

**Supplementary Table 1.** Shown are the properties, i.e. number of proteins and interactions, in the PPI networks used in our analysis. Y stands for yeast and H for human. We also show the number of proteins and complexes in each of the gold standards used in our analysis. Finally, we also show the number of nodes and edges in the intersection of the PPI networks and gold standards of yeast and human, respectively.

<b>PPI networks</b>						
	Collins (Y)	Gavin (Y)	KroganCore (Y)	KroganExt (Y)	STRING (H)	PIPS (H)
<b>#Proteins</b>	1,622	1,855	2,708	3,672	2,227	1,673
<b>#Interactions</b>	9,074	7,669	7,123	14,317	8,565	5,385
<b>Diameter</b>	15	13	12	10	21	18

### Gold standards

	SGD(Y)	CYC2008(Y)	Corum
<b>#proteins</b>	1,279	1,627	4,479
<b>#complexes</b>	323	408	4,274
<b>#complexes ≥ 3</b>	238	236	2,783

<b>Intersection of PPI networks and gold standards</b>				
MIPS	Collins(Y)	Gavin(Y)	KroganCore(Y)	KroganExt(Y)
<b>#Proteins</b>	773	766	780	888
<b>#interactions</b>	4,778	2,695	1,797	2,639
SGD	Collins(Y)	Gavin(Y)	KroganCore(Y)	KroganExt(Y)
<b>#Proteins</b>	830	776	944	1,057
<b>#interactions</b>	2,955	2,639	2,554	3,688
CYC2008	Collins(Y)	Gavin(Y)	KroganCore(Y)	KroganExt(Y)
<b>#Proteins</b>	1,116	1,047	1,149	1,263
<b>#interactions</b>	6,392	4,031	3,169	4,714
Corum	STRING(H)	PIPS(H)		
<b>#Proteins</b>	1,711	871		
<b>#interactions</b>	7,289	2,692		

**Supplementary Table 2.** Shown is the modularity of the clustering obtained by applying each of the eight compared algorithms on the PPI networks from yeast and human, respectively. The algorithms are ordered based on the year of publication.

Modularity-Yeast												
Method	Collins	Rank	Deviation of second best compared to PC2P	Gavin	Rank	Deviation of second best compared to PC2P	KroganCore	Rank	Deviation of second best compared to PC2P	KroganExt	Rank	Deviation of second best compared to PC2P
MCL	0.7450	1	<b>Not Best 2.2%</b>	0.7115	2	<b>1.12%</b>	0.1461	8	<b>27.63%</b>	0.3157	2	<b>11.48%</b>
MCODE	0.5817	5		0.5166	4		0.2522	5		0.1982	6	
CFinder	0.6116	4		0.5487	3		0.2953	3		0.1108	7	
AP	0.1350	8		0.2017	8		0.2314	6		0.1079	8	
CMC	0.3000	7		0.3065	7		0.2586	4		0.2040	4	
ClusterOne	0.5671	6		0.5003	5		0.2244	7		0.2005	5	
ProRank+	0.0341	10		0.0917	9		0.0338	9		0.0603	9	
Core&Peel	0.0346	9		0.0862	10		0.0102	10		0.0132	10	
IMHRC	0.6125	3		0.4652	6		0.3527	2		0.2107	3	
PC2P	0.7287	2		0.7196	1		0.4873	1		0.3566	1	

Modularity-Human						
Method	STRING	Rank	Deviation of PC2P Compared to the Best	PIPS	Rank	Deviation of second best compared to PC2P
MCL	0.7664	1	<b>Not Best 4.56%</b>	0.1413	7	<b>21.63%</b>
MCODE	0.5024	6		0.1908	5	
CFinder	0.6893	3		0.3742	2	
AP	0.1798	7		0.1880	6	
CMC	0.0726	8		0.0442	8	
ClusterOne	0.5799	5		0.2074	4	
ProRank+	0.0287	9		0.0243	9	
Core&Peel	0.0233	10		0.0069	10	
IMHRC	0.6423	4		0.3142	3	
PC2P	0.7314	2		0.4774	1	

**Supplementary Table 2.** Shown is the modularity of the clustering obtained by applying each of the eight compared algorithms on the PPI networks from yeast and human, respectively. The algorithms are ordered based on the year of publication.

Overlapped Modularity-Yeast												
Method	Collins	Rank	Deviation of second best compared to PC2P	Gavin	Rank	Deviation of second best compared to PC2P	KroganCore	Rank	Deviation of second best compared to PC2P	KroganExt	Rank	Deviation of second best compared to PC2P
MCL	0.6866	2	2.58%	0.2781	6	Not Best 3.77%	0.4969	1	Not Best 44.16%	0.0331	3	Not Best 26.69%
MCODE	0.5543	5		0.3211	5		0.2117	5		-0.0624	7	
CFinder	0.6783	3		0.3675	1		0.2307	4		-0.0713	8	
AP	0.5566	4		0.1804	8		0.2448	3		0.1145	1	
CMC	0.5347	6		0.2240	7		0.1911	7		-0.0588	6	
ClusterOne	0.4990	8		0.3381	3		0.2775	2		0.0839	2	
ProRank+	0.1347	9		0.1491	9		0.1090	9		0.0135	5	
Core&Peel	0.1193	10		0.0655	10		-0.0020	10		-0.0811	9	
IMHRC	0.5089	7		0.3313	4		0.1493	8		0.0149	4	
PC2P	0.7048	1		0.3536	2		0.1933	6		-0.0846	10	

Overlapped Modularity-Human						
Method	STRING	Rank	Deviation of PC2P Compared to the Best	PIPS	Rank	Deviation of second best compared to PC2P
MCL	0.6845	1	Not Best 3.58%	0.7908	1	Not Best 48.21%
MCODE	0.4742	6		0.2735	5	
CFinder	0.6050	3		0.4096	2	
AP	0.5916	4		0.3687	3	
CMC	0.2009	8		-0.0115	10	
ClusterOne	0.4603	7		0.1809	7	
ProRank+	0.1301	9		0.1078	8	
Core&Peel	0.0997	10		0.0208	9	
IMHRC	0.4999	5		0.2338	6	
PC2P	0.6600	2		0.3480	4	

**Supplementary Table 3.** Comparative analysis of eight algorithms for prediction of protein complexes with respect to nine performance measures as well as a composite score that combines five of them. Shown is also the modularity of the resulting clusterings.

