



HAL
open science

Clust&See: A Cytoscape plugin for the identification, visualization and manipulation of network clusters

Lionel Spinelli, Philippe Gambette, Charles E. Chapple, Benoît Robisson, Anaïs Baudot, Henri Garreta, Laurent Tichit, Alain Guénoche, Christine Brun

► To cite this version:

Lionel Spinelli, Philippe Gambette, Charles E. Chapple, Benoît Robisson, Anaïs Baudot, et al.. Clust&See: A Cytoscape plugin for the identification, visualization and manipulation of network clusters. *BioSystems*, 2013, 113 (2), pp.91-93. 10.1016/j.biosystems.2013.05.010 . hal-00832028v2

HAL Id: hal-00832028

<https://hal.science/hal-00832028v2>

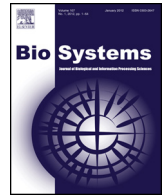
Submitted on 30 Jun 2013

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial - NoDerivatives 4.0 International License



Clust&See: A Cytoscape plugin for the identification, visualization and manipulation of network clusters ^{☆,☆☆}



Lionel Spinelli ^{a,d}, Philippe Gambette ^{a,d,1}, Charles E. Chapple ^{b,d}, Benoît Robisson ^{b,d}, Anaïs Baudot ^{a,d}, Henri Garreta ^{c,d}, Laurent Tichit ^{a,d}, Alain Guénoche ^{a,d}, Christine Brun ^{b,d,e,*}

^a Institut de Mathématiques de Luminy, CNRS – FRE3529, Avenue de Luminy, 13288 Marseille Cedex 9, France

^b Techniques Avancées pour le Génome et Clinique, INSERM – U1090, Avenue de Luminy, 13288 Marseille Cedex 9, France

^c Laboratoire d'Informatique Fondamentale de Marseille, CNRS – UMR7279, Avenue de Luminy, 13288 Marseille Cedex 9, France

^d Aix-Marseille Université, Campus de Luminy, 13288 Marseille Cedex 9, France

^e CNRS, France

ARTICLE INFO

Article history:

Received 3 April 2013

Received in revised form 22 May 2013

Accepted 22 May 2013

Keywords:

Interaction networks

Graph partitioning

Clustering

Visualization

ABSTRACT

Background and scope: Large networks, such as protein interaction networks, are extremely difficult to analyze as a whole. We developed Clust&See, a Cytoscape plugin dedicated to the identification, visualization and analysis of clusters extracted from such networks.

Implementation and performance: Clust&See provides the ability to apply three different, recently developed graph clustering algorithms to networks and to visualize: (i) the obtained partition as a quotient graph in which nodes correspond to clusters and (ii) the obtained clusters as their corresponding sub-networks. Importantly, tools for investigating the relationships between clusters and vertices as well as their organization within the whole graph are supplied.

© 2013 The Authors. Published by Elsevier Ireland Ltd. All rights reserved.

1. Introduction

The field of functional genomics is producing a large amount of data, often represented as interaction networks – or undirected graphs. These graphs typically contain thousands of vertices, rendering the extraction of pertinent biological information a daunting task. Graph partitioning or clustering methods have been used to highlight groups of densely connected vertices (Aittokallio and Schwikowski, 2006) which, in the field of protein interactions, often correspond to clusters of proteins involved in the same cellular process(es).

Cytoscape is a popular and versatile software platform (Shannon et al., 2003) for network visualization and analysis. While a number

of Cytoscape plugins such as ClusterMaker (Morris et al., 2011) or ClusterOne (Nepusz et al., 2012) can identify clusters from graphs, they mainly focus on visualizing the obtained clusters individually and independently as subnetworks to further investigate their node composition. However, exploring the relationships between clusters in detail is as important as studying their internal composition. Indeed, while proteins involved in the same process(es) interact within clusters, links between clusters correspond to crosstalk between processes. Communication between processes can also be performed by proteins belonging to several clusters. Consequently, considering the links between network clusters permits a better understanding of the modularity of biological networks and the functional transitions imposed by the integrative organization levels, from proteins to functional modules to entire systems.

