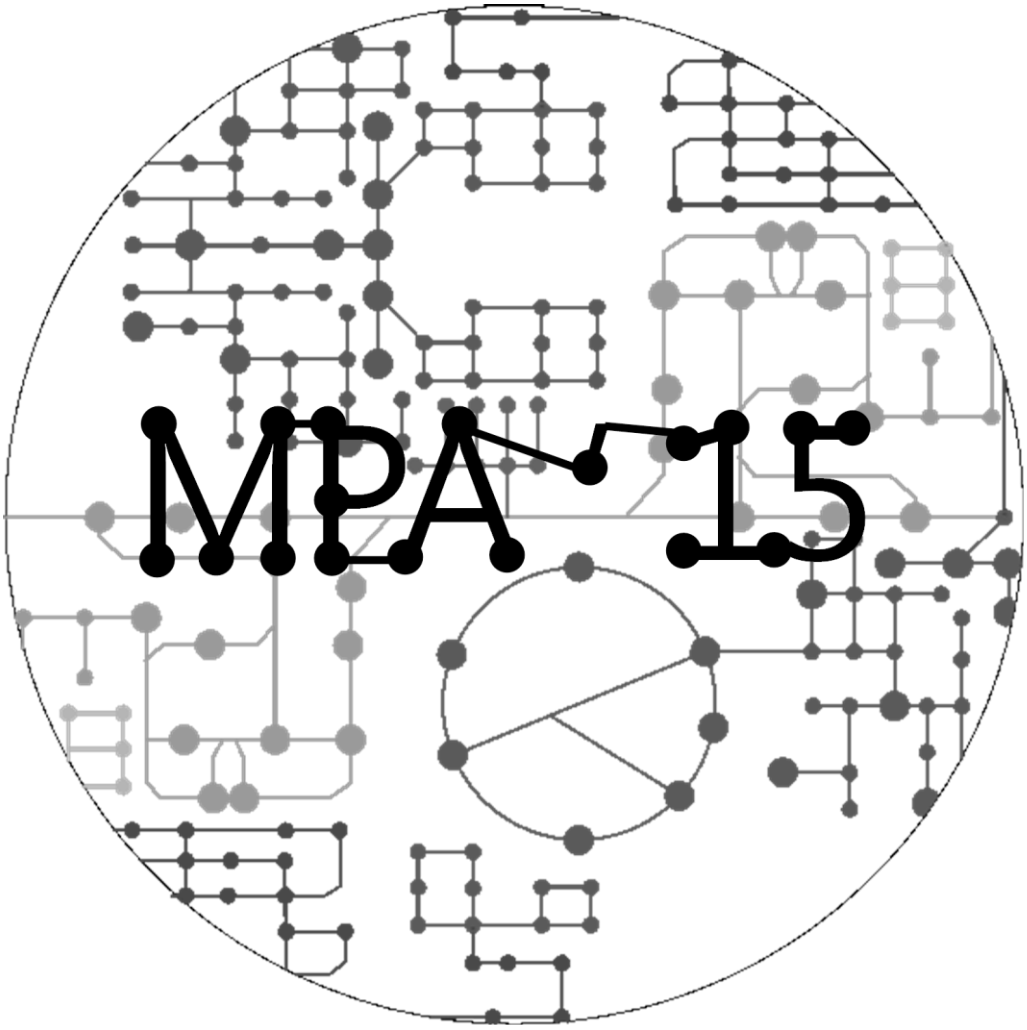
Programme & Abstracts

Metabolic Pathway Analysis 2015

8-12 June
Braga – Portugal



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Reconciling gene expression data with regulatory network models

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The reconstruction of genome-scale metabolic models from genome annotations has become a routine practice in Systems Biology research. The potential of metabolic models for predictive biology is widely accepted by the scientific community, but these same models still lack the capability to account for the effect of gene regulation on metabolic activity. Our focus organism, *Bacillus subtilis* is most commonly found in soil, being subject to a wide variety of external environmental conditions. This reinforces the importance of the regulatory mechanisms that allow the bacteria to survive and adapt to such conditions.

We introduce a manually curated regulatory network for *Bacillus subtilis*, tapping into the notable resources for *B. subtilis* regulation. We propose the concept of Atomic Regulon, as a set of genes that share the same “ON” and “OFF” gene expression profile across multiple samples of experimental data. Atomic regulon inference uses prior knowledge from curated SEED subsystems, in addition to expression data to infer regulatory interactions. We show how atomic regulons for *B. subtilis* are able to capture many sets of genes corresponding to regulated operons in our manually curated network. Additionally, we demonstrate how atomic regulons can be used to help expand/ validate the knowledge of the regulatory networks and gain insights into novel biology.