Comparative analysis																					
Yeast - CYC2008																					
Data-set	Method	# Clusters	MMR	FRM	SEP	PPV	SN	ACC	Prec	Rec	F-measure	CDAP_prec	CDAP_rec	CDAP_fmeas	CDAP_F_MMR	Modularity	Overlapped Modularity	Composite Score (CS) MMR + FRM + SEP + ACC + F-measure	CS Ranking	Deviation of PC2P to Max in CS	Deviation of second best in CS compared to PC2P (if PC2P is best)
Collin	MCL	193	0.558	0.840	0.743	0.648	0.950	0.785	0.912	0.693	0.787	0.870	0.573	0.691	1.250	0.799	0.776	3.713	1	3.05%	Not Best
	MCODE	93	0.255	0.389	0.528	0.665	0.633	0.649	0.892	0.331	0.483	0.849	0.270	0.409	0.665	0.623	0.669	2.304	6		
	CFinder	89	0.247	0.389	0.493	0.532	0.775	0.642	0.888	0.314	0.464	0.843	0.256	0.393	0.640	0.749	0.770	2.235	8		
	AP	413	0.511	0.785	0.416	0.506	0.717	0.603	0.392	0.645	0.488	0.356	0.502	0.416	0.928	0.270	0.618	2.803	4		
	CMC	119	0.205	0.324	0.333	0.646	0.538	0.590	0.622	0.266	0.373	0.571	0.232	0.330	0.535	0.343	0.363	1.825	9		
	ClusterOne	127	0.338	0.597	0.553	0.611	0.833	0.714	0.898	0.488	0.632	0.819	0.355	0.495	0.833	0.705	0.636	2.834	3		
	ProRank+	458	0.382	0.491	0.238	0.477	0.796	0.616	0.683	0.433	0.530	0.251	0.392	0.306	0.688	0.284	0.164	2.258	7		
	Core&Peel	210	0.181	0.266	0.198	0.647	0.499	0.568	0.457	0.218	0.296	0.276	0.198	0.231	0.412	0.249	0.174	1.509	10		
	IMHRC	118	0.322	0.584	0.549	0.605	0.851	0.718	0.907	0.437	0.590	0.839	0.338	0.482	0.804	0.731	0.671	2.762	5		
	PC2P	251	0.568	0.863	0.671	0.679	0.899	0.781	0.717	0.713	0.715	0.665	0.570	0.614	1.182	0.760	0.761	3.600	2		
Gavin	MCL	128	0.312	0.570	0.568	0.509	0.914	0.682	0.797	0.433	0.561	0.695	0.306	0.425	0.736	0.856	0.624	2.693	2	0.00%	12.00%
	MCODE	87	0.209	0.333	0.490	0.562	0.654	0.606	0.770	0.265	0.394	0.701	0.210	0.323	0.532	0.651	0.538	2.033	8		
	CFinder	103	0.245	0.443	0.465	0.485	0.816	0.629	0.806	0.337	0.475	0.718	0.254	0.376	0.620	0.796	0.605	2.258	6		
	AP	301	0.264	0.478	0.289	0.366	0.719	0.513	0.292	0.357	0.322	0.219	0.227	0.223	0.487	0.383	0.290	1.866	9		
	CMC	138	0.239	0.399	0.394	0.649	0.568	0.607	0.717	0.337	0.458	0.522	0.247	0.336	0.575	0.429	0.334	2.097	7		
	ClusterOne	140	0.301	0.564	0.494	0.574	0.801	0.678	0.757	0.426	0.545	0.621	0.299	0.404	0.705	0.726	0.513	2.582	3		
	ProRank+	395	0.363	0.553	0.265	0.523	0.808	0.650	0.770	0.457	0.574	0.273	0.371	0.315	0.678	0.429	0.173	2.405	5		
	Core&Peel	176	0.179	0.282	0.248	0.682	0.484	0.575	0.631	0.230	0.337	0.330	0.199	0.248	0.427	0.332	0.173	1.621	10		
	IMHRC	127	0.269	0.557	0.485	0.538	0.843	0.673	0.669	0.357	0.466	0.575	0.251	0.349	0.618	0.759	0.541	2.450	4		
	PC2P	203	0.417	0.722	0.578	0.622	0.841	0.723	0.685	0.567	0.620	0.571	0.399	0.470	0.887	0.791	0.541	3.060	1		
KroganCore	MCL	176	0.371	0.569	0.585	0.531	0.882	0.685	0.795	0.454	0.578	0.744	0.379	0.502	0.873	0.714	0.480	2.789	2	0.00%	17.91%
	MCODE	65	0.117	0.191	0.366	0.581	0.367	0.462	0.677	0.136	0.226	0.569	0.107	0.180	0.297	0.388	0.376	1.362	8		
	CFinder	87	0.176	0.289	0.388	0.494	0.643	0.564	0.828	0.228	0.358	0.759	0.191	0.305	0.481	0.623	0.462	1.774	7		
	AP	244	0.279	0.462	0.351	0.345	0.711	0.495	0.451	0.350	0.394	0.328	0.231	0.271	0.550	0.417	0.341	1.982	5		
	CMC	102	0.121	0.211	0.267	0.659	0.312	0.454	0.549	0.150	0.236	0.412	0.121	0.188	0.308	0.240	0.107	1.289	9		
	ClusterOne	189	0.315	0.540	0.470	0.619	0.748	0.680	0.762	0.425	0.546	0.556	0.303	0.393	0.708	0.594	0.321	2.551	3		
	ProRank+	340	0.246	0.350	0.206	0.512	0.661	0.582	0.741	0.301	0.428	0.262	0.257	0.259	0.505	0.271	0.136	1.811	6		
	Core&Peel	144	0.085	0.150	0.143	0.652	0.252	0.405	0.472	0.101	0.167	0.201	0.084	0.118	0.204	0.176	0.070	0.950	10		
	IMHRC	161	0.263	0.517	0.457	0.550	0.791	0.660	0.677	0.321	0.435	0.528	0.246	0.335	0.598	0.611	0.343	2.332	4		
	PC2P	338	0.556	0.815	0.618	0.697	0.788	0.741	0.642	0.694	0.667	0.530	0.517	0.523	1.079	0.643	0.402	3.397	1		
KroganExt	MCL	236	0.362	0.590	0.555	0.582	0.774	0.671	0.674	0.466	0.551	0.568	0.359	0.440	0.802	0.517	0.138	2.729	2	0.00%	12.54%
	MCODE	54	0.089	0.145	0.334	0.491	0.353	0.417	0.648	0.097	0.168	0.593	0.086	0.150	0.239	0.293	0.100	1.152	9		
	CFinder	69	0.119	0.188	0.299	0.302	0.681	0.453	0.739	0.150	0.250	0.681	0.126	0.213	0.331	0.290	0.217	1.308	8		
	AP	320	0.275	0.483	0.298	0.335	0.593	0.446	0.384	0.330	0.355	0.203	0.174	0.188	0.463	0.237	0.090	1.856	5		
	CMC	125	0.135	0.231	0.280	0.616	0.351	0.465	0.624	0.182	0.282	0.440	0.147	0.221	0.355	0.194	-0.013	1.393	7		
	ClusterOne	144	0.222	0.378	0.419	0.610	0.591	0.600	0.792	0.311	0.447	0.646	0.249	0.360	0.582	0.380	0.193	2.067	3		
	ProRank+	206	0.173	0.273	0.239	0.570	0.550	0.560	0.680	0.217	0.329	0.330	0.182	0.235	0.408	0.202	0.112	1.574	6		
	Core&Peel	185	0.097	0.164	0.144	0.589	0.290	0.413	0.535	0.123	0.200	0.222	0.110	0.147	0.244	0.128	0.009	1.018	10		
	IMHRC	192	0.229	0.491	0.365	0.472	0.802	0.615	0.490	0.239	0.321	0.359	0.185	0.244	0.473	0.471	0.137	2.020	4		
	PC2P	422	0.504	0.775	0.560	0.670	0.717	0.693	0.536	0.651	0.588	0.384	0.434	0.408	0.912	0.482	0.073	3.120	1		