To fill this gap, we have developed Clust&See, a truly interactive tool that can (i) automatically decompose a network into clusters; (ii) visualize those clusters as metanodes linked by several types of edges/relationships; (iii) manipulate the clusters for further detailed visualization, analyses and comparisons.

2. Software description

Clust&See is a Cytoscape plugin developed for Cytoscape version 2.8. Some GUI elements have been reused from code

[☆] This is an open-access article distributed under the terms of the Creative Commons Attribution-NonCommercial-No Derivative Works License, which permits non-commercial use, distribution, and reproduction in any medium, provided the original author and source are credited.

^{☆☆} Availability: <http://tagc.univ-mrs.fr/tagc/index.php/clustnsee>

* Corresponding author at: TAGC, U1090 Inserm-AMU, Parc Scientifique de Luminy case 928, 163, Avenue de Luminy, 13288 Marseille Cedex 09, France. Tel.: +33 491828712.

E-mail address: brun@tagc.univ-mrs.fr (C. Brun).

¹ Current address: Laboratoire d'Informatique Gaspard-Monge, CNRS – UMR8049, Cité Descartes, Bât Copernic – 5, bd Descartes, Champs sur Marne, 77454 Marne-la-Vallée Cedex 2, France.

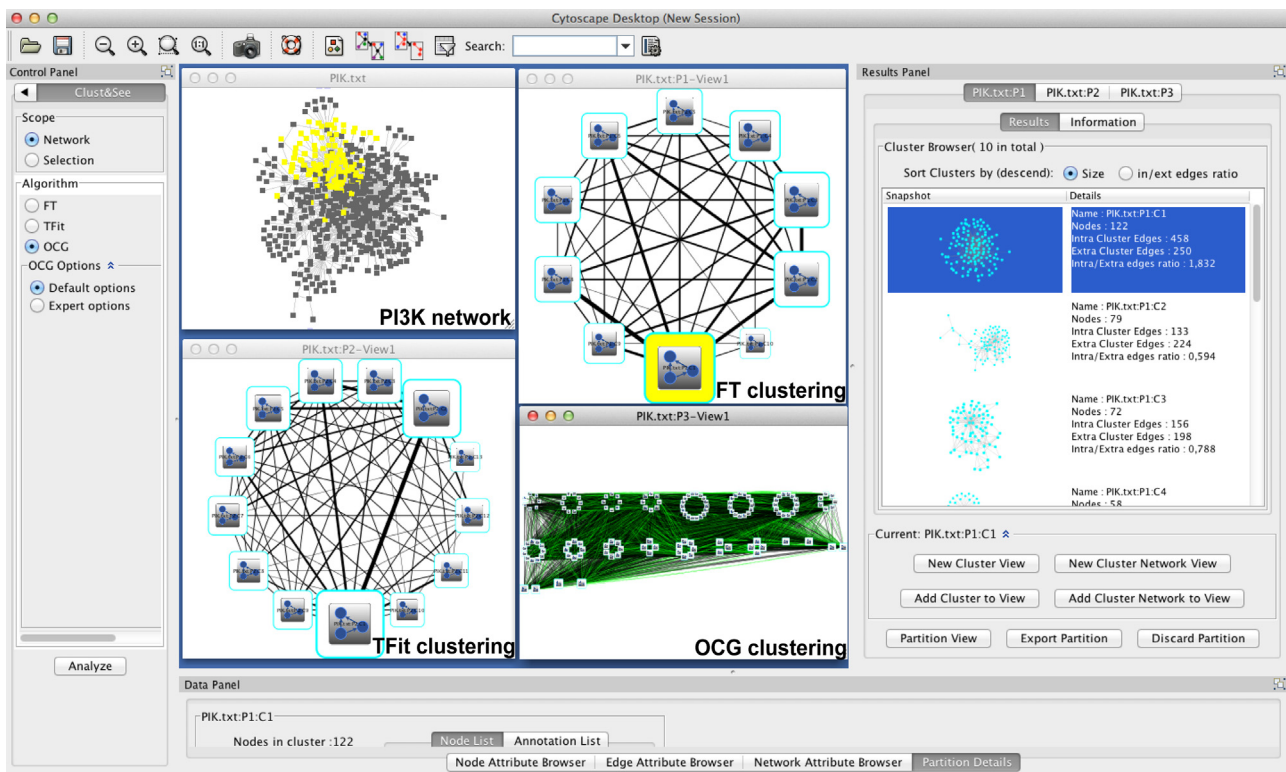


Fig. 1. Quotient graphs obtained when clustering the PI3K network with the 3 implemented algorithms.

from the MCODE (Bader and Hogue, 2003) and ClusterViz (<http://apps.cytoscape.org/apps/clusterviz>) plugins.

2.1. Implemented graph clustering algorithms

To date, three clustering algorithms based on the optimization of Newman's modularity (Newman, 2004) have been implemented in Clust&See. While TFit and FT lead to disjoint clusters, OCG leads to overlapping ones:

- (1) FT (for Fusion-Transfer) (Guénoche, 2011) is an ascending hierarchical method fusing two clusters iteratively if the fusion results in a modularity gain. The algorithm starts with singletons and stops when further fusions lead to a loss in modularity. Modularity is then further optimized by transferring vertices from one cluster to another.
- (2) TFit (for iterated Transfer-Fusion) (Gambette and Guénoche, 2012) is a multi-level algorithm in which a vertex transfer procedure is performed at every level. Level one corresponds to the network. While modularity increases, each node is associated to its best adjacent cluster. Classical transfers are then performed and a quotient graph is computed; clusters then become the nodes of the next level to be further optimized.
