Supplementary Text

1.1 Algorithm pseudocodes

1.1.1 Mining algorithms

Table A1 describes the main mining heuristic, which is based on finding at most one dense subgraph starting at each node in DAPG.

The core of our mining technique is Table A2. It starts at each node \( v \) in DAPG and walks its way to the previous node in the path up to a root. Along the path, we maintain in set \( S \) the intersection of the \texttt{vertexSet} of the nodes in a subset of the visited nodes (those which provide a better partial \textit{DSG}), while we maintain in set \( C \) the \textit{labels} of the nodes of the selected subset. Note that, at each point, \((S \cup C, S \times C)\) is indeed a valid graph. From all those DSGs, we retain only the “best one”. We determine the “best DSG” using and objective function \((f_{obj})\), which is a configuration parameter.
Table A1: Mining algorithm. Discovering DSGs in DAPG

Require: DAPG representation.
Ensure: list of maximal DSGs (at most $|N(DAPG)|$)

1: function GetDenseSubGraphs(DAPG)
2: $DSGs \leftarrow \emptyset$
3: for all node $\in V(DAPG)$ do
4:   $nodeDsg \leftarrow$ GetDenseSubgraphFrom(DAPG, node)
5:   if $nodeDsg$ is maximal w.r.t. $DSGs$ then
6:     $DSGs \leftarrow DSGs - \{dsg \in DSGs, \ dsg \subset nodeDsg\}$
7:     $DSGs \leftarrow DSGs \cup \{nodeDsg\}$
8:   end if
9: end for
10: return $DSGs$

Table A2: Detection of an DSG starting at a given node in DAPG.

Require: node $\in N(DAPG)$, DAPG, and $f_{obj}$
Ensure: $bestDSG = (S,C)$, with node $\in C$

1: function GetDenseSubGraphFrom(DAPG, node)
2: $bestDSG \leftarrow (node.vertexSet, \{node.label\})$
3: $nextNode \leftarrow$ getTravelerNextNode(DAPG, node)
4: while $nextNode \neq NULL$ do
5:   $candidate.C \leftarrow bestDSG.C \cup nextNode.label$
6:   $candidate.S \leftarrow bestDSG.S \cap nextNode.vertexSet$
7:   if $f_{obj}(bestDSG) < f_{obj}(candidate)$ then
8:     $bestDSG \leftarrow candidate$
9: end if
10: $nextNode \leftarrow$ getTravelerNextNode(DAPG, nextNode)
11: end while
12: return $bestDSG$
Table A3: Algorithms for redundancy-filtering.

Require: \textit{candidatesSet, threshold, filter}
Ensure: \( CC \subseteq \text{candidatesSet} \)

1. \( CC \leftarrow \emptyset \)
2. \textbf{for} candidate \( \in \text{candidatesSet} \) \textbf{do}
3. \hspace{1em} \textit{AddToFilteredSet}(CC, candidate, threshold, filter)
4. \textbf{end for}
5. \textbf{return} \( CC \)

Require: \( CC, \text{candidate, threshold, filter} \)

1. \( B \leftarrow \{ cc \in CC : \text{OS}(cc, \text{candidate}) \text{ is maximum} \} \)
2. \textbf{if} \( \text{filter} = \text{NONE} \text{ or OS}(B, \text{candidate}) < \text{threshold} \) \textbf{then}
3. \hspace{1em} \( CC \leftarrow CC \cup \{ \text{candidate} \} \)
4. \hspace{1em} \textbf{else}
5. \hspace{2em} \textbf{if} \( \text{filter} = \text{UNION} \) \textbf{then}
6. \hspace{3em} \( CC \leftarrow CC - \{ B \} \)
7. \hspace{3em} \( CC \leftarrow CC \cup \{ \text{candidate} \cup B \} \)
8. \hspace{2em} \textbf{end if}
9. \hspace{1em} \textbf{end if}

1.1.2 Protein complex prediction

Table A3 show the way we generate predicted complexes from candidate complexes based on two different filter options: NONE, where a predicted complex is always a candidate complex, and UNION, where a predicted complex is formed by the set union of the complex pairs with overlap score greater than a threshold (we used threshold = 0.8).

1.2 Weighted and unweighted DAPG

In this section we present all results we obtained in terms of clustering metrics using the unified version of DAPG on weighted and unweighted PPI networks. Therefore here we present the results using different orders and merge options and objective functions for the mining algorithm explained in the main manuscript. Tables A4, A6, A8, A10 show the results using \( f_{\text{obj}} = |S \cap C| \) and Tables A5, A7, A9, A11 show the results using \( f_{\text{obj}} \) based on weighted density definitions on small yeast PPI networks. Similarly we present the results on large PPI networks for yeast and human in Tables A12, A14, A16 with \( f_{\text{obj}} = |S \cap C| \) and Tables A13, A15, A17 with \( f_{\text{obj}} = WDEGREE \) for measuring the performance using weighted density metrics.

In all experiments we used yeast PPI networks and reference CYC2008 [1] provided by clusterONE software distribution for yeast and PCDq for human. All experiments were performed with total order function \( \phi \)

1.2.1 Unified DAPG
Table A4: Results of clustering using DAPGUU varying algorithm parameters in Collins with complexes of minimum size 3.

| order | merge | Complexes | FMeasure | Acc  | MMR  | Ex. time(s) |
|-------|-------|-----------|----------|------|------|-------------|
| ID    | NONE  | 537       | 0.7203   | 0.7188 | 0.6837 | 1.15        |
| ID    | UNION | 447       | 0.6782   | 0.7115 | 0.6749 | 1.06        |
| FREQ  | NONE  | 611       | 0.7245   | 0.7241 | 0.7014 | 3.41        |
| FREQ  | UNION | 479       | 0.6765   | 0.7175 | 0.6849 | 3.19        |

Table A5: Results of clustering using PPI weight density DAPGUW varying algorithm parameters in Collins with complexes of minimum size 3.