**Supplementary Table 3.** Comparative analysis of eight algorithms for prediction of protein complexes with respect to nine performance measures as well as a composite score that combines five of them. Shown is also the modularity of the resulting clusterings.

Comparative analysis																					
Yeast - SGD																					
Data-set	Method	# Clusters	MMR	FRM	SEP	PPV	SN	ACC	Prec	Rec	F-measure	CDAP_prec	CDAP_rec	CDAP_fmeas	CDAP_F_MMR	Modularity	Overlapped Modularity	Composite Score (CS) MMR + FRM + SEP + ACC + F-measure	CS Ranking	Deviation of PC2P to Max in CS	Deviation of second best in CS compared to PC2P (if PC2P is best)
Collins	MCL	156	0.508	0.791	0.671	0.566	0.863	0.699	0.859	0.643	0.735	0.821	0.514	0.632	1.140	0.891	0.804	3.404	2	0.00%	0.16%
	MCODE	85	0.262	0.438	0.503	0.541	0.630	0.584	0.800	0.333	0.471	0.800	0.273	0.407	0.670	0.713	0.700	2.258	8		
	CFinder	83	0.272	0.474	0.503	0.484	0.758	0.606	0.855	0.337	0.484	0.843	0.281	0.422	0.693	0.831	0.796	2.339	7		
	AP	272	0.507	0.787	0.425	0.452	0.698	0.562	0.515	0.635	0.568	0.445	0.486	0.464	0.972	0.462	0.692	2.850	3		
	CMC	74	0.203	0.349	0.370	0.525	0.534	0.529	0.851	0.285	0.427	0.757	0.225	0.347	0.549	0.521	0.557	1.879	9		
	ClusterOne	104	0.338	0.570	0.533	0.551	0.759	0.647	0.885	0.458	0.603	0.865	0.361	0.510	0.848	0.807	0.727	2.692	4		
	ProRank+	314	0.407	0.562	0.275	0.446	0.761	0.583	0.803	0.462	0.586	0.322	0.406	0.359	0.765	0.474	0.226	2.413	6		
	Core&Peel	106	0.181	0.305	0.243	0.496	0.502	0.499	0.736	0.241	0.363	0.472	0.201	0.282	0.463	0.405	0.319	1.592	10		
	IMHRC	103	0.335	0.566	0.527	0.548	0.766	0.648	0.883	0.438	0.585	0.854	0.353	0.500	0.835	0.784	0.718	2.661	5		
	PC2P	182	0.525	0.827	0.644	0.580	0.842	0.699	0.758	0.675	0.714	0.725	0.530	0.613	1.137	0.873	0.805	3.409	1		
	Gavin	MCL	97	0.291	0.510	0.537	0.430	0.895	0.621	0.825	0.382	0.523	0.753	0.291	0.420	0.711	0.827	0.709	2.481		
MCODE		77	0.220	0.394	0.464	0.504	0.648	0.572	0.779	0.267	0.398	0.714	0.219	0.335	0.555	0.647	0.576	2.047	7		
CFinder		83	0.244	0.470	0.462	0.437	0.808	0.594	0.795	0.303	0.439	0.771	0.255	0.383	0.627	0.793	0.668	2.209	6		
AP		226	0.277	0.498	0.297	0.349	0.636	0.471	0.332	0.339	0.335	0.261	0.235	0.247	0.524	0.450	0.334	1.878	9		
CMC		107	0.228	0.398	0.374	0.535	0.561	0.548	0.673	0.303	0.418	0.533	0.227	0.318	0.546	0.451	0.388	1.966	8		
ClusterOne		109	0.293	0.598	0.492	0.511	0.809	0.643	0.780	0.406	0.534	0.716	0.311	0.433	0.726	0.778	0.589	2.560	2		
ProRank+		290	0.352	0.554	0.273	0.455	0.797	0.602	0.759	0.406	0.529	0.310	0.359	0.333	0.685	0.480	0.211	2.310	5		
Core&Peel		132	0.187	0.319	0.245	0.510	0.493	0.501	0.621	0.227	0.333	0.364	0.191	0.251	0.437	0.370	0.237	1.585	10		
IMHRC		104	0.273	0.566	0.474	0.483	0.809	0.625	0.769	0.382	0.511	0.673	0.279	0.394	0.668	0.778	0.600	2.449	4		
PC2P		159	0.421	0.753	0.578	0.567	0.822	0.683	0.761	0.578	0.657	0.654	0.414	0.507	0.928	0.810	0.630	3.091	1		
KroganCore		MCL	140	0.374	0.565	0.546	0.460	0.804	0.608	0.800	0.471	0.593	0.736	0.373	0.495	0.869	0.785	0.536	2.686	2	0.00%
	MCODE	54	0.126	0.239	0.367	0.466	0.387	0.425	0.685	0.156	0.254	0.611	0.120	0.200	0.326	0.425	0.417	1.411	8		
	CFinder	73	0.193	0.333	0.399	0.422	0.632	0.516	0.877	0.257	0.398	0.795	0.210	0.332	0.526	0.635	0.493	1.839	7		
	AP	208	0.315	0.507	0.330	0.290	0.704	0.452	0.433	0.359	0.392	0.370	0.279	0.318	0.633	0.437	0.342	1.997	5		
	CMC	81	0.130	0.254	0.274	0.551	0.335	0.430	0.605	0.167	0.261	0.506	0.149	0.230	0.359	0.271	0.185	1.348	9		
	ClusterOne	137	0.324	0.507	0.475	0.516	0.703	0.602	0.796	0.428	0.556	0.664	0.330	0.441	0.765	0.622	0.374	2.465	3		
	ProRank+	297	0.278	0.399	0.210	0.423	0.639	0.520	0.717	0.341	0.462	0.269	0.290	0.279	0.557	0.283	0.140	1.867	6		
	Core&Peel	130	0.104	0.192	0.140	0.500	0.289	0.380	0.477	0.127	0.200	0.231	0.109	0.148	0.251	0.192	0.085	1.016	10		
	IMHRC	122	0.282	0.518	0.456	0.500	0.734	0.606	0.754	0.355	0.483	0.623	0.275	0.382	0.664	0.687	0.390	2.344	4		
	PC2P	256	0.516	0.793	0.564	0.583	0.738	0.656	0.637	0.681	0.658	0.543	0.504	0.523	1.039	0.698	0.469	3.187	1		
	KroganExt	MCL	71	0.170	0.243	0.357	0.189	0.906	0.414	0.704	0.189	0.298	0.662	0.159	0.256	0.426	0.194	0.475	1.483	6	
MCODE		39	0.080	0.122	0.310	0.338	0.372	0.355	0.692	0.098	0.172	0.667	0.088	0.155	0.235	0.318	0.227	1.038	10		
CFinder		57	0.127	0.209	0.303	0.253	0.639	0.402	0.789	0.162	0.269	0.684	0.132	0.221	0.348	0.276	0.271	1.311	8		
AP		235	0.239	0.422	0.279	0.299	0.543	0.403	0.340	0.287	0.312	0.221	0.176	0.196	0.435	0.286	0.109	1.655	4		
CMC		97	0.151	0.267	0.288	0.519	0.359	0.432	0.629	0.203	0.307	0.485	0.159	0.239	0.390	0.214	0.055	1.445	7		
ClusterOne		116	0.250	0.392	0.433	0.529	0.569	0.549	0.862	0.328	0.475	0.724	0.284	0.408	0.658	0.402	0.264	2.099	2		
ProRank+		185	0.207	0.318	0.249	0.453	0.530	0.490	0.692	0.257	0.375	0.351	0.220	0.270	0.477	0.212	0.124	1.638	5		
Core&Peel		149	0.114	0.199	0.153	0.495	0.310	0.392	0.510	0.142	0.222	0.242	0.122	0.162	0.276	0.149	0.038	1.080	9		
IMHRC		149	0.240	0.459	0.360	0.420	0.704	0.543	0.570	0.291	0.385	0.443	0.223	0.297	0.537	0.503	0.177	1.988	3		
PC2P		324	0.469	0.716	0.502	0.565	0.663	0.612	0.485	0.588	0.531	0.386	0.422	0.403	0.872	0.533	0.201	2.830	1		

**Supplementary Table 3.** Comparative analysis of eight algorithms for prediction of protein complexes with respect to nine performance measures as well as a composite score that combines five of them. Shown is also the modularity of the resulting clusterings.

