

## CT 1.4.5

### **CFinder: Efficient module finder in directed, undirected and weighted networks.**

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Networks are widely used for systems-level molecular biological analyses, for example, for the identification of related groups of proteins (motifs, modules, etc.). The clustering program CFinder identifies densely internally connected groups of nodes (modules) in networks and allows explicitly for overlaps among the identified modules. Recently, we have extended CFinder to weighted and directed networks.

In both graph models and directed real graphs we identify two types of directed network modules: in- and out-modules based on whether the overlaps of the modules contain mainly in- or out-hubs. We find in-modules in: the directed graph of Google's own webpages and a large word association net of English words. We find out-modules in an e-mail web and the transcription regulatory network of yeast. In biological and other networks, too, modules and the "background" are often hard to tell apart, and one cannot draw sharp boundaries for the modules. The extension of CFinder to weighted graphs allows one to identify densely internally connected groups of nodes (proteins in a PPI network) with higher confidence.

Publications and free software are available at  
<http://www.CFinder.org>

Selected publications:

G. Palla, I. J. Farkas, P. Pollner, I. Derényi and T. Vicsek  
[Directed network modules](#)  
*New J. Phys.* **9**, 186 (2007).

I. J. Farkas, D. Ábel, G. Palla and T. Vicsek  
[Weighted network modules](#)  
*New J. Phys.* **9**, 180 (2007).

B. Adamcsek, G. Palla, I. J. Farkas, I. Derényi and T. Vicsek  
[CFinder: Locating cliques and overlapping modules in biological networks](#)  
*Bioinformatics* **22**, 1021-1023 (2006).

G. Palla, I. Derényi, I. Farkas, and T. Vicsek  
[Uncovering the overlapping community structure of complex networks in nature and society](#)  
*Nature* **435**, 814 (2005).