

A metabolic approach to social interactions and microbial community robustness

Microbial communities drive processes ranging from human health to global nutrient cycling. There is also great hope that the power of microbial consortia can be harnessed for a wide range of industrial applications. We use genome-scale metabolic models and model laboratory communities to investigate how the physiology of cells generates social interactions to shape the content, function and dynamics of microbial communities. We computationally tested the impact that all possible single-gene knockouts have on community properties, and discovered that communities were more robust to genetic perturbations when bacteria were cooperating than when they were competing. In contrast, we show that when communities are disturbed with antibiotics cooperation makes species more sensitive to perturbation. We hope to use bottom-up approaches such as these to understand, predict and manage diverse microbial systems.