- (3) OCG (for Overlapping Cluster Generator) (Becker et al., 2012) is an ascending hierarchical method fusing two clusters at each step. Initially, an overlapping class system formed by either (i) maximal cliques, or (ii) edges or (iii) centered cliques is built. These classes are then merged, while modularity increases, resulting in overlapping clusters.

Performance values in terms of time and memory of the three algorithms are provided as Supplementary Material. Clustering results produced by Clust&See can be exported as text files, and subsequently re-imported and re-mapped to the original network, avoiding repetitive computation. Importantly, results from

external clustering tools can be analyzed with Clust&See. Currently, the R package "Linkcomm" (Kalinka and Tomancak, 2011), in which the LinkCommunities (Ahn et al., 2010) and OCG (Becker et al., 2012) algorithms are implemented, provides output files that are compatible with Clust&See (for further information on supported formats, see the online Documentation, <http://tagc.univ-mrs.fr/tagc/index.php/software/clustnsee/clustnseedocumentation>). Finally, the modular structure of Clust&See makes it easy to implement other clustering algorithms directly in Java.

2.2. Visualization and analysis

The clustering results can be visualized in Clust&See as a quotient graph in which clusters are represented as metanodes whose width is proportional to the number of their constituent vertices (Fig. 1). Metanodes can be linked by two types of "metaedges", one (black) whose width is proportional to the number of interactions between their vertices and, most importantly, one (green) whose width is proportional to the number of vertices shared by overlapping clusters computed by algorithms such as OCG. A docked Result Panel provides a sortable list of the clusters in which each cluster's subnetwork is displayed along with its relevant features, such as size or edge density.

Novel views, into which clusters of interest can be successively loaded, can be created on demand. An "Expand/collapse nodes" function allows the user to switch from the cluster/metanode representation to the corresponding subnetwork of vertices and *vice versa* (Fig. 2). Details provided in the Data Panel upon selection of the different objects (vertices, edges) facilitate the study of the relationships between clusters. The composition of each metanode is provided as well as, importantly, the composition of the metaedges representing the shared objects (nodes or edges) between cluster pairs.