| density | order | merge | Complexes | FMeasure | Acc  | MMR  | Ex. time(s) |
|---------|-------|-------|-----------|----------|------|------|-------------|
| WDEGR   | ID    | NONE  | 484       | 0.7013   | 0.6283 | 0.4024 | 2.47        |
| WDEGR   | ID    | UNION | 421       | 0.7109   | 0.7006 | 0.6396 | 2.38        |
| WDEGR   | FREQ  | NONE  | 530       | 0.7253   | 0.6485 | 0.4291 | 4.48        |
| WDEGR   | FREQ  | UNION | 447       | 0.7275   | 0.7065 | 0.6606 | 4.40        |
| WEDGE   | ID    | NONE  | 363       | 0.7583   | 0.6491 | 0.4532 | 1.50        |
| WEDGE   | ID    | UNION | 346       | 0.7825   | 0.6991 | 0.6442 | 1.44        |
| WEDGE   | FREQ  | NONE  | 397       | 0.7807   | 0.6541 | 0.4588 | 3.79        |
| WEDGE   | FREQ  | UNION | 347       | 0.7852   | 0.6891 | 0.6312 | 3.63        |
| FWDEG   | ID    | NONE  | 416       | 0.7172   | 0.6291 | 0.3962 | 2.80        |
| FWDEG   | ID    | UNION | 334       | 0.7130   | 0.6700 | 0.5324 | 2.64        |
| FWDEG   | FREQ  | NONE  | 424       | 0.7273   | 0.6536 | 0.4035 | 4.32        |
| FWDEG   | FREQ  | UNION | 320       | 0.7031   | 0.6666 | 0.4950 | 4.12        |
| FWEDG   | ID    | NONE  | 319       | 0.6865   | 0.6103 | 0.3721 | 1.51        |
| FWEDG   | ID    | UNION | 328       | 0.7189   | 0.6506 | 0.5332 | 1.50        |
| FWEDG   | FREQ  | NONE  | 359       | 0.7275   | 0.6280 | 0.3525 | 3.60        |
| FWEDG   | FREQ  | UNION | 328       | 0.7376   | 0.6548 | 0.4694 | 3.53        |

Table A6: Results of clustering DAPGUU varying algorithm parameters in Krogan Core with complexes of minimum size 3.

| order | merge | Complexes | FMeasure | Acc  | MMR  | Ex. time(s) |
|-------|-------|-----------|----------|------|------|-------------|
| ID    | NONE  | 584       | 0.6376   | 0.6470 | 0.4742 | 1.40        |
| ID    | UNION | 557       | 0.6198   | 0.6422 | 0.4807 | 1.32        |
| FREQ  | NONE  | 627       | 0.6379   | 0.6116 | 0.4550 | 6.23        |
| FREQ  | UNION | 582       | 0.5996   | 0.6137 | 0.4591 | 6.16        |
Table A7: Results of clustering using PPI weight density DAPGUW varying algorithm parameters in Krogan Core with complexes of minimum size 3.

| density | order | merge | Complexes | FMeasure | Acc  | MMR  | Ex. time(s) |
|---------|-------|-------|-----------|----------|------|------|-------------|
| WDEGR   | ID    | NONE  | 706       | 0.6404   | 0.6305| 0.4079| 2.57        |
| WDEGR   | ID    | UNION | 680       | 0.6136   | 0.6506| 0.4838| 2.48        |
| WDEGR   | FREQ  | NONE  | 756       | 0.6116   | 0.5992| 0.4016| 6.71        |
| WDEGR   | FREQ  | UNION | 733       | 0.5923   | 0.6119| 0.4555| 6.75        |
| WEDGE   | ID    | NONE  | 441       | 0.6568   | 0.6206| 0.3744| 1.93        |
| WEDGE   | ID    | UNION | 447       | 0.6558   | 0.6445| 0.4425| 1.89        |
| WEDGE   | FREQ  | NONE  | 506       | 0.6436   | 0.5920| 0.3878| 6.21        |
| WEDGE   | FREQ  | UNION | 486       | 0.6242   | 0.6015| 0.4318| 6.22        |
| FWDEG   | ID    | NONE  | 545       | 0.6519   | 0.6389| 0.3782| 2.31        |
| FWDEG   | ID    | UNION | 521       | 0.6259   | 0.6625| 0.4403| 2.23        |
| FWDEG   | FREQ  | NONE  | 575       | 0.6273   | 0.6308| 0.3700| 6.44        |
| FWDEG   | FREQ  | UNION | 549       | 0.6124   | 0.6146| 0.4121| 6.41        |
| FWEDG   | ID    | NONE  | 392       | 0.6428   | 0.6058| 0.3509| 1.93        |
| FWEDG   | ID    | UNION | 391       | 0.6379   | 0.6265| 0.4177| 1.95        |
| FWEDG   | FREQ  | NONE  | 481       | 0.6463   | 0.5653| 0.3439| 6.29        |
| FWEDG   | FREQ  | UNION | 467       | 0.6358   | 0.5785| 0.3900| 6.24        |

Table A8: Results of clustering using DAPGUU varying algorithm parameters in Krogan Extended with complexes of minimum size 3.

| order | merge | Complexes | FMeasure | Acc  | MMR  | Ex. time(s) |
|-------|-------|-----------|----------|------|------|-------------|
| ID    | NONE  | 896       | 0.5121   | 0.6147| 0.4352| 3.40        |
| ID    | UNION | 865       | 0.4847   | 0.6247| 0.4474| 3.26        |
| FREQ  | NONE  | 922       | 0.5027   | 0.6057| 0.4058| 15.07       |
| FREQ  | UNION | 906       | 0.4763   | 0.6129| 0.4166| 15.29       |

Table A9: Results of clustering using PPI weight density DAPGUW varying algorithm parameters in Krogan Extended with complexes of minimum size 3.

| density | order | merge | Complexes | FMeasure | Acc  | MMR  | Ex. time(s) |
|---------|-------|-------|-----------|----------|------|------|-------------|
| WDEGR   | ID    | NONE  | 1174      | 0.5503   | 0.5999| 0.4004| 8.31        |
| WDEGR   | ID    | UNION | 1118      | 0.5175   | 0.6144| 0.4581| 8.08        |
| WDEGR   | FREQ  | NONE  | 1209      | 0.5469   | 0.5809| 0.4096| 17.94       |
| WDEGR   | FREQ  | UNION | 1150      | 0.5244   | 0.5831| 0.4176| 17.46       |
| WEDGE   | ID    | NONE  | 529       | 0.6131   | 0.5778| 0.3637| 5.80        |
| WEDGE   | ID    | UNION | 532       | 0.5952   | 0.5982| 0.4039| 5.85        |
| WEDGE   | FREQ  | NONE  | 573       | 0.6039   | 0.5705| 0.3725| 15.70       |
| WEDGE   | FREQ  | UNION | 564       | 0.5850   | 0.5765| 0.3867| 15.84       |
| FWDEG   | ID    | NONE  | 963       | 0.6041   | 0.6130| 0.3987| 8.68        |
| FWDEG   | ID    | UNION | 906       | 0.5719   | 0.6199| 0.4484| 8.30        |
| FWDEG   | FREQ  | NONE  | 1027      | 0.6168   | 0.6086| 0.4083| 17.49       |
| FWDEG   | FREQ  | UNION | 950       | 0.5763   | 0.6078| 0.4220| 17.38       |
| FWEDG   | ID    | NONE  | 518       | 0.6204   | 0.5837| 0.3580| 7.19        |
| FWEDG   | ID    | UNION | 522       | 0.6026   | 0.5980| 0.4049| 7.02        |
| FWEDG   | FREQ  | NONE  | 592       | 0.6066   | 0.5768| 0.4018| 16.37       |
| FWEDG   | FREQ  | UNION | 590       | 0.5928   | 0.5839| 0.4121| 16.69       |
Table A10: Results of clustering using DAPGUU varying algorithm parameters in Gavin with complexes of minimum size 3.

