Journal of
Gastrointestinal & Digestive System

Editorial Open Access

Editorial on Systems Biology and Bioinformatics in Gastroenterology

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Editorial

Traditional medical research has gained significant improvement and garnered immense attention in terms of the detection and treatment of acute and chronic metabolic and inflammatory diseases as well as cancer. In particular, in the field of gastroenterology, significant advancements have been made with regard to Systems Biology. As is well known, the discovery of basic molecular and cellular disease mechanisms in the last 60 years has led to the development of reliable diagnostic tests and effective therapies. For instance, the discovery of several potential pathogenic variants has led to powerful diagnostic tools and drugs.

Next-generation sequencing has further helped in differential diagnoses to avoid misdiagnosis of gastrointestinal disorders mimicking genetic disorders. Equally, for many monogenetic liver diseases reliable diagnostic tests exist.

Although effective pharmacotherapy for some of these diseases exists (Wilson's disease), comparable treatments are not available for others (e.g., progressive familial intrahepatic cholestasis, PFIC). However, translation of gene knock-out mouse models has emerged as a powerful tool to understand the underlying disease processes and may eventually lead to successful gene therapy.

We may ask whether computational approaches and systems medicine are the only solution for complex and multifactorial diseases. Dynamic processes can be described mathematically with a set of differential equations. These equations can help in the generation of computational models, which can describe the time-resolved behavior of molecular reactions and cellular processes. Quantitative and semi-quantitative data derived from in vitro and in vivo models can be utilized to feed these mathematical constructs. Once a reliable and robust computational model is established, the model can be used for *in silico* research.

However, prior to establishing models, detailed insights into the biological functions of the liver and an understanding of its crosstalk with other human tissues and the gut microbiota should be used to develop novel strategies for the prevention and treatment of liver-associated diseases, including fatty liver disease, cirrhosis, hepatocellular carcinoma and type 2 diabetes mellitus. Then, biological network models, including metabolic, transcriptional regulatory, protein-protein interaction, signaling and co-expression networks, can provide a scaffold for studying the biological pathways operating in the liver in connection with disease development in a systematic manner.

Detailed insights into the biological functions of the liver and an understanding of its crosstalk with other human tissues and the gut microbiota can be used to develop novel strategies for the prevention and treatment of liver-associated diseases, including fatty liver disease, cirrhosis, hepatocellular carcinoma and type 2 diabetes mellitus. Biological network models, including metabolic, transcriptional regulatory, protein–protein interaction, signaling and co-expression networks, can provide a scaffold for studying the biological pathways operating in the liver in connection with disease development in a systematic manner. We need to review studies in which biological network models were used to integrate multiomics data to advance our understanding of the pathophysiological responses of complex liver diseases. We also need to discuss on how this mechanistic approach can contribute to the discovery of potential biomarkers and novel drug targets, which might lead to the design of targeted and improved treatment strategies. We also need to present a roadmap for the successful integration of models of the liver and other human tissues with the gut microbiota to simulate whole-body metabolic functions in health and disease. Thus, detailed characterization of human liver tissue and gut microbiota is enabled by omics technologies. Biologic network models are functional tools for the exploration and integration of multiomics data. Systems biology uses a holistic and integrative approach for comprehensive analysis of the biological functions in healthy and diseased states. Systems biology approaches have been successfully employed in gastroenterology and hepatology to identify biomarkers and drug targets. These integrative tools can be used for simulation of liver tissue functions and crosstalk of liver with other tissues.

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Received July 23, 2020; **Accepted** July 23, 2020; **Published** July 30, 2020

Citation: Amin A (2020) Editorial on Systems Biology and Bioinformatics in Gastroenterology. J Gastrointest Dig Syst 10: e624.