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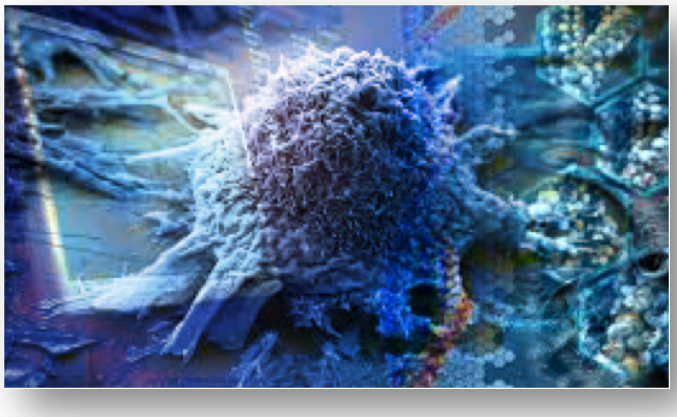


MISSION

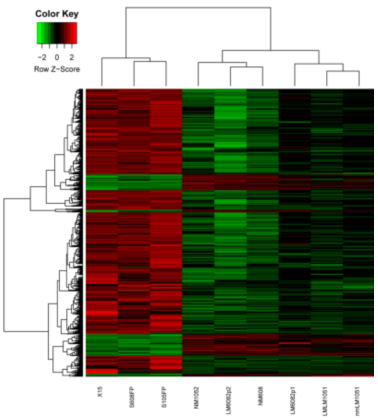
Using multidisciplinary approaches, based on computational and experimental competences, to identify anticancer targets and opportunities for drug repurposing.

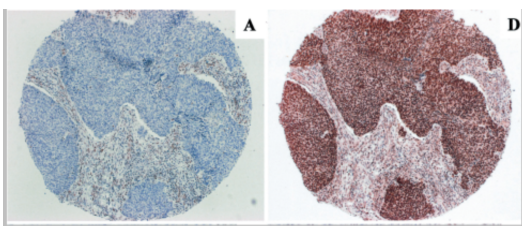
RESEARCH INTERESTS

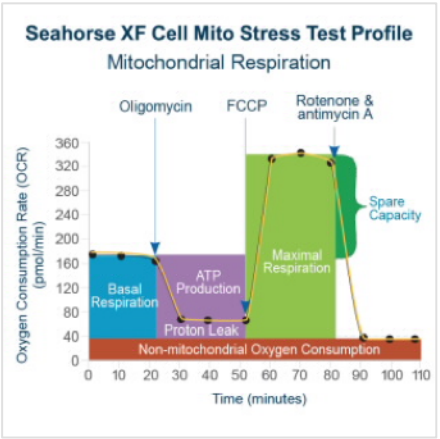
CANCER METABOLISM AND METASTASES

To investigate key metabolic vulnerabilities supporting metastases and immune-tolerance in breast cancer.

This project aims at identifying targets and therapeutics opportunities to reduce the risk of metastases in breast cancer and to inhibit metastases growth. To this purpose, we are investigating the complex metabolic adaptations of metastatic cancer cells and their interaction with the tumour microenvironment and the immune cells. Our methodologies involved both metabolomics profiles of cells, computational Genome-Scale Metabolic Modelling (GSMM) of cell metabolism through transcriptional gene expression profiles, and determination of immune-scores of tumours.







COMPUTER-AIDED DRUG REPOSITIONING IN ONCOLOGY
Identifying and re-using old drugs against fundamental anticancer targets.

This project is based on the development of methods and algorithm to extract information from the vast amounts of data generated by High Throughput technologies, such as trascriptomics, genomics, metabolomics, and epigenomics. The aim of the project is to elucidate biological mechanisms at the 'network' level, i.e. how genes, proteins, non-coding RNAs and metabolites interact with each other to perform a specific function in cancer cells. Furthermore, we aim at developing and applying experimental protocols and computational algorithms to elucidate mechanisms of cancer diseases and repurpose, among FDA-approved drugs, novel and targeted therapeutics with antitumor activity. This approach, called drug repurposing - i.e. the use of old drugs, already in clinical use, for a different therapeutic indication - is an appealing strategy to improve cancer therapy. Such computer-aided drug repurposing takes advantage of the use of big-data, data meaning, machine learning algorithms, and computational modelling. All these offer unprecedented knowledge of the biological mechanisms of cancers and drugs' modes of action, providing extensive availability for both disease-related data and drugs-related data. This offers the unique opportunity to generate, with time and cost-effective approaches, computational drug networks to predict, in-silico, the efficacy of approved drugs against relevant cancer targets, as well as to select better responder patients or disease' biomarkers.