| order | merge | Complexes | FMeasure | Acc | MMR | Ex. time(s) |
|-------|-------|-----------|----------|-----|-----|-------------|
| ID    | NONE  | 718       | 0.6042   | 0.6995 | 0.5557 | 1.44        |
| ID    | UNION | 641       | 0.5752   | 0.7055 | 0.5838 | 1.34        |
| FREQ  | NONE  | 592       | 0.6519   | 0.7039 | 0.5627 | 3.39        |
| FREQ  | UNION | 529       | 0.6097   | 0.6928 | 0.5561 | 3.29        |

Table A11: Results of clustering using PPI weight density DAPGUW varying algorithm parameters in Gavin with complexes of minimum size 3.

| density | order | merge | Complexes | FMeasure | Acc | MMR | Ex. time(s) |
|---------|-------|-------|-----------|----------|-----|-----|-------------|
| WDEGR   | ID    | NONE  | 699       | 0.6181   | 0.6624 | 0.4300 | 2.61        |
| WDEGR   | ID    | UNION | 657       | 0.5814   | 0.7039 | 0.5791 | 2.51        |
| WDEGR   | FREQ  | NONE  | 618       | 0.6489   | 0.6477 | 0.4294 | 3.80        |
| WDEGR   | FREQ  | UNION | 581       | 0.6165   | 0.6704 | 0.5632 | 3.77        |
| WEDGE   | ID    | NONE  | 511       | 0.6746   | 0.6600 | 0.4064 | 1.74        |
| WEDGE   | ID    | UNION | 489       | 0.6412   | 0.6903 | 0.5311 | 1.70        |
| WEDGE   | FREQ  | NONE  | 465       | 0.6389   | 0.6529 | 0.4054 | 3.44        |
| WEDGE   | FREQ  | UNION | 460       | 0.6250   | 0.6879 | 0.5243 | 3.40        |
| FWDEG   | ID    | NONE  | 530       | 0.6705   | 0.6751 | 0.4218 | 2.25        |
| FWDEG   | ID    | UNION | 482       | 0.6081   | 0.6774 | 0.4740 | 2.23        |
| FWDEG   | FREQ  | NONE  | 384       | 0.6766   | 0.6407 | 0.3247 | 3.71        |
| FWDEG   | FREQ  | UNION | 347       | 0.6175   | 0.6330 | 0.3779 | 3.60        |
| FWEDG   | ID    | NONE  | 436       | 0.6239   | 0.6387 | 0.3842 | 1.78        |
| FWEDG   | ID    | UNION | 461       | 0.6076   | 0.6702 | 0.4735 | 1.77        |
| FWEDG   | FREQ  | NONE  | 425       | 0.5889   | 0.6046 | 0.3224 | 3.98        |
| FWEDG   | FREQ  | UNION | 426       | 0.5740   | 0.6326 | 0.4031 | 3.51        |

Table A12: Results of clustering using DAPGUU varying algorithm parameters in Biogrid yeast with complexes of minimum size 3.

| order | merge | Complexes | FMeasure | Acc | MMR | Ex. time(s) |
|-------|-------|-----------|----------|-----|-----|-------------|
| ID    | NONE  | 4,992     | 0.1490   | 0.5692 | 0.3385 | 345.77      |
| ID    | UNION | 4,945     | 0.1444   | 0.5693 | 0.3371 | 346.42      |
| FREQ  | NONE  | 5,012     | 0.1528   | 0.5663 | 0.3455 | 757.74      |
| FREQ  | UNION | 4,980     | 0.1486   | 0.5702 | 0.3523 | 751.00      |

Table A13: Results of clustering using DAPGUWD varying algorithm parameters in Biogrid yeast with complexes of minimum size 3.

| density | order | merge | Complexes | FMeasure | Acc | MMR | Ex. time(s) |
|---------|-------|-------|-----------|----------|-----|-----|-------------|
| WDEGR   | ID    | NONE  | 5,199     | 0.0620   | 0.4000 | 0.1506 | 798.1       |
| WDEGR   | ID    | UNION | 5,153     | 0.0600   | 0.4016 | 0.1521 | 806.2       |
| WDEGR   | FREQ  | NONE  | 4,803     | 0.0331   | 0.3514 | 0.0769 | 1,315.1     |
| WDEGR   | FREQ  | UNION | 4,747     | 0.0323   | 0.3519 | 0.0771 | 1,324.6     |
1.3 Methods used for comparison

In order to evaluate DAPG in detecting protein complexes, we used the following state-of-the-art methods: ClusterONE [2], MCL [3], Cfinder [4], and GMFTP [5]. The performance of each method depends on its parameter setting and the reference (gold standard) of protein complexes used as ground truth. Therefore, we first describe the main features of each of algorithms and provide the parameter tuning using the reference CYC2008 [1]. We optimized the parameters that achieved the best results based on MMR (Maximum Matching Ratio), proposed by clusterONE, and used the implementation for measuring clustering metrics provided by them and available at [http://www.paccanarolab.org/static_content/clusterone/additional_information.html]. All experiments report the parameters and the clustering metrics: FMeasure, Acc, MMR as well as the execution time in seconds.

1.3.1 ClusterONE

ClusterONE detects overlapping protein complexes from weighted and unweighted PPI networks, and it is based on overlapping neighborhood expansion. The main parameter of clusterONE is \( d \), which is the minimum density of clusters, and we keep the other parameters as given by default as has been used in previous work [5]. Tables A18, A19, A20, A21, and A24 present the results for Collins, KroganCore, KroganExt, Gavin and Biogrid.

1.3.2 MCL

MCL is based on detecting clusters using a model that uses random walks on the input graph adopting Markov Chains trying to discover where the flows concentrate forming clusters. The Inflation (\( I \)) parameter is its key parameter, which tunes the granularity of the clusters. We executed MCL using different inflations for all input PPI networks and we provide the results in Tables A25, A26, A27, A28, and A29.

