

Towards the digital *Escherichia coli*

Pierre Millard

Role of post-transcriptional regulation in control of *E. coli* metabolism

Modelling of *E. coli* metabolism



2007

BSc in Biochemistry and Molecular biology

2009

MSc in Structural biochemistry, Proteomics and Metabolomics

2012

PhD in Systems biology of micro-organisms

CJS fellowship, INRA

LISBP, INSA of Toulouse, France

2013

Post doctoral position in Systems biology

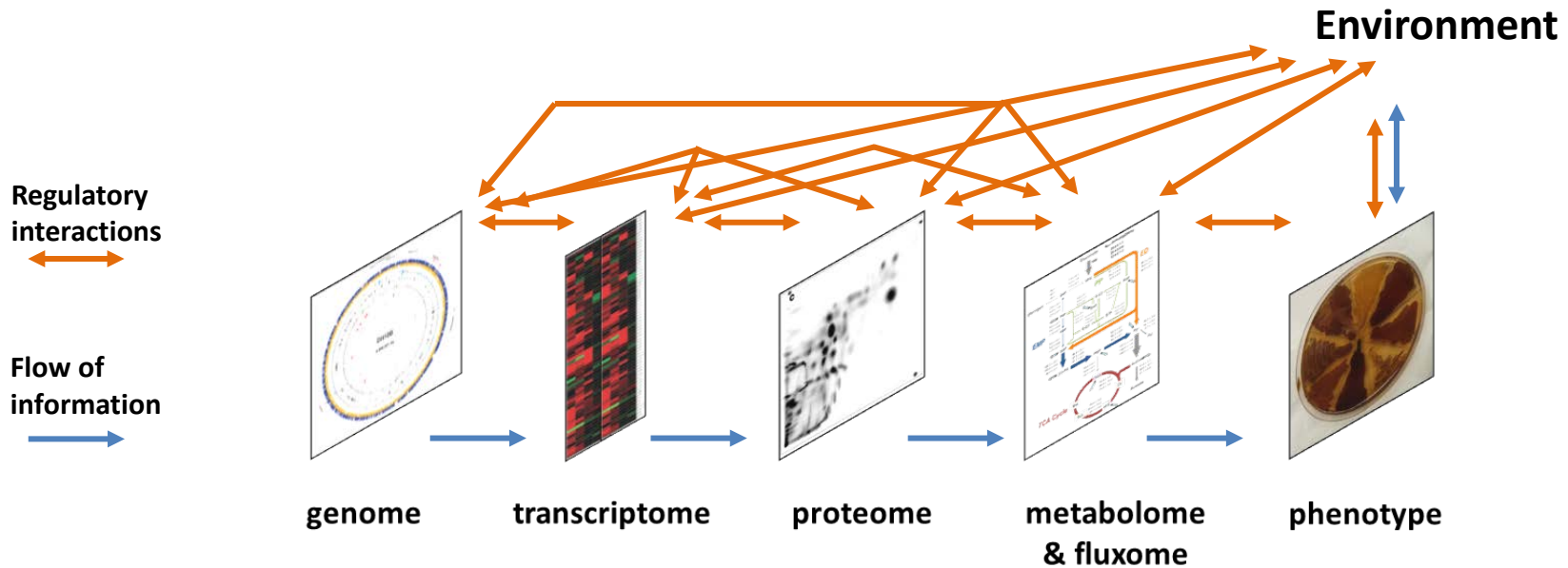
CJS fellowship, INRA

Agreenskills fellowship

MCISB, University of Manchester, UK
LISBP, INSA of Toulouse, France



Why developing a model of *Escherichia coli* metabolism?

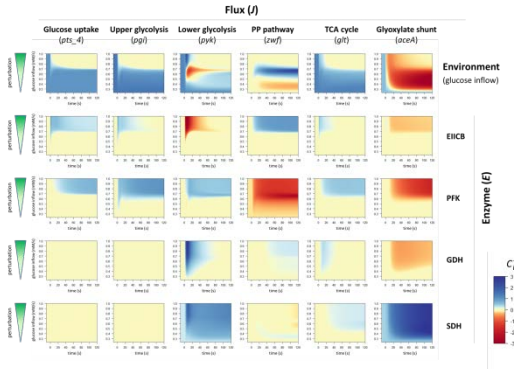
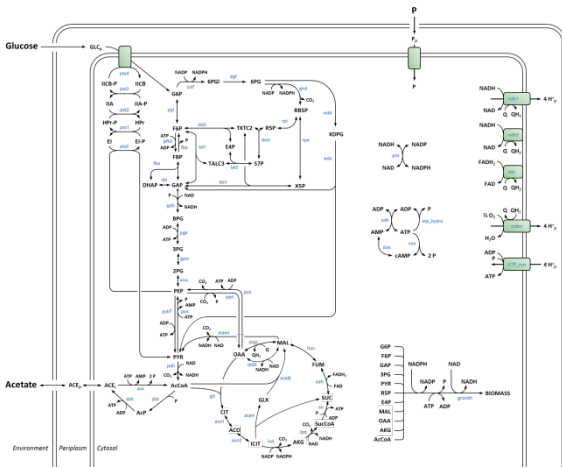


Mathematical models are needed to explain and predict how cells respond to their environment

Expected impacts:

- in **biology in general**, to understand how cells respond to the environment
- in **biotechnology**, to enable the rational design of production strains
- in **biomedecine**, to develop new strategies to deal with food-borne infections

- i. **Build a core model: detailed kinetic model of the central metabolism of *E. coli***
- ii. Include signalling and gene regulation for specific external perturbations (i.e. environmental changes)
- iii. Expand this model to genome scale



Data

≈ 100 publications

Mathematical description

75 ODEs

440 parameters

Dynamic metabolic control analysis

Model topology

3 compartments

60 metabolites

70 proteins

75 reactions

Simulations of the metabolic response to nutritional perturbations

Understand the metabolic response to environmental changes