Comparative analysis																					
Human - Corum																					
Data-set	Method	# Clusters	MMR	FRM	SEP	PPV	SN	ACC	Prec	Rec	F-measure	CDAP_prec	CDAP_rec	CDAP_fmeas	CDAP_F_MMR	Modularity	Overlapped Modularity	Composite Score (CS) MMR + FRM + SEP + ACC + F-measure	CS Ranking	Deviation of PC2P to Max in CS	Deviation of second best in CS compared to PC2P (if PC2P is best)
STRING	MCL	384	0.089	0.606	0.237	0.139	0.754	0.323	0.802	0.404	0.537	0.664	0.085	0.150	0.239	0.721	0.655	1.792	2	0.00%	0.15%
	MCODE	114	0.026	0.198	0.156	0.145	0.378	0.234	0.763	0.119	0.206	0.728	0.028	0.053	0.079	0.523	0.495	0.820	8		
	CFinder	119	0.030	0.263	0.159	0.125	0.569	0.266	0.866	0.146	0.249	0.807	0.032	0.061	0.091	0.693	0.621	0.967	7		
	AP	501	0.078	0.512	0.160	0.098	0.738	0.268	0.537	0.342	0.418	0.419	0.070	0.119	0.197	0.316	0.558	1.435	3		
	CMC	132	0.023	0.132	0.094	0.148	0.283	0.205	0.636	0.089	0.155	0.523	0.023	0.044	0.067	0.330	0.246	0.608	9		
	ClusterOne	243	0.053	0.419	0.183	0.128	0.652	0.289	0.794	0.234	0.362	0.646	0.052	0.096	0.149	0.651	0.491	1.305	4		
	ProRank+	587	0.083	0.349	0.080	0.140	0.579	0.285	0.714	0.235	0.354	0.443	0.086	0.144	0.227	0.275	0.145	1.151	6		
	Core&Peel	206	0.025	0.091	0.049	0.143	0.241	0.186	0.515	0.059	0.106	0.374	0.026	0.048	0.073	0.191	0.124	0.458	10		
	IMHRC	213	0.047	0.398	0.188	0.127	0.732	0.304	0.756	0.196	0.311	0.648	0.046	0.085	0.133	0.679	0.517	1.248	5		
	PC2P	462	0.094	0.616	0.227	0.141	0.755	0.326	0.723	0.421	0.532	0.546	0.084	0.145	0.239	0.721	0.651	1.795	1		
Data-set	Method	# Clusters	MMR	FRM	SEP	PPV	SN	ACC	Prec	Rec	F-measure	CDAP_prec	CDAP_rec	CDAP_fmeas	CDAP_F_MMR	Modularity	Overlapped Modularity	Composite Score (CS) MMR + FRM + SEP + ACC + F-measure	CS Ranking	Deviation of PC2P to Max in CS	Deviation of second best in CS compared to PC2P (if PC2P is best)
PIPS	MCL	73	0.018	0.119	0.127	0.043	0.906	0.196	0.740	0.099	0.174	0.452	0.014	0.027	0.044	0.298	0.593	0.634	4	0.00%	24.35%
	MCODE	32	0.006	0.060	0.106	0.069	0.292	0.141	0.406	0.015	0.029	0.281	0.004	0.007	0.013	0.221	0.192	0.341	9		
	CFinder	36	0.008	0.061	0.090	0.043	0.621	0.163	0.556	0.023	0.044	0.417	0.006	0.012	0.020	0.391	0.435	0.366	8		
	AP	222	0.051	0.371	0.142	0.064	0.687	0.210	0.635	0.267	0.376	0.392	0.036	0.066	0.117	0.293	0.356	1.150	2		
	CMC	68	0.009	0.103	0.077	0.057	0.359	0.143	0.338	0.065	0.108	0.235	0.007	0.013	0.022	0.132	0.024	0.440	7		
	ClusterOne	83	0.015	0.131	0.124	0.075	0.477	0.189	0.386	0.048	0.085	0.301	0.010	0.020	0.035	0.394	0.297	0.544	6		
	ProRank+	212	0.030	0.234	0.059	0.054	0.569	0.176	0.396	0.096	0.154	0.250	0.022	0.040	0.070	0.128	0.113	0.653	3		
	Core&Peel	123	0.010	0.063	0.046	0.058	0.300	0.132	0.203	0.026	0.047	0.138	0.007	0.013	0.023	0.088	0.031	0.298	10		
	IMHRC	99	0.017	0.110	0.126	0.062	0.699	0.208	0.374	0.055	0.097	0.303	0.012	0.024	0.041	0.470	0.278	0.557	5		
	PC2P	302	0.078	0.495	0.218	0.098	0.713	0.264	0.689	0.351	0.465	0.454	0.057	0.101	0.178	0.494	0.366	1.520	1		



Supplementary Table 4. Result of the post-hoc Tukey test between means of GO semantic similarity over the clusters for biological process (BP), molecular function (MF), and cellular compartment (CC). Results are shown for min and mean analyses for four data sets of yeast and two data sets of human.