1.3.3 CFinder

CFinder is based on Clique Percolation Method (CPM) [6] to detect overlapping modules in biological networks. The CPM method consists of building communities from k-cliques where a community is defined as the maximal union of k-cliques that are connected through a series of adjacent cliques. The keys parameters in CFinder are the parameter \( k \) (for size \( k \) in k-clique) and the parameter \( t \) which represents the time in seconds allowed for searching a clique.
Table A15: Results of clustering using DAPGUWD varying algorithm parameters in HPRD with complexes of minimum size 3 and reference PCDq.

| density | order | merge | Complexes | FMeasure | Acc  | MMR  | Ex. time(s) |
|---------|-------|-------|-----------|----------|------|------|-------------|
| WDEGR   | ID    | NONE  | 3,791     | 0.3390   | 0.2821 | 0.1790 | 121.2       |
| WDEGR   | ID    | UNION | 3,751     | 0.3346   | 0.2869 | 0.1832 | 120.5       |
| WDEGR   | FREQ  | NONE  | 3,592     | 0.3190   | 0.2588 | 0.1506 | 287.9       |
| WDEGR   | FREQ  | UNION | 3,562     | 0.3216   | 0.2631 | 0.1603 | 291.7       |

Table A16: Results of clustering using DAPGUU varying algorithm parameters in Biogrid human with complexes of minimum size 3.

| order | merge | Complexes | FMeasure | Acc  | MMR  | Ex. time(s) |
|-------|-------|-----------|----------|------|------|-------------|
| ID    | NONE  | 7,178     | 0.1496   | 0.3534 | 0.1247 | 900.0       |
| ID    | UNION | 7,105     | 0.1469   | 0.3529 | 0.1249 | 900.2       |
| FREQ  | NONE  | 7,360     | 0.1577   | 0.3470 | 0.1303 | 3,238.2     |
| FREQ  | UNION | 7,314     | 0.1542   | 0.3485 | 0.1319 | 3,210.3     |

Table A17: Results of clustering using DAPGUWD varying algorithm parameters in Biogrid human with complexes of minimum size 3.

| density | order | merge | Complexes | FMeasure | Acc  | MMR  | Ex. time(s) |
|---------|-------|-------|-----------|----------|------|------|-------------|
| WDEGR   | ID    | NONE  | 11,160    | 0.0932   | 0.2516 | 0.0951 | 1,803.2     |
| WDEGR   | ID    | UNION | 10,871    | 0.0978   | 0.2529 | 0.0964 | 1,795.3     |
| WDEGR   | FREQ  | NONE  | 11,233    | 0.1037   | 0.2386 | 0.1028 | 3,013.2     |
| WDEGR   | FREQ  | UNION | 10,727    | 0.0986   | 0.2407 | 0.1009 | 3,012.4     |

Table A18: Results of clustering using ClusterONE varying algorithm parameters in Collins with complexes of minimum size 3.

| D     | Complexes | FMeasure | Acc  | MMR  | Ex. time(s) |
|-------|-----------|----------|------|------|-------------|
| 0.1   | 172       | 0.6936   | 0.7448 | 0.5626 | 1.35         |
| 0.2   | 177       | 0.6844   | 0.7469 | 0.5656 | 1.34         |
| 0.3   | 194       | 0.6646   | 0.7343 | 0.5707 | 1.39         |
| 0.4   | 187       | 0.6940   | 0.7677 | 0.5711 | 1.37         |
| 0.5   | 169       | 0.7273   | 0.7676 | 0.5477 | 1.33         |
| 0.6   | 136       | 0.7594   | 0.7376 | 0.5132 | 1.30         |
| 0.7   | 128       | 0.7836   | 0.7208 | 0.5061 | 1.28         |
| 0.8   | 117       | 0.7615   | 0.6816 | 0.4559 | 1.24         |
| 0.9   | 100       | 0.6996   | 0.6564 | 0.3861 | 1.19         |

from a node in the graph. For all PPI networks we found that our best results we for \( k = 3 \) for Collins, and KroganCore, \( k = 4 \) for KroganExtended and Gavin, and \( K = 6 \) for Biogrid. For the \( t \) parameters we found that using \( t = 1 \) or \( t = 10 \) in Collins, KroganCore, KroganExtended and Gavin all results were the same so we reported execution times for \( t = 1 \). However, in the case of Biogrid the execution time with \( t = 10 \) took more than 2 days so we used \( t = 1 \).
Table A19: Results of clustering using ClusterONE varying algorithm parameters in Krogan Core with complexes of minimum size 3.

| D | Complexes | FMeasure | Acc | MMR | Ex. time(s) |
|---|-----------|----------|-----|-----|-------------|
| 0.1 | 372 | 0.4852 | 0.7494 | 0.4424 | 1.80 |
| 0.2 | 456 | 0.5099 | 0.7674 | 0.4600 | 1.79 |
| 0.3 | 522 | 0.4637 | 0.7683 | 0.4817 | 1.68 |
| 0.4 | 411 | 0.5844 | 0.7416 | 0.5068 | 1.65 |
| 0.5 | 240 | 0.6836 | 0.7075 | 0.4598 | 1.63 |
| 0.6 | 183 | 0.7128 | 0.6622 | 0.4055 | 1.56 |
| 0.7 | 139 | 0.6729 | 0.6203 | 0.3598 | 1.44 |
| 0.8 | 111 | 0.5903 | 0.5637 | 0.2753 | 1.39 |
| 0.9 | 79 | 0.5649 | 0.4859 | 0.2099 | 1.31 |

Table A20: Results of clustering using ClusterONE varying algorithm parameters in Krogan Extended with complexes of minimum size 3.

| D | Complexes | FMeasure | Acc | MMR | Ex. time(s) |
|---|-----------|----------|-----|-----|-------------|
| 0.1 | 421 | 0.4550 | 0.7145 | 0.4081 | 2.34 |
| 0.2 | 504 | 0.4587 | 0.7229 | 0.4197 | 2.33 |
| 0.3 | 530 | 0.4693 | 0.7334 | 0.4342 | 2.21 |
| 0.4 | 402 | 0.5751 | 0.7050 | 0.4553 | 2.18 |
| 0.5 | 257 | 0.6497 | 0.6614 | 0.4188 | 1.98 |
| 0.6 | 200 | 0.6923 | 0.6478 | 0.3850 | 1.88 |
| 0.7 | 142 | 0.6334 | 0.5915 | 0.3211 | 1.84 |
| 0.8 | 112 | 0.5879 | 0.5320 | 0.2505 | 1.82 |
| 0.9 | 82 | 0.5512 | 0.4733 | 0.1922 | 1.79 |

Table A21: Results of clustering using ClusterONE varying algorithm parameters in Gavin with complexes of minimum size 3.

