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Automated reconstruction of tissue specific human metabolic networks and its potential impact on personalized medicine

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Metabolic diseases have been recognized as an important emerging global public health problem that have been associated with commonly occurring disorders such as obesity, diabetes, hypertension, dyslipidemia and certain types of cancer. It is difficult to identify the exact causes of such diseases since they are complex to study and they involve interplay between different tissues in human body. Therefore, scientists focus on human metabolism and its regulation since such diseases could be explained through the use of computational modeling of human metabolic processes and the reconstruction of tissue-specific human metabolic networks. These networks can be analyzed using genome-scale metabolic models and can also be employed for the treatment of human metabolism. However, human metabolism involves a very large number of metabolic reactions in different tissues and the entire reconstruction of tissue-specific human metabolism requires more effort after the presentation of first generic human metabolic networks. Recently, several tissue specific models for liver and brain have been published and there is still a need for improving the existing models and generating new models for other tissues in human body. In this study, we develop a model building algorithm and automatically generate 69 preliminary tissue specific metabolic networks from the generic human model by merging publicly available omics data. Furthermore, for validation of our model building algorithm, generated genome-scale model of hepatocytes is simulated for the known biological central functions of the liver metabolism such as gluconeogenesis and detoxification of ammonia and compared with the recently published tissue specific liver model.

Biography

Adil Mardinoglu had his PhD from Waterford Institute of Technology in Ireland and his PhD thesis entitled “Inclusion of interactions in implant assisted magnetic drug targeting” is accepted without any corrections. He worked as a postdoctoral researcher in Development of Artificial Neuronal Networks for Molecular Communication in Trinity College Dublin, Ireland. Currently, he is working in Prof Jens Nielsen’s Systems and Synthetic Biology group in Chalmers, Sweden on the development and validation of model building algorithms in Automated Reconstruction of Tissue Specific Human Metabolic Networks. He has published papers in reputed journals and had talks in different international conferences.