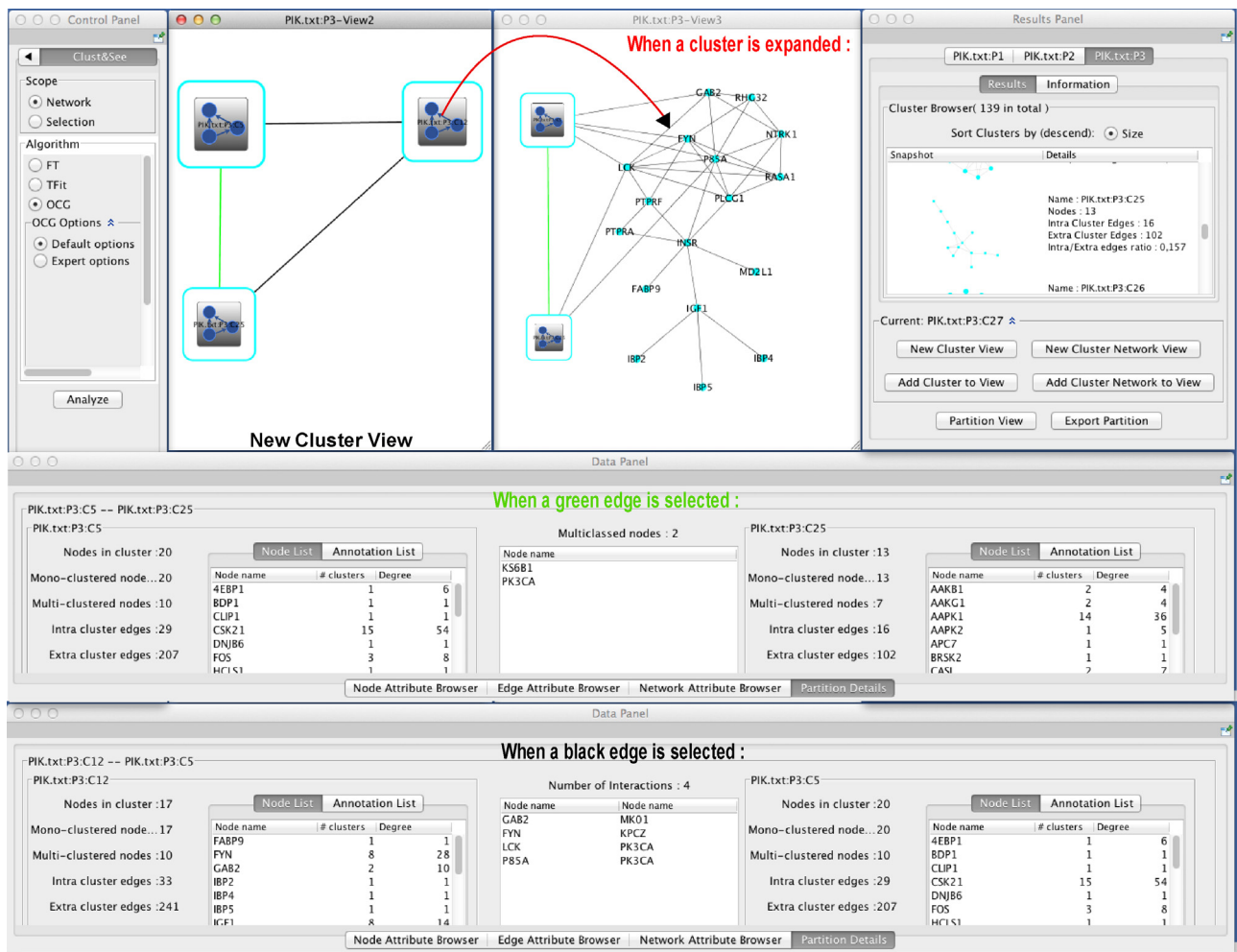


Fig. 2. A ‘New Cluster View’ showing the clusters 5, 12 and 25 generated by the OCG algorithm as metanodes and the two edge types linking them. Black metaedges connect vertices of one cluster to those of another. Green metaedges represent the nodes shared between the clusters. Details are shown in the Data Panel when selecting a green or a black metaedge. An example of an expanded metanode is also given.