| D | Complexes | FMeasure | Acc | MMR | Ex. time(s) |
|---|-----------|----------|-----|-----|-------------|
| 0.1 | 254 | 0.5383 | 0.7548 | 0.4949 | 1.45 |
| 0.2 | 239 | 0.5706 | 0.7626 | 0.5102 | 1.46 |
| 0.3 | 196 | 0.6852 | 0.7523 | 0.5378 | 1.41 |
| 0.4 | 173 | 0.7842 | 0.6953 | 0.5171 | 1.43 |
| 0.5 | 153 | 0.7740 | 0.6229 | 0.4214 | 1.42 |
| 0.6 | 89 | 0.5868 | 0.4757 | 0.2769 | 1.29 |
| 0.7 | 34 | 0.3626 | 0.2991 | 0.1239 | 1.16 |
| 0.8 | 5 | 0.0556 | 0.1089 | 0.0126 | 1.17 |

1.3.4 GMFTP

GMFTP is based on a generative model with functional and topological properties tending to predict protein complexes that are formed by group of proteins which frequently interact with each other and have similar functional patterns. The method transform the detection problem into a parameter estimation problem. The objective function in GMFTP is not convex and then the multiplicative updating rules of the algorithm does not necessarily converge to the global minimum. As a result, the method cannot guarantee the final estimator is the
globally optimum solution and the result is not deterministic. This issue is addressed by the method having a parameter for repeating the entire calculation, which is the repeat times parameter. By default this parameter is set to 100.

In our experiments, when trying to execute GMFTP on all PPI networks, we found that using all the default parameters of GMFTP was impossible to get results before a day of execution time. Therefore, we left all parameters as the defaults, except the repeat time which we set to 10 instead of 100. Doing this we were able to get results in a little more than 12 hours of execution with
Table A25: Results of clustering using MCL varying algorithm parameters in Collins with complexes of minimum size 3.

| T     | Complexes | FMeasure | Acc   | MMR   | Ex. time(s) |
|-------|-----------|----------|-------|-------|-------------|
| 1.2   | 99        | 0.5764   | 0.6562 | 0.3797 | 0.74        |
| 1.4   | 130       | 0.6857   | 0.7351 | 0.4604 | 0.74        |
| 1.6   | 145       | 0.6899   | 0.7447 | 0.4899 | 0.74        |
| 1.8   | 152       | 0.6816   | 0.7435 | 0.4992 | 0.74        |
| 2.0   | 155       | 0.6815   | 0.7474 | 0.5121 | 0.74        |
| 2.2   | 158       | 0.6813   | 0.7487 | 0.5165 | 0.74        |
| 2.4   | 160       | 0.6787   | 0.7465 | 0.5161 | 0.74        |
| 2.6   | 165       | 0.6690   | 0.7486 | 0.5215 | 0.74        |
| 2.8   | 168       | 0.6690   | 0.7522 | 0.5231 | 0.74        |
| 3.0   | 171       | 0.6806   | 0.7870 | 0.5363 | 0.74        |
| 3.2   | 173       | 0.6804   | 0.7908 | 0.5452 | 0.74        |
| 3.4   | 172       | 0.6807   | 0.7888 | 0.5408 | 0.74        |
| 3.6   | 174       | 0.6781   | 0.7841 | 0.5361 | 0.74        |
| 3.8   | 176       | 0.6847   | 0.7830 | 0.5366 | 0.74        |
| 4.0   | 180       | 0.6756   | 0.7842 | 0.5418 | 0.74        |
| 4.2   | 181       | 0.6733   | 0.7845 | 0.5519 | 0.74        |
| 4.4   | 181       | 0.6733   | 0.7835 | 0.5510 | 0.74        |
| 4.6   | 181       | 0.6800   | 0.7852 | 0.5561 | 0.74        |
| 4.8   | 183       | 0.6821   | 0.7814 | 0.5572 | 0.74        |
| 5.0   | 184       | 0.6776   | 0.7803 | 0.5591 | 0.74        |
| 5.2   | 186       | 0.6707   | 0.7801 | 0.5621 | 0.74        |
| 5.4   | 186       | 0.6820   | 0.7803 | 0.5625 | 0.74        |
| 5.6   | 185       | 0.6842   | 0.7762 | 0.5614 | 0.74        |
| 5.8   | 186       | 0.6820   | 0.7720 | 0.5607 | 0.74        |
| 6.0   | 187       | 0.6732   | 0.7693 | 0.5577 | 0.74        |
| 6.2   | 187       | 0.6710   | 0.7690 | 0.5581 | 0.74        |
| 6.4   | 187       | 0.6731   | 0.7679 | 0.5580 | 0.74        |
| 6.6   | 186       | 0.6818   | 0.7680 | 0.5611 | 0.74        |
| 6.8   | 188       | 0.6817   | 0.7685 | 0.5675 | 0.74        |
| 7.0   | 189       | 0.6837   | 0.7689 | 0.5726 | 0.74        |
| 7.2   | 193       | 0.6751   | 0.7681 | 0.5722 | 0.74        |
| 7.4   | 196       | 0.6875   | 0.7641 | 0.5760 | 0.74        |
| 7.6   | 196       | 0.6916   | 0.7626 | 0.5746 | 0.74        |
| 7.8   | 196       | 0.6854   | 0.7627 | 0.5735 | 0.74        |
| 8.0   | 196       | 0.6854   | 0.7577 | 0.5707 | 0.74        |
| 8.2   | 198       | 0.6935   | 0.7537 | 0.5741 | 0.74        |
| 8.4   | 198       | 0.6935   | 0.7533 | 0.5729 | 0.74        |
| 8.6   | 201       | 0.6850   | 0.7484 | 0.5712 | 0.74        |
| 8.8   | 201       | 0.6869   | 0.7463 | 0.5658 | 0.74        |
| 9.0   | 202       | 0.6848   | 0.7447 | 0.5650 | 0.74        |

all PPI networks.

1.3.5 **DCAFP**

DCAFP is a method that predict protein complexes based on two main properties. The first considers the idea of dense connected proteins in the PPI network and the second is based on the idea that proteins in the same protein complexes are at least similar in specific subsets of functional GO categories in the context of functional information given in the Gene ontology. DCAFP has three main parameters: `minsize attributes`, `delta`, `wmin`, `osmax`, `maxloops`, where the parameters `wmin` and `osmax` are the more relevant, where `wmin` has more impact in the size of the clusters found and `osmax` is more important in the performance. We modified these parameters between 0.2 and 1.0, keeping the other by default, to obtain our results.

