Abstract:
Human metabolism, an essential and highly organized process, which is required to run and maintain cellular processes, can be described as a complex and interconnected network of metabolic pathways. Computational systems biology provides a suitable framework to study the mechanisms and interactions of this network and to address questions that are difficult to reproduce in vitro or in vivo. In this presentation two computational strategies which help to investigate aspects of human metabolism and metabolic-related disorders are presented.

In the first part, we introduce a mathematical model of folate-mediated one-carbon metabolism in the cytoplasm and subsequently in the nucleus. A hybrid-stochastic framework is applied to investigate the behavior and stability of the complete metabolic network in response to genetic and nutritional factors.

In the second part, we focus on metabolic syndrome, a highly prevalent cluster of metabolic disorders. We develop a computational workflow based on network analysis to characterise underlying molecular mechanisms of the disorder and to explore possible novel therapeutic strategies by means of drug repurposing.

Supervisor: Corrado Priami