

## Tecnologie Convergenti per i Sistemi Biomolecolari

## Converging Technologies for Biomolecular Systems

<b>Progetto di ricerca Research project</b>	<i>"Systems metabolomics Approaches in Biomedical Research"</i>
<b>Tipo/Type</b>	Borsa finanziata dal Dipartimento di Biotecnologie e Bioscienze
<b>Borse/Scholarships</b>	1
<b>Abstract</b>	<p>Changes in metabolite levels and their corresponding fluxes are sensitive indicators of biological systems' responses to genetic and environmental perturbations. Systems metabolomics integrates experimental and computational approaches to uncover the design principles of metabolic regulation. In this context The SYSBIO research network aims at utilizing systems metabolomics to:</p> <ul style="list-style-type: none"> <li>• Integrate metabolism, with cell mass growth and cell cycle progression into a low-granularity, multiscale computational model (from cell to population) to offer a framework for organizing molecular knowledge and predicting cell phenotypes under various genetic and environmental conditions. This will likely allow to refine predictions from the cellular to the molecular level by incorporating molecular details of cellular subsystems.</li> <li>• Investigate the links between metabolism and important physiological properties, such as cell proliferation or metastatic spread to establish a solid foundation for developing personalized precision oncology therapies.</li> <li>• Develop personalized mathematical models of metabolism that synergize with AI and deep learning methods to identify key regulatory mechanisms to be validated using advanced cellular models, including patient-derived cell lines, spheroids, organoids, organs-on-chip, and xenotransplants (PDXs).</li> </ul> <p>The objectives of this PhD project include:</p> <ol style="list-style-type: none"> <li>1. Use the coarse-grained mathematical model described above for massive <i>in silico</i> experiments on populations describing both steady-state exponential growth and nutritional/genetic perturbations.</li> <li>2. Develop reliable and reproducible 3D cancer models of solid tumors (such as heterotypic spheroids containing various cell types alongside ECM components) to investigate the morpho-functional and metabolic alterations occurring in these cellular models through the integrative application of spatial transcriptomic and metabolomic analyses, metabolic flux analysis, and high-content analysis/quantitative imaging using confocal and multi-photon microscopy.</li> <li>3. Integrate multi-omics data, including gene expression, proteomics, and metabolomics, at the single-cell and spatially resolved levels to develop a biologically informed framework that incorporates metabolic network architecture.</li> </ol>
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