1.3.6 **RNSC**

RNSC is a stochastic algorithm based on a search meta-heuristic aiming to optimize the network partition to define clusters based on a cost function. The
Table A26: Results of clustering using MCL varying algorithm parameters in Krogan Core with complexes of minimum size 3.

| T | Complexes | FMeasure | Acc | MMR | Ex. time(s) |
|---|-----------|----------|-----|-----|-------------|
| 1.2 | 386 | 0.2122  | 0.5220  | 0.0814 | 8.62 |
| 1.4 | 203 | 0.4265  | 0.7088  | 0.2604 | 8.62 |
| 1.6 | 297 | 0.4282  | 0.7462  | 0.3451 | 8.62 |
| 1.8 | 367 | 0.4207  | 0.7568  | 0.4072 | 8.62 |
| 2.0 | 369 | 0.4225  | 0.7499  | 0.4062 | 8.62 |
| 2.2 | 385 | 0.4134  | 0.7378  | 0.4127 | 8.62 |
| 2.4 | 393 | 0.4118  | 0.7211  | 0.4077 | 8.62 |
| 2.6 | 393 | 0.4073  | 0.7196  | 0.4075 | 8.62 |
| 2.8 | 391 | 0.3963  | 0.7052  | 0.4022 | 8.62 |
| 3.0 | 392 | 0.3905  | 0.6957  | 0.3914 | 8.62 |
| 3.2 | 393 | 0.3867  | 0.6799  | 0.3860 | 8.62 |
| 3.4 | 388 | 0.3684  | 0.6741  | 0.3589 | 8.62 |
| 3.6 | 378 | 0.3674  | 0.6687  | 0.3522 | 8.62 |
| 3.8 | 372 | 0.3712  | 0.6629  | 0.3509 | 8.62 |
| 4.0 | 371 | 0.3719  | 0.6619  | 0.3495 | 8.62 |
| 4.2 | 369 | 0.3636  | 0.6496  | 0.3395 | 8.62 |
| 4.4 | 366 | 0.3643  | 0.6442  | 0.3313 | 8.62 |
| 4.6 | 363 | 0.3664  | 0.6397  | 0.3301 | 8.62 |
| 4.8 | 359 | 0.3654  | 0.6359  | 0.3273 | 8.62 |
| 5.0 | 358 | 0.3661  | 0.6346  | 0.3269 | 8.62 |
| 5.2 | 355 | 0.3643  | 0.6332  | 0.3268 | 8.62 |
| 5.4 | 355 | 0.3636  | 0.6290  | 0.3240 | 8.62 |
| 5.6 | 354 | 0.3682  | 0.6246  | 0.3237 | 8.62 |
| 5.8 | 355 | 0.3668  | 0.6214  | 0.3200 | 8.62 |
| 6.0 | 352 | 0.3689  | 0.6292  | 0.3175 | 8.62 |
| 6.2 | 346 | 0.3622  | 0.6141  | 0.3054 | 8.62 |
| 6.4 | 346 | 0.3590  | 0.6133  | 0.3067 | 8.62 |
| 6.6 | 344 | 0.3604  | 0.6163  | 0.3076 | 8.62 |
| 6.8 | 344 | 0.3604  | 0.6148  | 0.3071 | 8.62 |
| 7.0 | 339 | 0.3655  | 0.6124  | 0.3068 | 8.62 |
| 7.2 | 339 | 0.3655  | 0.6108  | 0.3074 | 8.62 |
| 7.4 | 336 | 0.3589  | 0.6066  | 0.3085 | 8.62 |
| 7.6 | 336 | 0.3556  | 0.6030  | 0.2975 | 8.62 |
| 7.8 | 335 | 0.3522  | 0.6005  | 0.2936 | 8.62 |
| 8.0 | 333 | 0.3537  | 0.5994  | 0.2922 | 8.62 |
| 8.2 | 332 | 0.3455  | 0.5951  | 0.2877 | 8.62 |
| 8.4 | 329 | 0.3436  | 0.5950  | 0.2868 | 8.62 |

algorithm has several parameters such as the tabu length, number of experiments, diversification length, and diversification frequency. We run RNSC with default parameters.

1.3.7 MCODE

MCODE is one of the earliest algorithms that provide a solution for protein complex prediction. We use a command line application for linux platform to run the experiments. The method has several parameters, among the most important parameters are the neighborhood density percentage which varies from 0 to 1.0 and the maxdepth parameter, which we set in 1000 and 10000. We defined the other parameters in their default values.

1.3.8 SPICI

SPICI is a method that has a web site to run it and it also has the software available for download at [http://compbio.cs.princeton.edu/spici/](http://compbio.cs.princeton.edu/spici/). The method is based on ranking nodes by weighted degree and build clusters greedily.
Table A27: Results of clustering using MCL varying algorithm parameters in Krogan Extended with complexes of minimum size 3.

