[P15] Biconnectivity of the cellular metabolism: A cross-species study and its implication for human diseases

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The maintenance of stability during perturbations is essential for living organisms, and cellular networks organize multiple pathways to enable elements to remain connected and communicate, even when some pathways are broken. Here, we evaluated the biconnectivity of the metabolic networks of 506 species in terms of the clustering coefficients and the largest biconnected components (LBCs), wherein a biconnected component (BC) indicates a set of nodes in which every pair is connected by more than one path. Via comparison with the rewired networks, we illustrated how biconnectivity in cellular metabolism is achieved on small and large scales. Defining the biconnectivity of individual metabolic compounds by counting the number of species in which the compound belonged to the LBC, we demonstrated that biconnectivity is significantly correlated with the evolutionary age and functional importance of a compound. The prevalence of diseases associated with each metabolic compound quantifies the compounds vulnerability, i.e., the likelihood that it will cause a metabolic disorder. Moreover, the vulnerability depends on both the biconnectivity and the lethality of the compound. This fact can be used in drug discovery and medical treatments.