Yc	Mean				Min							
	BP		MF		BP		MF					
	diff	p-val	diff	p-val	diff	p-val	diff	p-val				
Yc	MCODE-MCL	-0.00592	0.13319	0.00275	1.00000	0.02275	0.81707	-0.04485	0.04413	0.04077	0.81824	
	Cfinder-MCL	0.00873	0.99999	-0.03550	0.61714	0.00001	1.00000	-0.00772	1.00000	-0.00914	0.99954	
	AP-MCL	-0.10953	0.00000	-0.10308	0.00000	-0.06513	0.00000	-0.13888	0.00000	-0.00000	AP < MCL	
	CMC-MCL	0.13170	0.99982	-0.02572	0.99862	0.22292	0.99999	0.16286	0.99999	0.28181	0.99999	
	Hc	ClusterOne-MCL	-0.02499	0.85199	-0.05766	0.00270	ClusterOne > MCL	-0.02568	0.17628	-0.09266	0.01233	ClusterOne < MCL
		ProRank-MCL	0.03253	0.42805	-0.02005	0.00018	ProRank > MCL	0.00395	0.99999	-0.14480	0.00000	ClusterOne < MCL
		CorePeel-MCL	0.12370	0.00000	0.00444	1.00000	0.00241	0.00000	0.13027	0.00000	ProRank < MCL	
		IMHRC-MCL	-0.14858	0.00000	IMHRC < MCL	-0.07455	0.00000	IMHRC < MCL	-0.00190	0.00000	IMHRC < MCL	
		PCFP-MCL	-0.00821	0.99991	-0.00074	0.81812	-0.00074	1.00000	-0.01894	0.99979	-0.04246	0.00000





**Supplementary Table 5.** Empirical running time on the four PPI networks of yeast and the two PPI networks of human.

<b>Yeast</b>	<b>Empirical time</b>
Collins	0 hour, 8 minutes and 43 seconds
Gavin	0 hours, 32 minutes and 0 seconds
KroganCore	0 days, 4 hours, 31 minutes and 35 seconds
KroganExt	1 day, 13 hours, 20 minutes and 31 seconds

<b>Human</b>	<b>Empirical time</b>
PIPS	0 hours, 18 minutes and 2 seconds
STRING	0 hours, 5 minutes and 18 seconds

**Supplementary Table 6.** The average of enrichment score of predicted complexes with at least one enriched annotation over all clusters are compared for the nine approaches across all datasets.

Yeast				
	method	BP	MF	CC
Collins	MCL	0.818	0.376	0.545
	MCODE	0.937	0.559	0.649
	CFinder	0.956	0.500	0.667
	AP	0.817	0.396	0.536
	CMC	<b>0.989</b>	0.645	<b>0.817</b>
	ClusterOne	0.961	0.552	0.670
	ProrankPlu	0.965	<b>0.771</b>	0.785
	Core&Peel	0.977	0.761	0.651
	IMHRC	0.963	0.590	0.691
	PC2P	0.949	0.582	0.646

	method	BP	MF	CC
Gavin	MCL	0.907	0.398	0.610
	MCODE	0.918	0.566	0.713
	CFinder	0.924	0.533	0.734
	AP	0.911	0.572	0.678
	CMC	0.957	0.558	0.726
	ClusterOne	0.969	0.558	0.713
	ProrankPlu	0.956	<b>0.716</b>	<b>0.781</b>
	Core&Peel	0.971	0.681	0.741
	IMHRC	<b>0.973</b>	0.579	0.699
	PC2P	0.959	0.594	0.771

	method	BP	MF	CC
KroganCore	MCL	0.768	0.354	0.405
	MCODE	0.896	0.519	0.597
	CFinder	0.930	0.487	0.617
	AP	0.846	0.542	0.594
	CMC	<b>0.975</b>	0.679	<b>0.778</b>
	ClusterOne	0.885	0.424	0.576
	ProrankPlu	0.927	0.628	0.701
	Core&Peel	0.880	<b>0.696</b>	0.749
	IMHRC	0.951	0.548	0.692
	PC2P	0.929	0.506	0.597

**Supplementary Table 6.** The average of enrichment score of predicted complexes with at least one enriched annotation over all clusters are compared for the nine approaches across all datasets.