| T   | Complexes | FMeasure | Acc  | MMR  | Ex. time(s) |
|-----|------------|----------|------|------|-------------|
| 1.2 | 85         | 0.1298   | 0.4373 | 0.0370 | 19.50       |
| 1.4 | 232        | 0.3375   | 0.6739 | 0.1871 | 19.50       |
| 1.6 | 336        | 0.3386   | 0.7132 | 0.2500 | 19.50       |
| 1.8 | 400        | 0.3422   | 0.7337 | 0.2810 | 19.50       |
| 2.0 | 436        | 0.3389   | 0.7309 | 0.2895 | 19.50       |
| 2.2 | 467        | 0.3333   | 0.7235 | 0.2972 | 19.50       |
| 2.4 | 497        | 0.3243   | 0.7168 | 0.3090 | 19.50       |
| 2.6 | 517        | 0.3110   | 0.7039 | 0.3079 | 19.50       |
| 2.8 | 521        | 0.3059   | 0.6947 | 0.3026 | 19.50       |
| 3.0 | 528        | 0.3024   | 0.6921 | 0.3042 | 19.50       |
| 3.2 | 531        | 0.2955   | 0.6850 | 0.2999 | 19.50       |
| 3.4 | 529        | 0.2882   | 0.6759 | 0.2915 | 19.50       |
| 3.6 | 534        | 0.2752   | 0.6674 | 0.2854 | 19.50       |
| 3.8 | 531        | 0.2735   | 0.6607 | 0.2785 | 19.50       |
| 4.0 | 536        | 0.2663   | 0.6549 | 0.2726 | 19.50       |
| 4.2 | 542        | 0.2637   | 0.6443 | 0.2702 | 19.50       |
| 4.4 | 538        | 0.2652   | 0.6422 | 0.2690 | 19.50       |
| 4.6 | 536        | 0.2595   | 0.6386 | 0.2638 | 19.50       |
| 4.8 | 536        | 0.2535   | 0.6411 | 0.2576 | 19.50       |
| 5.0 | 535        | 0.2507   | 0.6444 | 0.2557 | 19.50       |
| 5.2 | 534        | 0.2511   | 0.6307 | 0.2553 | 19.50       |
| 5.4 | 535        | 0.2451   | 0.6261 | 0.2506 | 19.50       |
| 5.6 | 532        | 0.2433   | 0.6199 | 0.2470 | 19.50       |
| 5.8 | 530        | 0.2411   | 0.6157 | 0.2424 | 19.50       |
| 6.0 | 529        | 0.2408   | 0.6091 | 0.2377 | 19.50       |
| 6.2 | 528        | 0.2383   | 0.6069 | 0.2359 | 19.50       |
| 6.4 | 529        | 0.2323   | 0.6014 | 0.2331 | 19.50       |
| 6.6 | 525        | 0.2308   | 0.5905 | 0.2319 | 19.50       |
| 6.8 | 523        | 0.2340   | 0.5994 | 0.2291 | 19.50       |
| 7.0 | 521        | 0.2346   | 0.5965 | 0.2264 | 19.50       |
| 7.2 | 520        | 0.2350   | 0.5939 | 0.2264 | 19.50       |
| 7.4 | 518        | 0.2324   | 0.5927 | 0.2252 | 19.50       |
| 7.6 | 516        | 0.2377   | 0.5896 | 0.2203 | 19.50       |
| 7.8 | 516        | 0.2277   | 0.5883 | 0.2198 | 19.50       |
| 8.0 | 513        | 0.2287   | 0.5845 | 0.2182 | 19.50       |
| 8.2 | 512        | 0.2261   | 0.5826 | 0.2168 | 19.50       |
| 8.4 | 509        | 0.2271   | 0.5804 | 0.2151 | 19.50       |
| 8.6 | 510        | 0.2238   | 0.5758 | 0.2096 | 19.50       |
| 8.8 | 510        | 0.2264   | 0.5748 | 0.2088 | 19.50       |
| 9.0 | 511        | 0.2261   | 0.5725 | 0.2077 | 19.50       |

starting at seed nodes with decreasing degree. Clusters are formed by increasing adding neighbors of seed vertexes that incrementing their densities. We tried different values for minimum density, including default 0.5 and different values of minimum support threshold. We varied these parameters between 0.2 and 0.8. We also defined the sparcity parameter (-m) with its possible values of 0,1, and 2.

1.3.9 COREPEEL

COREPEEL is a method that predict protein complexes in polynomial running time and works well in large PPI networks. The method is available for running in [http://bioalgo.iit.cnr.it/](http://bioalgo.iit.cnr.it/) The approach is based on finding dense communities of the form of quasi-cliques. The method has two basic step, the first consist of applying a core decomposition of the graph where for each vertex in a graph provides a tight upper bound to the size of the largest quasi-clique that includes that vertex. And the second step consists of discarding (peeling out) loosely connected vertices from the quasi-cliques. The method has several parameters, such as the minimum density, maximum size, subgraph min size, 

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Table A28: Results of clustering using MCL varying algorithm parameters in Gavin with complexes of minimum size 3.

| T   | Complexes | FMeasure | Acc  | MMR  | Ex. time(s) |
|-----|-----------|----------|------|------|-------------|
| 1.2 | 63        | 0.5117   | 0.7194| 0.1320| 2.01        |
| 1.4 | 154       | 0.5111   | 0.7294| 0.2984| 2.01        |
| 1.6 | 198       | 0.5119   | 0.7516| 0.3791| 2.01        |
| 1.8 | 218       | 0.5119   | 0.7555| 0.4062| 2.01        |
| 2.0 | 224       | 0.5131   | 0.7613| 0.4268| 2.01        |
| 2.2 | 227       | 0.5187   | 0.7609| 0.4450| 2.01        |
| 2.4 | 236       | 0.5098   | 0.7600| 0.4528| 2.01        |
| 2.6 | 236       | 0.5112   | 0.7575| 0.4558| 2.01        |
| 2.8 | 243       | 0.5193   | 0.7557| 0.4655| 2.01        |
| 3.0 | 246       | 0.5246   | 0.7443| 0.4726| 2.01        |
| 3.2 | 253       | 0.5308   | 0.7448| 0.4794| 2.01        |
| 3.4 | 254       | 0.5372   | 0.7437| 0.4856| 2.01        |
| 3.6 | 253       | 0.5333   | 0.7331| 0.4726| 2.01        |
| 3.8 | 253       | 0.5294   | 0.7380| 0.4801| 2.01        |
| 4.0 | 252       | 0.5201   | 0.7367| 0.4760| 2.01        |
| 4.2 | 252       | 0.5269   | 0.7361| 0.4804| 2.01        |
| 4.4 | 252       | 0.5241   | 0.7312| 0.4782| 2.01        |
| 4.6 | 253       | 0.5227   | 0.7321| 0.4817| 2.01        |
| 4.8 | 250       | 0.5187   | 0.7286| 0.4775| 2.01        |
| 5.0 | 250       | 0.5187   | 0.7245| 0.4770| 2.01        |
| 5.2 | 248       | 0.5147   | 0.7184| 0.4659| 2.01        |
| 5.4 | 248       | 0.5187   | 0.7130| 0.4628| 2.01        |
| 5.6 | 244       | 0.5217   | 0.7092| 0.4552| 2.01        |
| 5.8 | 242       | 0.5232   | 0.7070| 0.4516| 2.01        |
| 6.0 | 240       | 0.5151   | 0.7049| 0.4437| 2.01        |
| 6.2 | 240       | 0.5205   | 0.7046| 0.4451| 2.01        |
| 6.4 | 239       | 0.5220   | 0.7038| 0.4432| 2.01        |
| 6.6 | 238       | 0.5289   | 0.7035| 0.4432| 2.01        |
| 6.8 | 238       | 0.5289   | 0.7011| 0.4443| 2.01        |
| 7.0 | 239       | 0.5275   | 0.6990| 0.4432| 2.01        |
| 7.2 | 239       | 0.5275   | 0.6972| 0.4410| 2.01        |
| 7.4 | 240       | 0.5220   | 0.6960| 0.4399| 2.01        |
| 7.6 | 240       | 0.5301   | 0.6928| 0.4366| 2.01        |
| 7.8 | 238       | 0.5289   | 0.6947| 0.4353| 2.01        |
| 8.0 | 237       | 0.5249   | 0.6942| 0.4341| 2.01        |
| 8.2 | 237       | 0.5193   | 0.6894| 0.4284| 2.01        |
| 8.4 | 235       | 0.5167   | 0.6889| 0.4250| 2.01        |
| 8.6 | 236       | 0.5111   | 0.6883| 0.4250| 2.01        |
| 8.8 | 234       | 0.5125   | 0.6819| 0.4171| 2.01        |
| 9.0 | 233       | 0.5140   | 0.6823| 0.4167| 2.01        |

Filter type (strict, medium, loose) and maximum jaccard separation. We tried between 50 and 100 minimum density, maximum jaccard separation between 0.5 and 1.0 and all the three filter types in all PPI networks.

