Editörden/Editorial

From the Editorial Board

As the number of scientific publications rises, readers are increasingly seeking concise information, precise results, and definitive answers within these materials. Many authors gather a substantial amount of data for their experimental works in an attempt to understand the mechanisms and etiology of stress. However, this needs laborious writing, careful arrangement, and lengthy papers. Of course, this would discourage readers from perusing the entire article and hinder their ability to quickly grasp the concept. Almost in all areas of scientific studies, we use sophisticated software, statistical tools, and graphical illustrations with excellent quality. As we noted from the recent publications, internationally reputed scientific authors have started using new tools to add value to their manuscripts. Unlike the manuscripts in the previous decade, the authors have started to use new tools to analyze their data to reach a definite verdict. Researchers are now evaluating the same old manuscripts using a new concept.

Correlation-based network analysis (CNA) and pathway-based metabolic analysis have reached out to a broad audience, and they have been employed in many recent scientific articles and books. With a single illustration, we could say many things about what we are going to say. We could easily evaluate, understand, interpret, and develop mechanisms and establish a network between metabolites. So, rather than comparing two parameters in terms of significance, we could see the whole picture and understand the mechanism in normal and stress conditions. By means of this approach, we could even notice the relations that could have a high impact under stress conditions before the occurrence of stress. When we want to breed or develop a new variety, most of the time we choose or select a gene or gene groups either on the basis of references from the published works or on the basis of the "try and error" principle. This approach, which has been used, is costly, time-consuming, and needs meticulous work. A modification, upregulation, or downregulation of a gene would be assessed at a later stage after the modification has been completed. By using biochemicals on living things and watching what happens afterward, we could make them more tolerant or resistant without changing their genomic structures. All scientific disciplines, such as botany, zoology, medicine, and agriculture, could debate this approach. However, if we know what we are going to assess and if we are able to predict the potential changes in advance of the application, we would be very pleased, and we are going to follow the right pathway in a living cell. As long as you have data, you can follow up on any minor changes in a cell using metabolic pathway and correlation network analyses. Data do not have to belong to one family of compounds; they may vary and be quite distant from each other in terms of their nature. For example, you can compare plant height, weight, biochemical compounds, and even gene regulations in a single pathway employing network analysis. With the use of artificial intelligence and machine learning, we could even analyze the cells with millions of possibilities without an invasive approach.

Correlation-based network analysis (CNA) uses complex dendrograms to show multiple correlations between components, with similarities and differences between them being mathematically defined. "Heads" or "nodes" represent metabolites or parameters, while lines called "edges" represent relationships among them. Edges could be directed or undirected, which means connections between two nodes may be bilateral, directed, or not. The thickness of the edges determines the level of significance of the interactions. The color of the edges represents positive or negative correlations. The analysis of parameters determines the node size, which in turn represents the value of the parameters. With the use of CNA and pathway-based metabolic analyses, we do not have to go into data reduction. Every single data point, regardless of its magnitude, holds a significant value in the network map. We could describe this with a simple example. For example, cities in a country connected to each other via roads represent a map. However, ignoring side roads or village roads prevents us from understanding the city transition. Some important products may be transferred via shortcut roads to save energy between cities. The cell mechanisms follow the same example. This approach allows for a detailed evaluation of proteomics and metabolomics studies. We believe publications employing these methods might have a higher chance and value in highly regarded scientific journals.

Some free package programs that could be used with these programs are Pajek, Gephi, Cytoscape, social network analysis (SNA), and network visualization software (NVS). As long as the codes that define metabolites are written correctly in an algorithmic way, these programs could be used with no hassle.

As old in age but new in concept, we are happy to accept good quality articles written within the above frame. Since we are a strong candidate for the Scopus and WOS databases, we could only achieve this with authors submitting their high-quality works and readers appreciating and citing the high-quality papers. We recently renewed our Editorial Board with dynamic and highly regarded scientists worldwide to achieve our goals. Our members of the team are from different universities around the globe. We are now welcoming new members to join us to expand our team capacity. Meanwhile, we would like to express our sincere gratitude to the former Editorial Board members who worked hard to bring the journal to this stage.

With our kind regards,

Prof. Dr. Murat Dikilitaş,
On Behalf of the Editorial Board