Laurent Tichit (MMG-IML)

Résumé

Large networks such as protein-protein interaction networks are usually extremely difficult to understand as a whole. We developed two novel modularity-based clustering algorithms for weighted graphs: FT and TFit. Their results are compared both on random graphs and on benchmarks where the optimal partition is known. Both algorithms are implemented in ModClust, a Cytoscape plugin for large network modularity-based clustering. The aim of this plugin is first to establish classes of high density edges. It also allows to understand the relations between these classes, and how they are assembled within the whole graph. It can be used to predict new protein functions