Computational Approaches to Study Metabolism for C1 Bioconversion

김동혁†
UNIST
(1234@1234.com†)

Fossil fuels have the finite reservation, which necessitated developing renewable energy sources. Bioenergy became one of powerful renewable energy sources with recent advances in synthetic biology encompassing systems biology and metabolic engineering. This enable us to engineer and/or create tailor made microorganisms to produce alternative biofuels for the future bio-era. The efficient transformation of biomass to bioenergy requires maximum performance of cellular metabolism to be designed and engineered. Toward this end, investigation of bacterial metabolism with systems biology became one of powerful tools. Here, genome-scale metabolic models for industrially relevant methylotroph and Clostridium will be covered on how these models can be used for explanatory and predictive capabilities in understanding and designing bacterial metabolism. In addition, machine-learning based investigation of uncharacterized transcription factors will be discussed. E. coli, the most-well studied microorganism, still has 20% of its transcription factors unknown of their functions.