When two different partitions are computed on the same network (using different algorithms or different parameters), they are compared using the Jaccard index (Jaccard, 1901) which provides a measure of the partitions’ similarity. A contingency table listing the number of shared nodes between the clusters of each partition is provided for further analysis.

In addition, because launching an analysis on a very large network or selection may lead, at best, unmanageable results (too many clusters) and, at worst, to memory issues and very long computation times, Clust&See offers the user the choice of extracting sub-networks of interest on which to continue the analysis by using the ‘Build neighborhood network’ functionality.

Finally, the provided search function can identify a specific node among the clusters of all partitions under investigation.

3. Application

3.1. From clusters to nodes

Fig. 1 shows the results obtained when applying the 3 algorithms currently implemented in Clust&See to the PI3K interactome network (Pilot-Storck et al., 2010). A global view of each partition as a quotient graph, in which the obtained clusters are represented as metanodes, is given. Note that the default view is shown when the partition contains no more than 15 clusters/metanodes, but can

always be displayed on demand for larger partitions. These views are one of the original features provided by the plug-in.

The PI3K pathway transmits signals from receptors located at the cell surface to transcription factors in the nucleus, *via* an intracellular signaling cascade involving several kinases. To illustrate the value of a local analysis using Clust&See, we have chosen to explore the connections between 3 overlapping clusters generated by the OCG algorithm, containing a majority of receptor-binding proteins (Cluster 12), serine/threonine kinases (Cluster 25) and nuclear acid binding proteins (Cluster 5) respectively. The 3 clusters are represented as metanodes in Fig. 2, which shows a ‘New Cluster View’ created on the fly. In addition, Cluster 25, formed by 13 nodes linked by 16 intra-cluster edges, is shown in the Cluster Browser of the Results Panel. Details on the mono/multi-clustered status of vertices are given in the Data Panel. Clusters sharing vertices (like Clusters 5 and 25), are easily identifiable since they are linked by a green metaedge whose details are shown in the Data Panel upon selection: two kinases, KS6B1 and PK3CA, belong to both clusters, suggesting a possible functional link between those proteins. Interestingly, particular variants of the genes encoding these proteins have been found to interact genetically in a case-control study for colorectal cancers (Slattery et al., 2011). A visual exploration of the organization of the clusters with Clust&See can therefore help building hypothesis and pointing toward relevant functional objects (represented as nodes, metanodes, edges or metaedges) and their relationships. Finally, metanodes can be expanded (and