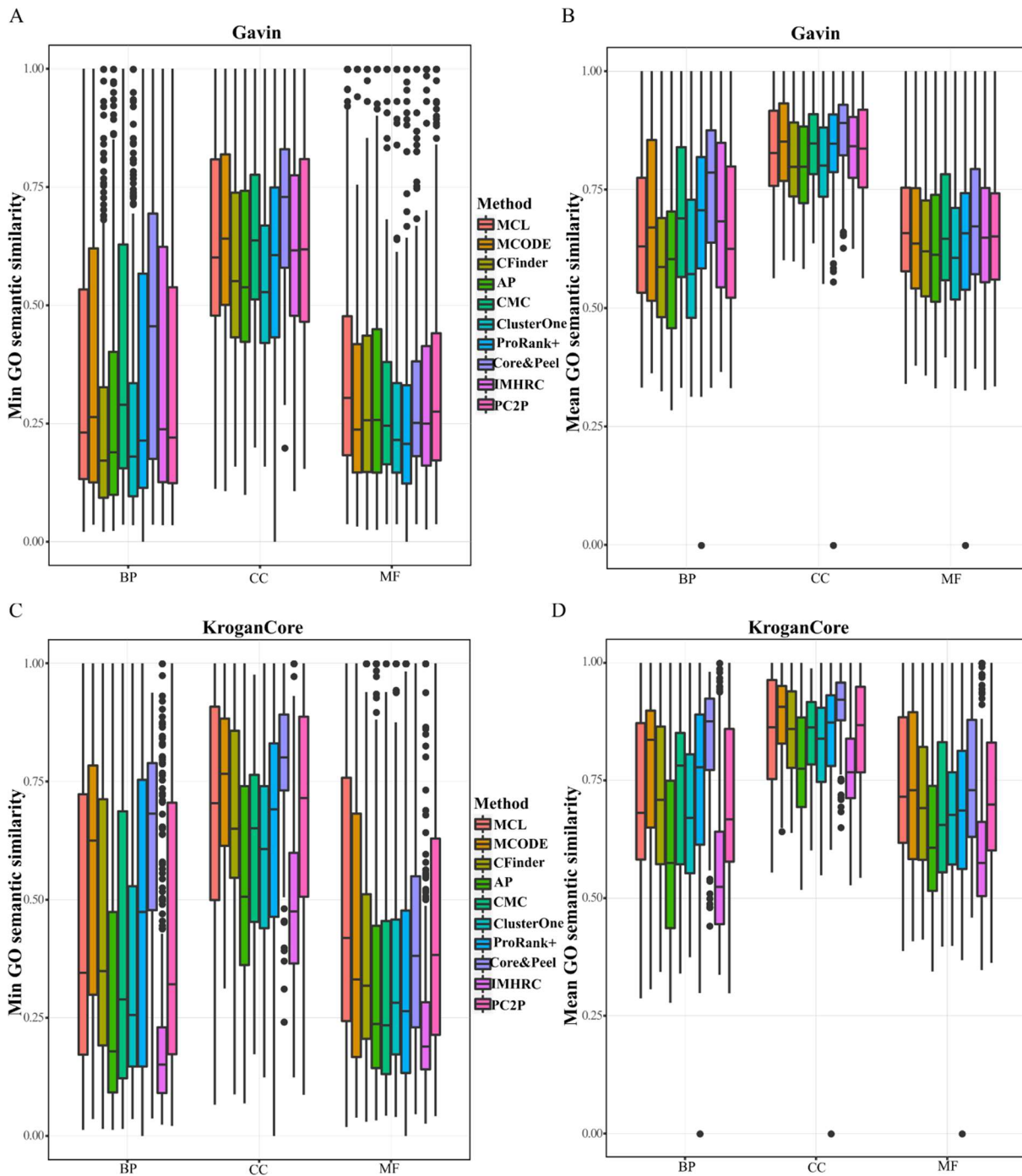
	method	BP	MF	CC
KroganExt	MCL	0.810	0.441	0.499
	MCODE	0.894	0.723	0.660
	CFinder	0.901	0.405	0.570
	AP	0.879	0.637	0.621
	CMC	0.944	0.702	0.742
	ClusterOne	0.867	0.471	0.550
	ProrankPlu	0.897	0.551	0.627
	Core&Peel	0.918	0.709	0.775
	IMHRC	0.950	0.556	0.671
	PC2P	0.887	0.504	0.613

Human

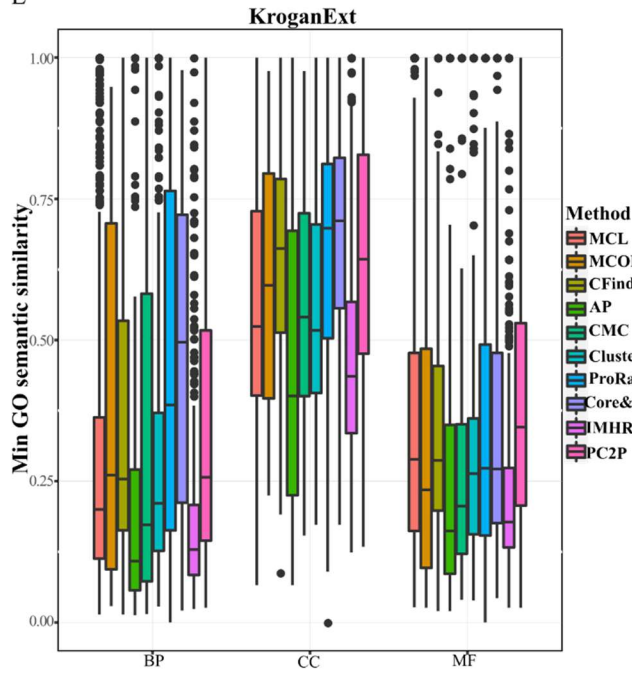
	method	BP	MF	CC
STRING	MCL	0.868	0.424	0.679
	MCODE	0.884	0.465	0.736
	CFinder	0.911	0.563	0.830
	AP	0.827	0.383	0.678
	CMC	0.919	0.466	0.758
	ClusterOne	0.925	0.544	0.797
	ProrankPlu	0.935	0.576	0.809
	Core&Peel	0.949	0.474	0.682
	IMHRC	0.917	0.547	0.811
