Modeling the multi-scale mechanisms of macromolecular resource allocation

As microbes face changing environments, they dynamically allocate macromolecular resources to produce a particular phenotypic state. Broad 'omics' data sets have revealed several interesting phenomena regarding how the proteome is allocated under differing conditions, but the functional consequences of these states and how they are achieved remain open questions. Various types of multi-scale mathematical models have been used to elucidate the genetic basis for systems-level adaptations. In this review, we outline several different strategies by which microbes accomplish resource allocation and detail how mathematical models have aided in our understanding of these processes. Ultimately, such modeling efforts have helped elucidate the principles of proteome allocation and hold promise for further discovery.