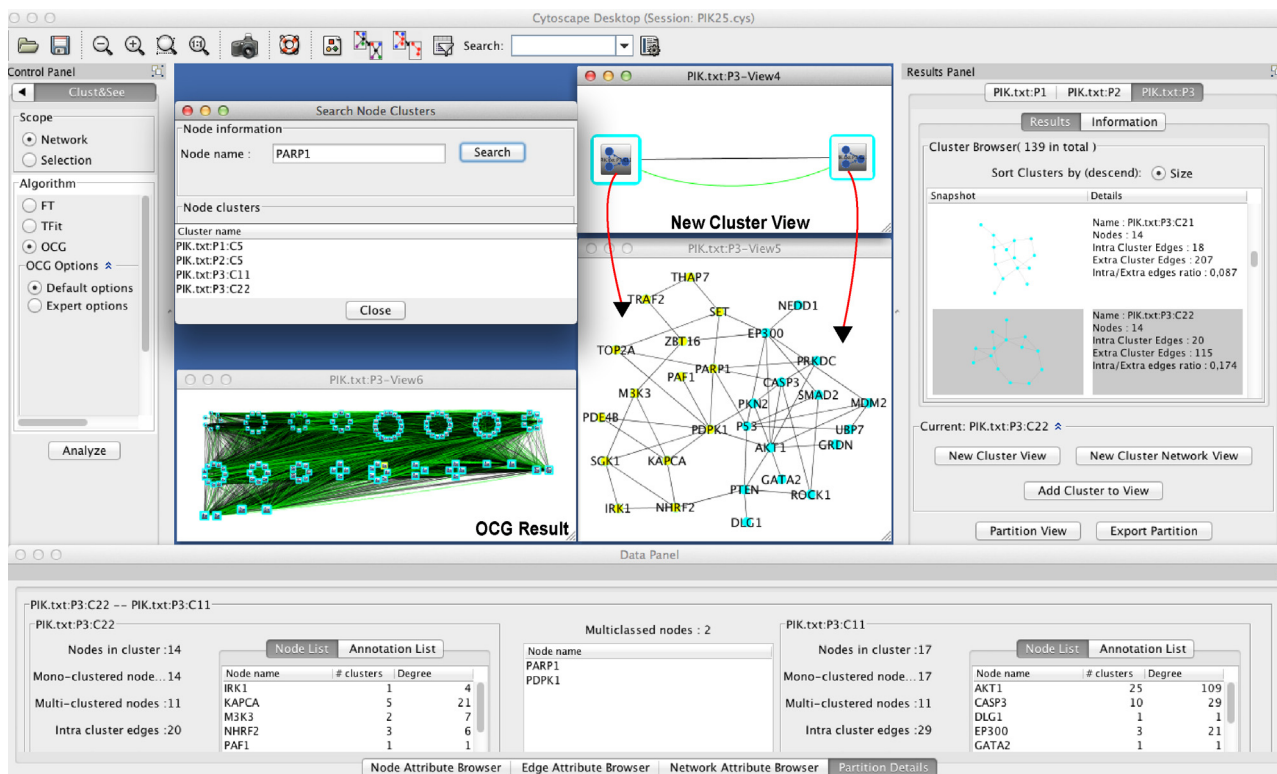


Fig. 3. The result of a search for PARP1 in the clusters obtained from the different algorithms is shown. The two clusters containing PARP1 according to OCG are provided as a 'New Cluster View' and the expanded metanodes are shown below them.

subsequently collapsed) in order to visualize the underlying sub-network. The combination of the details shown in the Data Panel and the visualization of the composite subnetwork greatly facilitates the study of the identified clusters and their connections.

3.2. From nodes to clusters

Fig. 3 illustrates the search for a particular node, PARP1, across the different partitions obtained when using all three algorithms on the same network. PARP1 belongs to two OCG clusters (P3 partition in the Results Panel). Interestingly, when both clusters are loaded in a "New Cluster View" for further analysis, the Data Panel shows that PDK1 is also shared by the same clusters, suggesting a possible functional link between PARP1 and PDK1. This is further confirmed when the expanded cluster view is generated, showing that both proteins interact directly. This interaction could in part explain the fact that co-targeting the PI3K pathway improves the response of cancer cells to PARP1 inhibition (Kimbung et al., 2012).

4. Conclusion

The Cytoscape plug-in Clust&See aims to facilitate network clustering and analysis for biologists not only by providing several original functionalities but also by providing them within a single analysis framework. While ClusterMaker (Morris et al., 2011) can represent clusters as metanodes, it provides neither intra/extra-edge visualization nor the possibility to expand/collapse the metanodes. Similarly, while ClusterOne (Nepusz et al., 2012) can identify overlapping clusters, studying the relationships between these clusters is not possible because their combined representation is not supported. In addition, Clust&See enables (i) better evaluation of the biological meaning of network clustering, (ii) better understanding of the underlying reasons for a particular node classification, (iii) better estimation of the quality of

the network under scrutiny and (iv) adjusting the clustering algorithm choice to the studied network. In summary, the originality of Clust&See lies in its providing users with a complete tool for the creation and analysis of network clusters and the relationships between them.

