Programme & Abstracts

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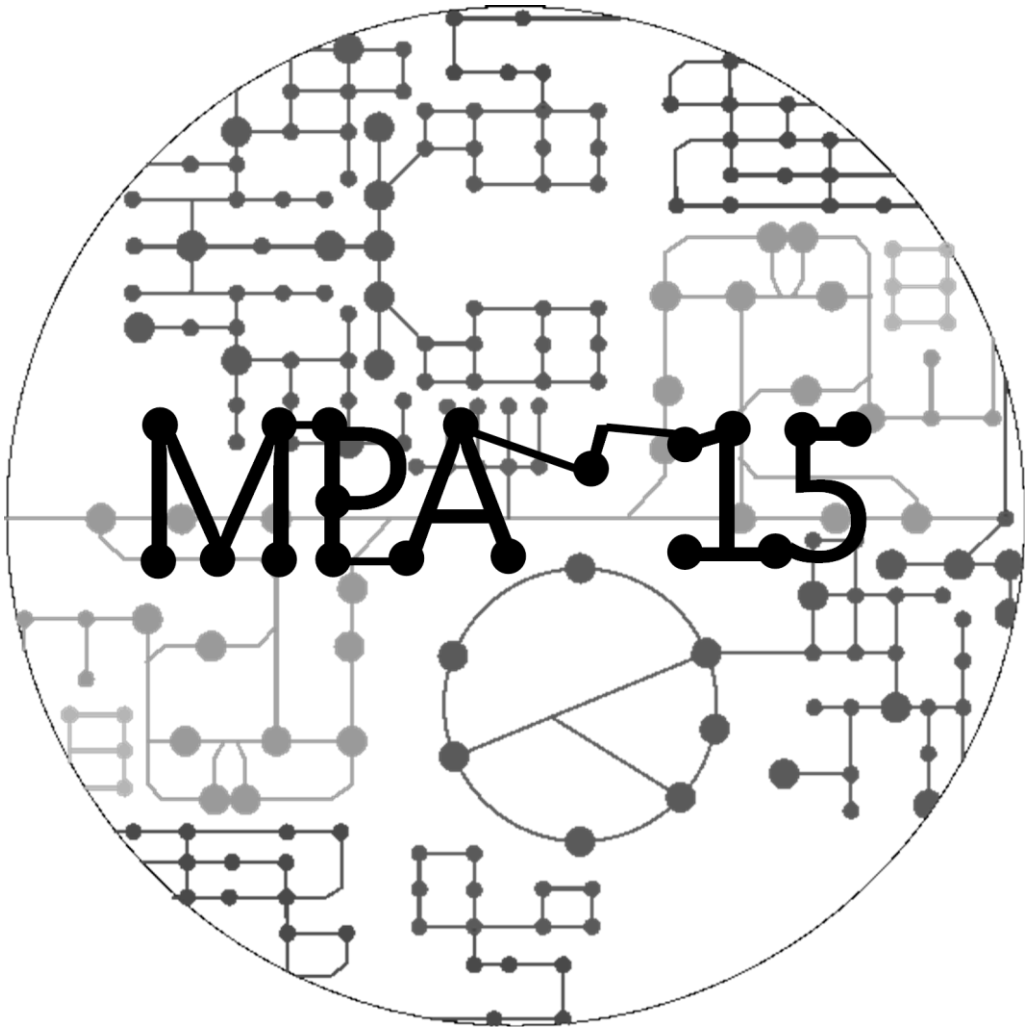

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Transcriptional vs post-transcriptional regulation of the central carbon metabolism of *E. coli*

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Transcriptomics data are currently one of the most available types of large-scale biological data. A large number of methods have been developed to improve constraint-based simulations using these data. We recently performed a systematic comparison of these methods and observed that, at least for central carbon metabolism, there is no significant improvement in the prediction of flux distributions when gene expression data is used. These results are consistent with recent studies, in different organisms, showing that central carbon metabolism is predominantly regulated at post-transcriptional levels. Central carbon metabolism provides the precursors for the production of multiple compounds used in industrial biotechnology. Hence, it is the main target for intervention in most rational strain design strategies. However, its complexity is still not completely understood. In this work, we analyze the role of allosteric regulation, one of the main mechanisms of post-transcriptional regulation, for the control of central carbon metabolism. We extend a model of central carbon metabolism of *E. coli* with allosteric interactions, revealing a hidden topology in metabolic networks. We use this model to integrate a multi-*omic* dataset containing transcript, protein, flux and metabolite levels to further dissect the contribution of different types of regulation for metabolic flux control in these central pathways. Situations of predominant allosteric control could be identified, highlighting the importance of this kind of regulation in central carbon metabolism.