PAASE Webinars: Lecture #8

Socio-Ecological Network Structures from Process Graphs

May 22, 2020
Friday
08:00—09:00
Philippine Standard Time

Dr. Angelyn Lao

The webinar will be held on Friday, 22nd of May at 8 AM (Philippine Time) or Thursday, 21st of May at 8 PM (Eastern Time)

To register please go to:
https://bit.ly/AngieLao

With a special guest lecturette on P-graph fundamentals by the Process Integration guru, **Prof. Raymond Tan** of De La Salle University

Angie is currently an Associate Professor in the Mathematics & Statistics Department and the Assistant Dean for Research & Advanced Studies of College of Science at De La Salle University (DLSU). She joined DLSU after the completion of her Doctorate degree in Systems Biology at the University of Rostock (Germany). She held a Research Fellowship and two Professorial Chairs in Mathematics namely the Br. C. John Lynan FSC Professorial Chair in Mathematics and the Br. Albinus Peter FSC Professorial Chair in Mathematics. Several of her most notable publications include her work on establishing the first mathematical and compartmental models to describe and analyze the influence of the receptor SORLA in the amyloidogenic processing of Alzhemier's disease. Her recent works apply bioinformatics and machine-learning approaches to study and discover the patterns in the topological structures of the disease networks, and identify biomarkers associated with different diseases.

About this webinar

In this study, we propose the novel application of the process graph (P-graph) methodology to the analysis of ecological networks. P-graph was originally developed for engineering design problems; in our work, we show how its five axioms and two algorithms - maximal structure generation (MSG) and solution structure generation (SSG) can be adapted to the problem of understanding complex interactions in ecosystems. The methodology allows multiple types of interactions among ecosystem components to be handled simultaneously based on representation as a bipartite graph. Complete network structures can be deduced from knowledge of local interactions of components using MSG. Finally, all structurally feasible networks of viable ecosystems can be identified with SSG. We illustrate the features of the P-graph methodology with a stylized illustrative example.