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Changes in metabolic modules under environmental variations

EIVIND ALMAAS, Lawrence Livermore National Laboratory

During the last few years, network approaches have shown great promise as a tool to both analyze and provide understanding of complex systems as disparate as the world-wide web and cellular metabolism. Much effort has been focused on characterizing topological properties of such systems. However, in order to develop detailed descriptions of complex networks, we need to look beyond their topology and incorporate dynamical aspects. The cellular metabolism, where nodes correspond to metabolites and links indicate chemical reactions, is an excellent model system where theoretical predictions can be compared with experimental results. I will present recent insights into the principles governing the modular utilization of the cellular metabolism [1,2,3]. We find that, while most metabolic reactions have small fluxes, the metabolism's activity is dominated by an interconnected sub-network of reactions with very high fluxes [1]. For the bacteria *H. pylori* and *E. coli* and the yeast *S. cerevisiae*, the metabolism responds to changes in growth conditions by reorganizing the rates of select reactions predominantly within this high-flux backbone. Furthermore, these networks are organized around the metabolic core – a set of reactions that are always in use [2]. Strikingly, the activity of the metabolic core reactions is highly synchronized, and the core reactions are significantly more essential and evolutionary conserved than the non-core ones.

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