	PC2P	0.922	0.498	0.812

	method	BP	MF	CC
PIPS	MCL	0.846	0.500	0.526
	MCODE	0.895	0.561	0.737
	CFinder	0.942	0.609	0.783
	AP	0.912	0.573	0.754
	CMC	1.000	0.661	0.831
	ClusterOne	0.943	0.631	0.723
	ProrankPlu	0.967	0.640	0.804
	Core&Peel	1.000	0.724	0.846
	IMHRC	0.967	0.687	0.810
	PC2P	0.925	0.653	0.755

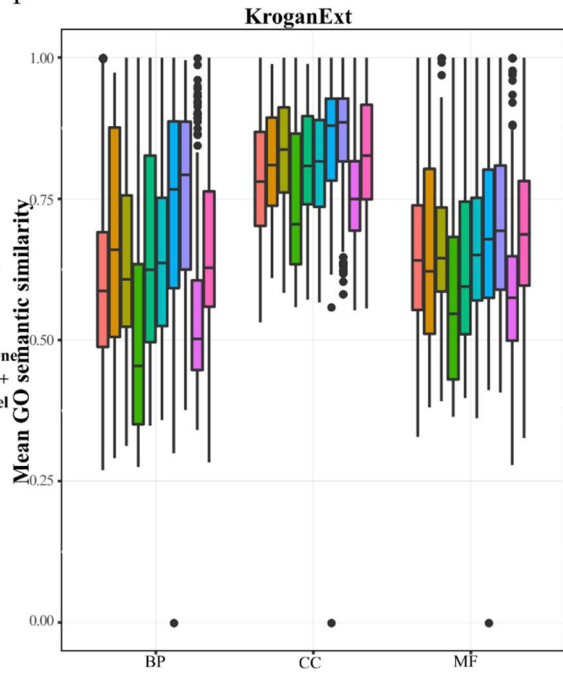
**Supplementary Figure 1. Distribution of minimum and mean semantic similarities over clusters.** The distribution of minimum and mean semantic similarities are given for (A – B) Gavin, (C – D) KroganCore, (E – F) KroganExt, (G - H) PIPS, as well as the mean for (I-J) Collin and STRING PPI networks.



