Clust&See: a Cytoscape plugin for identification, visualization and manipulation of network clusters
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Large networks, such as protein-protein interaction networks, are extremely difficult to analyze as a whole. We developed Clust&See, a Cytoscape [1] plug-in dedicated to the identification, visualization and analysis of clusters extracted from such networks.

Since visualizing and manipulating graph partitions constitute an important issue regarding the subsequent biological interpretation, a real improvement in this direction is desirable.

For this, we propose herein Clust&See, a real interactive data analysis tool allowing to:

• automatically decompose a network
• visualize the obtained partition as a quotient graph
• manipulate the clusters for further detailed visualization and analyses
• iteratively decompose chosen clusters

Clust&See provides:

• (i) the use of different, recently developed validated graph clustering algorithms: TFit [2] outputs a strict partition while OCG [3] outputs a set of overlapping classes
• (ii) the ability to visualize a partition as a quotient graph
• (iii) tools for investigating the relationships between vertices and clusters as well as their organization within the whole graph

This software will be demoed to partition a functional interactome core, consisting of proteins linked by their interactions.

In summary, the originality of Clust&See lies in its ability to provide users with a complete tool for the creation and investigation of clusters and their relationships.

The current version of the Java plugin, tested on Cytoscape 2.7 and 2.8, is available on http://tagc.univ-mrs.fr/tagc/index.php/clustnsee

