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VABILO NA PREGLOV KOLOKVIJ /
INVITATION TO THE PREGL COLLOQUIUM

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Velika predavalnica Kemijskega inštituta / Lecture Hall at the National Institute of Chemistry; Hajdrihova 19, Ljubljana

Genome-Wide Reprogramming of Human Metabolism in Response to Obesity and Cancer

Metabolism is highly complex involving a very large number of chemical reactions. These reactions are traditionally grouped into pathways with dedicated functions, but recent analysis of metabolism has shown that there is a high degree of connectivity between these pathways due to common sharing of co-factors and key metabolites. It is therefore necessary to study metabolism in its whole, and this can be done through the use of the so-called genome scale metabolic models (GEMs). These models represent comprehensive reconstruction of all known metabolic reactions operating in a cell, and these GEMs represent knowledge databases that link genes, proteins, enzymes, metabolic reactions and metabolites. We have recently reconstructed the to date most comprehensive GEM for human metabolism, HMR2.0. This reconstruction represents human metabolism in general and includes 3,765 genes, 3,160 metabolites, and 8,181 metabolic reactions. In order to study specific cell types and their associated diseases we developed a computational platform, INIT, that enables reconstruction of cell type specific GEMs from HMR2.0 using different types of omics data, e.g. proteomics data or RNAseq data. In this presentation HMR2.0 and INIT will be presented. It will further be demonstrated how high quality models for adipocytes, hepatocytes and myocytes could be used for studies of how these cell types respond to obesity, NAFLD, NASH and type-2-diabetes. By combining these cell type specific GEMs with high-throughput experimental data, in particular RNAseq data, it will be demonstrated how metabolic reprogramming is occuring in these cell types in response to disease development. It will further be shown how HMR2.0 and INIT can be used for reconstruction of functional metabolic networks in cancer cells, and how analysis of these metabolic networks can be used to gain insight into metabolic reprogramming occurring in connection with cancer progression, examplified for clear cell renal carcinoma. It will also be shown how patient specific proteomics data can be used for reconstruction of personalized GEMs for hepatocellular carcinoma, and that these personalized GEMs offer opportunity for improved therapy compared with the use of a generic model.

Vljudno vabljeni! / Kindly invited!

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