Dr. Karl E. Peace was presented with the Sellers-McCroan Award for his lifelong commitment to improving public health through academia and laboratory advancements. The award was presented during the Sellers-McCroan luncheon, part of the 85th Annual Meeting and Conference of the Georgia Public Health Association in Atlanta on Monday, March 10th.

Peace provided the leadership and endowments to create the Jiann Ping Hsu College of Public Health at Georgia Southern University, which was named in honor of his late wife. Peace is also a recognized authority on clinical trials methodology, measurement and analysis. He currently serves as Professor and a Distinguished Georgia Cancer Coalition Scholar at the Jiann Ping Hsu College of Public Health.

Peace was introduced by Dr. Wade Sellers, District Health Director of the Northwest Georgia Health District. “He’s enabled folks who’ve heard the calling to go into public health to become educated, get their degrees and go out and be launched and supported,” said Sellers.

Peace’s contributions were further outlined in the program for today’s event. “His national leadership has raised the visibility of both Georgia and Georgia Southern University, and his lifework and contributions have been a great credit to both the state and university. His commitment to battling cancer not just in a laboratory or library but in practice has resulted in many more South Georgians being screened. And his longtime work in biopharmaceuticals has helped create many of the lifesaving and life-improving drugs we can access today.”

The program goes on to say, “He has shown many that a poor boy from a small farm in southwest Georgia can accomplish great things.”

To read more, visit gapha.org.
A collaborative study including Dr. Daniel Linder, an assistant professor of biostatistics expands the algebraic statistical model for biochemical network dynamics inference. With modern molecular quantification methods, like, for instance, high throughput sequencing, biologists may perform multiple complex experiments and collect longitudinal data on RNA and DNA concentrations. Such data may be then used to infer cellular level interactions between the molecular entities of interest. One method which formalizes such inference is the stoichiometric algebraic statistical model (SASM) of Ref. [2] which allows to analyze the so-called conic (or single source) networks. Despite its intuitive appeal, up until now the SASM has been only heuristically studied on few simple examples. The current paper provides a more formal mathematical treatment of the SASM, expanding the original model to a wider class of reaction systems decomposable into multiple conic subnetworks.