

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>

[1] Shannon, P., Markiel, A., Ozier, O., Baliga, NS., Wang, JT., Ramage, D., Amin, N., Schwikowski, B. and Ideker, T. (2003) Cytoscape: A software environment for integrated models of biomolecular interaction networks, *Genome Research*, 13(11), 2498–2504.

[2] Gambette, P. and Guénoche, A. (2011) Bootstrap Clustering for Graph Partitioning. *RAIRO-Operations Research*, 45(4), 339-352.

[3] Becker, E., Robisson, B., Chapple, C.E., Guénoche, A. Brun, C. (2012) Multifunctional proteins revealed by overlapping clustering in protein interaction network. *Bioinformatics*, 28(1), 84-90.