2019 Annual Meeting of the American Association for the Advancement of Science (AAAS), Special Session on Mathematical Modeling of Diseases: Translational Approaches (sponsored by the Mathematical Section of the AAAS).   Friday, February 15, 2019, 1:30 PM to 3:00 PM: https://aaas.confex.com/aaas/2019/meetingapp.cgi/Session/21409

The world's largest multidisciplinary scientific society established in 1848 and a leading publisher of cutting-edge research through its *Science* family of journals, AAAS has individual members in more than 91 countries around the globe.

Synopsis of the Special Session: Progress in understanding and modeling disease processes based on the availability of data about individual patients has the potential to greatly improve medical treatments by personalizing them, thus leading to what is known as precision medicine. Precision medicine's promise is to customize treatments by making use of patient-specific data, such as genomic, physiological, or lifestyle information. The overarching challenges then is to connect individual features of a patient's data to the outcome of certain interventions. Computational models are used that range from data-driven and correlation-based associations to mechanistic predictive models, often integrating processes that span several spatial and temporal scales.

This session presents three examples of personalized mathematical models. These translational modeling projects integrate an understanding of the relevant individual variability of physiology or biochemistry with fundamental insights into disease dynamics. All these projects are based on close collaborations between mathematical and computational scientists and clinicians. The result is a very timely and important bench-to-bedside paradigm. The first model is called an artificial pancreas and it is used to treat patients with type I diabetes. The second model provides a guide to surgical treatment of tumors. The third project uses medical image-based multi-scale computational modeling to generate new strategies for improving diagnosis, patient selection and therapy optimization in heart failure patients and has promise to improve outcomes of therapies such as cardiac resynchronization therapy for dyssynchronous heart failure.

Society for Mathematical Biology

2021 Annual Meeting of the Society for Mathematical Biology (SMB) will be held at the University of California Riverside from June 13-17, 2021. The Society for Mathematical Biology was founded in 1973 to promote the development and dissemination of research and education at the interface between the mathematical and biological sciences. It does so through its meetings, awards, and publications. The Society serves a diverse community of researchers and educators in academia, in industry, and government agencies throughout the world.

Scientific Program of the 2021 SMB Annual Meeting. The proposed conference theme is "Mathematics & Personalized Medicine". Modern mathematical models could soon lead to customizing treatments for specific patients by incorporating patient-specific data. Development of multi-scale mathematical models of the key molecular biology and cellular biology processes, biochemical networks personalized with omics data, structural and physicochemical analyses, heterogeneous tissue architecture, and physiology, could lead to detailed comparison of many different treatments, including different drugs, routes of administration, doses and schedules by virtual clinical trials that incorporate models of many patients.

Due to the multi-scale nature of the models, clinicians could identify emergent therapeutic or toxic effects of treatments, as well as conditions under which therapies fail. These models can translate knowledge from in vitro cell culture to in vivo preclinical and clinical studies, which is important because it is known that observed mechanisms in vitro do not always hold in vivo. These models can help researchers and clinicians translate therapies from animals to humans, or from microphysiological systems ('body-on-a-chip') to patients. Also, combining omics data, machine learning approaches and other statistical methods with novel mechanistic mathematical modeling approaches could lead to better understanding and treatment of many human disease including, among others, cancer, hematological diseases, both genetic and infectious, chronic wounds in diabetic patients as well as brain diseases. At the same time, it would be crucial to develop uncertainty quantification methods for automated parameter estimation for clinical data assimilation.