2 False positive predicted protein complexes

Predicted protein complexes considered as false positive, i.e, protein complexes that are absent in gold standards are analyzed based on the information stored in PDBe containing protein complexes that have been characterized structurally. Many of these PDB ids are present in the Periodic table of protein complexes [7]. We report the complete lists for these candidate complexes in files with the extension .csv. Additionally we report predicted protein complexes found to be false positive that include these candidate protein complexes. This information is stored in files with the extension .xml. Both types of files are included in the results directory included in the software distribution developed in our approach (http://doi.org/10.6084/m9.figshare.5297314.v1).
Table A29: Results of clustering using MCL varying algorithm parameters in Biogrid with complexes of minimum size 3.

| I  | Complexes | FMeasure | Acc | MMR | Ex. time(s) |
|----|-----------|----------|-----|-----|-------------|
| 1.6 | 7         | 0.0082   | 0.0436 | 0.0021 | 59.13       |
| 1.8 | 35        | 0.0444   | 0.1208 | 0.0040 | 59.13       |
| 2.0 | 88        | 0.0807   | 0.2015 | 0.0129 | 59.13       |
| 2.2 | 167       | 0.1100   | 0.2976 | 0.0190 | 59.13       |
| 2.4 | 224       | 0.1641   | 0.3621 | 0.0298 | 59.13       |
| 2.6 | 265       | 0.2195   | 0.4164 | 0.0316 | 59.13       |
| 2.8 | 300       | 0.2661   | 0.4620 | 0.0344 | 59.13       |
| 3.0 | 315       | 0.2960   | 0.4645 | 0.0340 | 59.13       |
| 3.2 | 330       | 0.2648   | 0.4653 | 0.0340 | 59.13       |
| 3.4 | 340       | 0.2355   | 0.4695 | 0.0340 | 59.13       |
| 3.6 | 347       | 0.2134   | 0.4717 | 0.0340 | 59.13       |
| 3.8 | 338       | 0.2372   | 0.4748 | 0.0340 | 59.13       |
| 4.0 | 334       | 0.2384   | 0.4751 | 0.0340 | 59.13       |
| 4.2 | 326       | 0.2274   | 0.4567 | 0.0340 | 59.13       |
| 4.4 | 315       | 0.2308   | 0.4539 | 0.0340 | 59.13       |
| 4.6 | 310       | 0.2230   | 0.4603 | 0.0340 | 59.13       |
| 4.8 | 306       | 0.2097   | 0.4533 | 0.0340 | 59.13       |
| 5.0 | 301       | 0.1966   | 0.4486 | 0.0340 | 59.13       |
| 5.2 | 296       | 0.1985   | 0.4479 | 0.0340 | 59.13       |
| 5.4 | 292       | 0.1962   | 0.4442 | 0.0340 | 59.13       |
| 5.6 | 288       | 0.2054   | 0.4415 | 0.0340 | 59.13       |
| 5.8 | 281       | 0.2074   | 0.4361 | 0.0340 | 59.13       |
| 6.0 | 275       | 0.2099   | 0.4337 | 0.0340 | 59.13       |
| 6.2 | 275       | 0.2059   | 0.4498 | 0.0340 | 59.13       |
| 6.4 | 272       | 0.2072   | 0.4438 | 0.0340 | 59.13       |
| 6.6 | 271       | 0.2036   | 0.4355 | 0.0340 | 59.13       |
| 6.8 | 269       | 0.2004   | 0.4305 | 0.0340 | 59.13       |
| 7.0 | 263       | 0.1947   | 0.4287 | 0.0340 | 59.13       |
| 7.2 | 258       | 0.1926   | 0.4176 | 0.0340 | 59.13       |
| 7.4 | 253       | 0.1860   | 0.4089 | 0.0340 | 59.13       |
| 7.6 | 249       | 0.1792   | 0.4020 | 0.0340 | 59.13       |
| 7.8 | 246       | 0.1719   | 0.3950 | 0.0340 | 59.13       |
| 8.0 | 243       | 0.1688   | 0.3895 | 0.0340 | 59.13       |
| 8.2 | 242       | 0.1691   | 0.3866 | 0.0340 | 59.13       |
| 8.4 | 241       | 0.1695   | 0.3852 | 0.0340 | 59.13       |
| 8.6 | 234       | 0.1591   | 0.3751 | 0.0340 | 59.13       |
| 8.8 | 233       | 0.1548   | 0.3729 | 0.0340 | 59.13       |
| 9.0 | 231       | 0.1469   | 0.3672 | 0.0340 | 59.13       |

References

[1] Pu, S., Wong, J., Turner, B., Cho, E., Wodak, S.J.: Up-to-date catalogues of yeast protein complexes. Nucleic acids research 37(3), 825–831 (2009)

[2] Nepusz, T., Yu, H., Paccanaro, A.: Detecting overlapping protein complexes in protein-protein interaction networks. Nature methods 9(5), 471–472 (2012)

[3] Enright, A.J., Van Dongen, S., Ouzounis, C.A.: An efficient algorithm for large-scale detection of protein families. Nucleic acids research 30(7), 1575–1584 (2002)

[4] Adamcsek, B., Palla, G., Farkas, I.J., Derényi, I., Vicsek, T.: Cfinder: locating cliques and overlapping modules in biological networks. Bioinformatics 22(8), 1021–1023 (2006)

[5] Zhang, X.-F., Dai, D.-Q., Ou-Yang, L., Yan, H.: Detecting overlapping protein complexes based on a generative model with functional and topological properties. BMC bioinformatics 15(1), 186 (2014)
[6] Palla, G., Derényi, I., Farkas, I., Vicsek, T.: Uncovering the overlapping community structure of complex networks in nature and society. Nature 435(7043), 814–818 (2005)

[7] Ahnert, S.E., Marsh, J.A., Hernández, H., Robinson, C.V., Teichmann, S.A.: Principles of assembly reveal a periodic table of protein complexes. Science 350(6266) (2015). doi:10.1126/science.aaa2245. http://science.sciencemag.org/content/350/6266/aaa2245.full.pdf