

Table S1. Summary of experimental results using MIPS protein complexes as evaluation dataset.

Algorithms	Percentage of successful prediction	Absolute number of predictions	Mean Score of valid predicted complexes	Mean predicted size of valid clusters	Sn	PPV	Acc_g
<u>DIP dataset</u>							
MCL	9,91%	84/848	0,468	6,988	48,96%	52,97%	50,93%
Spectral	11,04%	50/453	0,441	7,801	66,84%	33,46%	47,29%
Affinity	9,40%	42/447	0,422	6,690	37,39%	36,73%	37,06%
RNSC	10,83%	99/914	0,483	6,717	49,64%	57,40%	53,38%
<u>MIPS dataset</u>							
MCL	9,57%	83/867	0,482	5,373	45,69%	52,67%	49,06%
Spectral	10,47%	53/506	0,457	5,962	58,68%	37,37%	46,83%
Affinity	8,35%	36/431	0,426	5,833	38,47%	35,97%	37,20%
RNSC	11,35%	95/837	0,443	5,442	43,83%	56,25%	49,65%
<u>Gavin_2002 dataset</u>							
MCL	33,98%	70/206	0,579	8,214	74,26%	56,97%	65,04%
Spectral	37,27%	41/110	0,536	8,951	75,84%	43,85%	57,67%
Affinity	32,67%	49/150	0,534	7,510	64,47%	47,25%	55,19%
RNSC	35,26%	67/190	0,475	6,925	67,78%	54,51%	60,79%
<u>Gavin_2006 dataset</u>							
MCL	32,02%	57/178	0,531	10,053	76,42%	53,97%	64,22%
Spectral	42,19%	54/128	0,488	8,333	75,03%	49,59%	61,00%
Affinity	31,47%	45/143	0,511	7,533	61,80%	45,61%	53,09%
RNSC	33,16%	62/187	0,482	8,323	65,32%	55,99%	60,48%
<u>Krogan dataset</u>							
MCL	15,72%	83/528	0,520	7,506	63,07%	56,09%	59,48%
Spectral	18,46%	48/260	0,500	9,188	70,45%	40,30%	53,28%
Affinity	16,28%	49/301	0,506	6,592	52,01%	41,71%	46,58%
RNSC	23,73%	75/316	0,424	9,000	61,84%	54,59%	58,10%
<u>Tong Dataset</u>							
MCL	4,44%	15/338	0,357	4,733	43,95%	40,89%	42,39%
Spectral	6,15%	11/179	0,405	3,545	55,83%	32,32%	42,48%
Affinity	2,44%	6/246	0,317	3,333	41,14%	31,29%	35,88%
RNSC	4,26%	12/282	0,386	6,000	47,87%	44,72%	46,27%

Table S2. Summary of experimental results using BT_409 protein complexes collection as evaluation dataset.

Algorithms	Percentage of successful prediction	Absolute number of predictions	Mean Score of valid predicted complexes	Mean predicted size of valid clusters	Sn	PPV	Acc_g
<u>DIP dataset</u>							
MCL	19,22%	163/848	0,421	5,785	59,94%	65,29%	62,56%
Spectral	17,44%	79/453	0,420	9,114	73,16%	43,26%	56,26%
Affinity	13,20%	59/447	0,413	5,847	45,50%	40,72%	43,04%
RNSC	18,27%	167/914	0,453	6,234	58,52%	72,94%	65,33%
<u>MIPS dataset</u>							
MCL	14,99%	130/867	0,397	4,200	46,14%	57,98%	51,72%
Spectral	14,43%	73/506	0,408	4,315	58,63%	40,03%	48,45%
Affinity	11,60%	50/431	0,378	5,060	43,91%	37,56%	40,61%
RNSC	14,70%	123/837	0,394	4,675	47,06%	63,27%	54,57%
<u>Gavin 2002 dataset</u>							
MCL	64,56%	133/206	0,617	7,850	86,66%	74,63%	80,42%
Spectral	66,36%	73/110	0,603	9,370	87,25%	61,66%	73,35%
Affinity	60,67%	91/150	0,531	7,462	72,58%	60,69%	66,37%
RNSC	63,68%	121/190	0,535	6,512	74,95%	73,57%	74,26%
<u>Gavin 2006 dataset</u>							
MCL	71,91%	128/178	0,615	8,914	92,60%	71,08%	81,13%
Spectral	85,16%	109/128	0,572	9,330	86,82%	61,91%	73,32%
Affinity	65,73%	94/143	0,583	7,617	75,93%	58,35%	66,56%
RNSC	71,12%	133/187	0,530	7,647	81,64%	73,53%	77,48%
<u>Krogan dataset</u>							
MCL	45,27%	239/528	0,601	5,841	77,12%	79,12%	78,11%
Spectral	51,92%	135/260	0,558	6,904	81,04%	54,69%	66,57%
Affinity	34,88%	105/301	0,544	5,838	60,76%	50,88%	55,60%
RNSC	71,12%	133/187	0,530	7,647	81,64%	73,53%	77,48%
<u>Tong Dataset</u>							
MCL	8,88%	30/338	0,373	5,833	53,77%	44,37%	48,84%
Spectral	13,41%	24/179	0,351	4,333	66,31%	34,77%	48,02%
Affinity	4,88%	12/246	0,355	3,167	51,20%	33,21%	41,24%
RNSC	7,45%	21/282	0,414	6,524	57,37%	46,92%	51,88%

Table S3. MCL algorithm behavior depending on the inflation parameter, using MIPS protein complexes as evaluation dataset.

