

Inference and modelling of regulatory transcriptional networks from transcriptomic data

The design of organisms hosting synthetic biological devices will require an appropriate characterisation and modelling of the corresponding chassis. We will analyse several transcriptomic data to characterise and model a large portion of the promoters of a cyanobacterial chassis. The methodology inputs previous knowledge of transcription factors to infer promoter regulation from microarray data. We consider that the promoters may have a combinatorial regulation by transcription factor complexes. We use our model to make prediction of protein expression that we compare with experimental data. Our methodology will contribute to the design of a cyanobacterial chassis able to accommodate synthetic circuits for biofuel production.