillermo Leal et al., J Proteomics Bioinform 2013, 6:8
http://dx.doi.org/10.4172/0974-276X.S1.002

OMICS Group Conferences
Accelerating Scientific Discovery
International Conference on
Omics Studies
September 04-05, 2013 Holiday Inn Orlando International Airport, Orlando, FL, USA

A multivariate analysis approach to compare gene co-expression networks from pathogen infected plants

Luis Guillermo Leal, Camilo López and Liliana Lopez-Kleine
Universidad Nacional de Colombia, Colombia

Gene co-expression networks (GCNs) are graphic representations that depict the coordinated transcription of genes to certain external stimuli. GCNs have been useful in studies of translational functional genomics such as networks alignment and comparisons based on principal component analysis (PCA). For the PCA comparison, networks are described by topological variables and then a PCA on these variables is applied to characterize them. Closeness of networks on the Principal Component (PC) space indicates their structural similarity. However, network description using topological variables has for now only allowed the discovery of similar graph motifs while valuable biological conclusions remain unrevealed. In this work, a novel methodology improving network comparison is proposed. Microarray datasets from pathogen infected plants (*Arabidopsis thaliana*, rice, soybean, tomato and cassava) were used to construct a total of 59 GCNs. The GCNs construction was undertaken using the mutual information coefficient as gene similarity metric and a clustering coefficient based method for similarity threshold selection. We added new non-topological variables to describe the networks from a biological perspective, such as tolerance to pathogen attacks and assortativity coefficients from functional annotations. The K-Means clustering algorithm was used to find groups of similar GCNs on the PCA space. Results confirm that some clustered networks represent similar immune responses and that our methodology was able to retain the complexity of the experiments analyzed. The current biological knowledge on model organisms and less studied species is widened with our results and can be a starting point for emitting biological hypothesis related to plant immunity processes.

Biography

Luis Guillermo Leal has a BS in Chemical Engineering and is a Master of Science student in the Statistics program at Universidad Nacional de Colombia. Together with Ph.D. Liliana López-Kleine and Ph.D. Camilo López, he is working on a common project regarding the reconstruction and comparison of GCNs in plants. He published a review on biostatistical methods for the reconstruction of GCNs. He has also worked on the prediction of immunity genes in *Arabidopsis* and cassava using heterogeneous genomic data.