Algorithms	Percentage of successful prediction	Absolute number of predictions	Mean Score of valid predicted complexes	Mean predicted size of valid clusters	Sn	PPV	Acc_g
<u>DIP dataset</u>							
1.8	9,91%	84/848	0,468	6,988	48,96%	52,97%	50,93%
2	10,05%	101/1005	0,449	6,000	46,90%	56,98%	51,70%
2.2	9,04%	105/1161	0,454	4,952	45,12%	59,15%	51,66%
<u>MIPS dataset</u>							
1.8	9,57%	83/867	0,482	5,373	45,69%	52,67%	49,06%
2	9,22%	93/1009	0,487	4,559	42,96%	56,74%	49,37%
2.2	9,07%	102/1125	0,501	4,049	41,76%	58,31%	49,35%
<u>Gavin_2002 dataset</u>							
1.8	33,98%	70/206	0,579	8,214	74,26%	56,97%	65,04%
2	29,79%	70/235	0,584	7,671	70,69%	58,50%	64,31%
2.2	29,44%	73/248	0,591	6,890	67,71%	59,25%	63,34%
<u>Gavin_2006 dataset</u>							
1.8	32,02%	57/178	0,531	10,053	76,42%	53,97%	64,22%
2	30,92%	64/207	0,531	9,625	74,60%	55,58%	64,39%
2.2	29,69%	68/229	0,548	8,044	72,84%	57,53%	64,73%
<u>Krogan dataset</u>							
1.8	15,72%	83/528	0,520	7,506	63,07%	56,09%	59,48%
2	14,53%	86/592	0,523	7,186	60,43%	57,05%	58,72%
2.2	14,80%	94/635	0,508	6,468	59,05%	58,48%	58,76%
<u>Tong Dataset</u>							
1.8	4,44%	15/338	0,357	4,733	43,95%	40,89%	42,39%
2	4,89%	18/368	0,346	4,389	43,18%	43,18%	43,18%
2.2	4,81%	19/395	0,344	4,263	42,21%	44,76%	43,47%

Table S4. MCL algorithm behavior depending on the inflation parameter, using BT_409 protein complexes collection as evaluation dataset.

Algorithms	Percentage of successful prediction	Absolute number of predictions	Mean Score of valid predicted complexes	Mean predicted size of valid clusters	Sn	PPV	Acc_g
<u>DIP dataset</u>							
1.8	19,22%	163/848	0,421	5,785	59,94%	65,29%	62,56%
2	18,71%	188/1005	0,427	4,920	56,97%	71,04%	63,62%
2.2	18,35%	213/1161	0,425	4,291	55,71%	75,26%	64,75%
<u>MIPS dataset</u>							
1.8	14,99%	130/867	0,397	4,200	46,14%	57,98%	51,72%
2	14,97%	151/1009	0,388	3,748	45,23%	63,37%	53,54%
2.2	14,67%	165/1125	0,411	3,412	45,75%	66,67%	55,23%
<u>Gavin 2002 dataset</u>							
1.8	64,56%	133/206	0,617	7,850	86,66%	74,63%	80,42%
2	58,72%	138/235	0,610	6,790	81,65%	76,59%	79,08%
2.2	58,06%	144/248	0,599	6,410	78,93%	77,43%	78,18%
<u>Gavin 2006 dataset</u>							
1.8	71,91%	128/178	0,615	8,914	92,60%	71,08%	81,13%
2	71,50%	148/207	0,600	7,764	92,28%	75,11%	83,25%
2.2	69,43%	159/229	0,592	7,069	88,98%	76,99%	82,77%
<u>Krogan dataset</u>							
1.8	45,27%	239/528	0,601	5,841	77,12%	79,12%	78,11%
2	43,41%	257/592	0,593	5,191	73,51%	81,01%	77,17%
2.2	42,52%	270/635	0,591	4,781	71,96%	83,52%	77,52%
<u>Tong Dataset</u>							
1.8	8,88%	30/338	0,373	5,833	53,77%	44,37%	48,84%
2	8,15%	30/368	0,373	5,333	53,37%	46,28%	49,70%
2.2	7,85%	31/395	0,374	5,129	52,63%	47,84%	50,18%

Table S5. Summary of experimental results with altered datasets, using MIPS protein complexes as evaluation dataset.

Algorithms	Percentage of successful prediction	Absolute number of predictions	Mean Score of valid predicted complexes	Mean predicted size of valid clusters	Sn	PPV	Acc_g
<u>Complexes rm 10 ad 10</u>							
MCL	79.57%	74/93	0.789	10.432	81.11%	51.05%	64.34%
Spectral	97.32%	109/112	0.760	9.624	89.76%	61.82%	74.49%
Affinity	88.76%	79/89	0.673	12.215	83.19%	55.10%	67.71%
RNSC	99.25%	133/134	0.935	8.098	95.09%	68.95%	80.97%
<u>Complexes rm 20 ad 20</u>							
MCL	85.00%	68/80	0.745	10.353	83.32%	53.92%	67.02%
Spectral	92.93%	92/99	0.710	10.848	93.03%	58.34%	73.67%
Affinity	81.44%	79/97	0.528	12.127	71.17%	50.03%	59.67%
RNSC	97.06%	132/136	0.813	8.008	92.58%	67.19%	78.87%
<u>Complexes rm 40 ad 40</u>							
MCL	74.47%	35/47	0.374	4.086	88.73%	60.21%	73.09%
Spectral	81.00%	81/100	0.590	11.074	81.25%	52.98%	65.61%
Affinity	50.57%	44/87	0.337	15.364	51.89%	37.20%	43.94%
RNSC	64.29%	117/182	0.612	7.692	77.31%	60.09%	68.16%