

Reaction networks as languages for biology computing

Jinsu Kim¹

1) *Department of Mathematics, POSTECH, Pohang 37673, KOREA*

Corresponding Author: Jinsu Kim, jinsukim@postech.ac.kr

ABSTRACT

Biological computing (or natural computing) refers to performing computational tasks using biochemical species such as DNA and proteins. It is believed that biology computing could offer solutions to the bottlenecks faced by traditional computational systems—particularly energy efficiency and massive parallelization. In this talk, we explore biology computing from a mathematical perspective using reaction networks as a computational language. Reaction networks are mathematical constructs that graphically represent the interactions between biochemical species. They enable us to analyze theoretical aspects of biological computing. Using this formalism, we will address open mathematical problems in the field, including stability of systems, convergence rates, the range of functions that biochemical systems can implement, approaches to managing noise.