Metabolic optimization in a minimal photosynthetic picocyanobacterium

Submitted by: John Casey, Jens B. Nielsen, Saeed Shoaie, Boyang Ji, Adil Mardinogu, Partho Sarathi Sen and David Karl

Earth's most prolific photosynthetic organism, the tiny marine cyanobacterium *Prochlorococcus*, accounts for much of ocean productivity and is therefore relevant to global carbon dynamics. High light adapted *Prochlorococcus* strains capitalize on numerous physiological adaptations which allow them to thrive in the most nutrient-depleted surface oceans; however, their metabolism has not been studied in detail. We constructed a whole genome-scale metabolic network (iJCMED4) for the high light adapted strain MED4 to evaluate its metabolic niche. By combining transcriptomic, proteomic, and exometabolomic data with physiological measurements, we were able to employ several constraint-based modeling techniques to simulate MED4 metabolism under a wide range of conditions experienced in the natural environment. Our simulations of growth, nutrient utilization, photosynthetic performance, and metabolite excretion matched quite closely with experimental results from the MED4 literature, suggesting the model is suitable for simulations. Using phenotype phase plane analysis, we also aligned MED4 phenotypes within a range of nutrient concentrations and light intensities typical of Station ALOHA, and found that optimal growth was possible even at extremely low nutrient concentrations. Our results suggest that the MED4 metabolic network could operate near several theoretical optima at Station ALOHA.
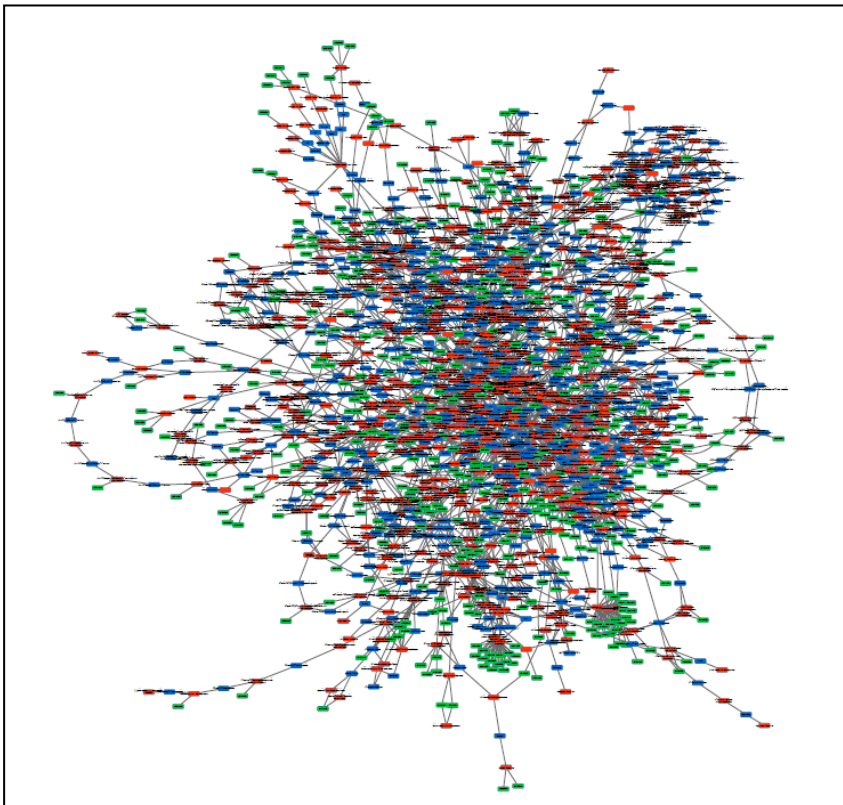

Figure. iJCMED4 network of gene (green), enzyme (red), and metabolite (blue) associations.