Acknowledgements

We thank Marine Veyssi re for the update of the PI3K interactome. This work is supported by the "Agence Nationale de la Recherche" as a Piribio grant (09-PIRI-0028, Moonlight project to C.B) and as a partner of the ERASysbio+ initiative supported under the EU ERANET Plus scheme in FP7 (ModHeart Project). B.R. is a PhD fellow of the AXA Research Fund. C.C. is a postdoctoral fellow of the "Fondation pour la Recherche M dicale".

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.biosystems.2013.05.010>.

References

- Ahn, Y.-Y., Bagrow, J.P., Lehmann, S., 2010. Link communities reveal multiscale complexity in networks. *Nature* 466, 761–764.
- Aittokallio, T., Schwikowski, B., 2006. Graph-based methods for analysing networks in cell biology. *Brief Bioinform.* 7, 243–255.
- Bader, G.D., Hogue, C.W., 2003. An automated method for finding molecular complexes in large protein interaction networks. *BMC Bioinform.* 4, 2.
- Becker, E., Robisson, B., Chapple, C.E., Gu enoche, A., Brun, C., 2012. Multifunctional proteins revealed by overlapping clustering in protein interaction network. *Bioinformatics* 28, 84–90.
- Gambette, P., Gu enoche, A., 2012. Bootstrap clustering for graph partitioning. *RAIRO – Oper. Res.* 45, 339–352.
- Gu enoche, A., 2011. Consensus of partitions: a constructive approach. *Adv. Data Anal. Classification* 5, 215–229.

- Jaccard, P., 1901. Distribution de la flore alpine dans le bassin des Dranses et de quelques régions voisines. *Bull. Soc. Vaud. Sci. Nat.* 37, 241–272.
- Kalinka, A.T., Tomancak, P., 2011. linkcomm: an R package for the generation, visualization, and analysis of link communities in networks of arbitrary size and type. *Bioinformatics* 27, 2011–2012.
- Kimbung, S., Biskup, E., Johansson, I., Aaltonen, K., Ottosson-Wadlund, A., Grubberger-Saal, S., Cunliffe, H., Fadeel, B., Loman, N., Berglund, P., et al., 2012. Co-targeting of the PI3K pathway improves the response of BRCA1 deficient breast cancer cells to PARP1 inhibition. *Cancer Lett.* 319, 232–241.
- Morris, J.H., Apeltsin, L., Newman, A.M., Baumbach, J., Wittkop, T., Su, G., Bader, G.D., Ferrin, T.E., 2011. clusterMaker: a multi-algorithm clustering plugin for Cytoscape. *BMC Bioinform.* 12, 436.
- Nepusz, T., Yu, H., Paccanaro, A., 2012. Detecting overlapping protein complexes in protein–protein interaction networks. *Nat. Methods* 9, 471–472.
- Newman, M.E., 2004. Fast algorithm for detecting community structure in networks. *Phys. Rev. E Stat. Nonlin. Soft Matter Phys.* 69, 066133.
- Pilot-Storck, F., Chopin, E., Rual, J.-F., Baudot, A., Dobrokhotov, P., Robinson-Rechavi, M., Brun, C., Cusick, M.E., Hill, D.E., Schaeffer, L., et al., 2010. Interactome mapping of the phosphatidylinositol 3-kinase-mammalian target of rapamycin pathway identifies deformed epidermal autoregulatory factor-1 as a new glycogen synthase kinase-3 interactor. *Mol. Cell Proteomics* 9, 1578–1593.
- Shannon, P., Markiel, A., Ozier, O., Baliga, N.S., Wang, J.T., Ramage, D., Amin, N., Schwikowski, B., Ideker, T., 2003. Cytoscape: a software environment for integrated models of biomolecular interaction networks. *Genome Res.* 13, 2498–2504.
- Slattery, M.L., Lundgreen, A., Herrick, J.S., Wolff, R.K., 2011. Genetic variation in RPS6KA1, RPS6KA2, RPS6KB1, RPS6KB2, and PDK1 and risk of colon or rectal cancer. *Mutat. Res.* 706, 13–20.