Model-driven analysis of cancer-associated alterations in lipid profile by developing novel algorithm-based metabolic network reconstruction

It is increasingly clear that significant alterations in the lipid profile of cancer cells accompany tumor progression and metastasis. These changes are induced by a metabolic reprogramming which is aimed to enhance malignant phenotype in cancer cells.

In this context, genome-scale metabolic models (GSMM) have emerged as a valuable platform to integrate different omic data to study cancer metabolism from a holistic perspective. However, far too often lipid associated pathways are poorly annotated in these metabolic networks which limits the scope of GSMM-based methods to study the altered tumor metabolism.

Thus, it is imperative to develop novel computational tools that allowing a better integration of high-throughtput lipidomic data into the current GSMM reconstruction analyses. It is expected that these computational tools will enable a more in-dept understanding of the metabolic mechanisms underlying lipid profiles alterations of multifactorial diseases with a strong metabolic component such as cancer with potential clinical applications

The project: The project is aimed to develop and test a computational framework for automatically expand and improve the lipid-associated metabolic pathways of the current computational models of cell metabolism.

As a case of concept we will study the metabolic alterations associated to the chronic exposure to Endocrine disruptors (ED) in prostate cancer . To achieve this aim the student will apply different strategies to integrate transcriptomic, metabolomic and lipidomic data into a computational analysis of the whole metabolism. This study will provide a holistic view of the molecular processes and mechanisms underlying tumor progression and metastasis associated to the chronic exposure to EDs in prostate cancer which ultimately can unveil potential therapeutic targets. This project is a joint venture between Prof. Lars Keld Nielsen lab (DTU, Denmark) and Prof. Romà Tauler's group (IDAEA-CSIC, Spain) that will be under the direct supervision of Dr. Igor Marín.

The role: The successful appointee will develop and apply a pipeline based on constraint-based methods to expand and improve the lipid-associated metabolic pathways of a current GSMM. Secondly, the student will integrate and analyze transcriptomic, metabolomic and lipidomic data from DU145 before and after a chronic exposure to different EDs. Finally the results will be analyzed and interpreted in order to describe the evolutionary mechanisms underlying the metabolic reprogramming associated to the chronic exposure to EDs in prostate cancer

Criteria: We are seeking for a highly motivated, independent, and well organized person, who is passionate about computational biology. Background on biostatistics and previous knowledge of some programming language (R, Matlab, Python, ...) are desirable but not exclusive.

Those students who are interested in join this project can contact to Igor Marín (igmar@biosustain.dtu.dk)