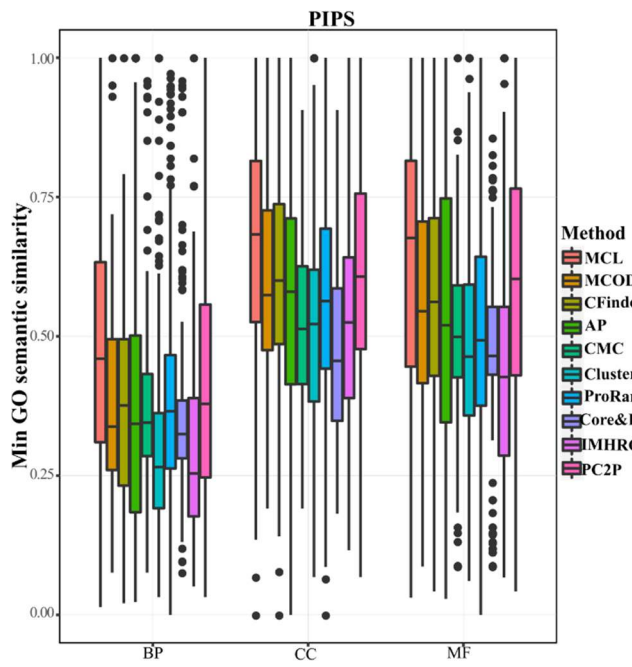
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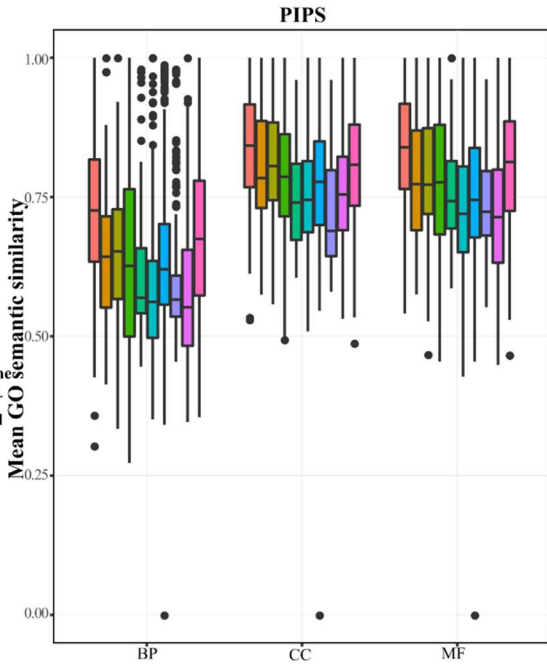
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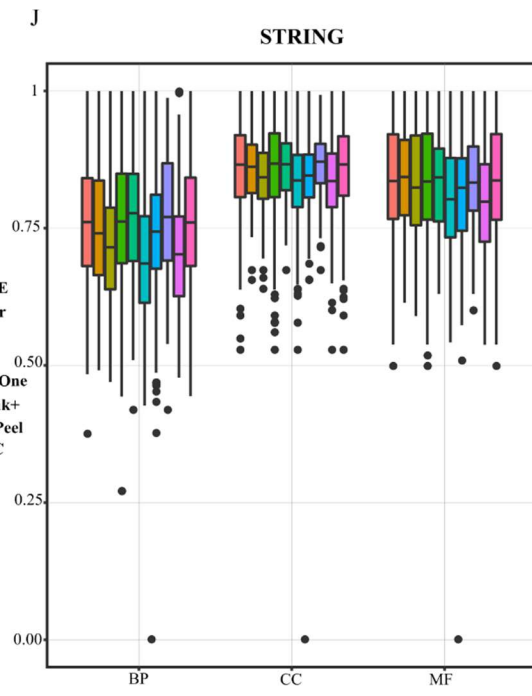
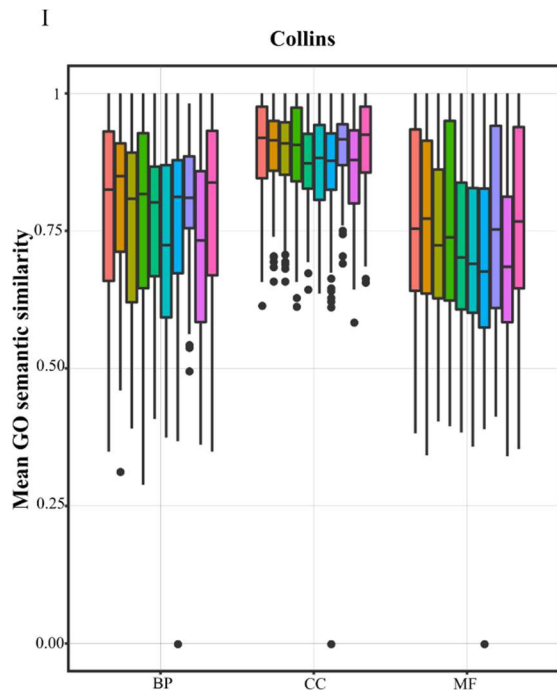


G

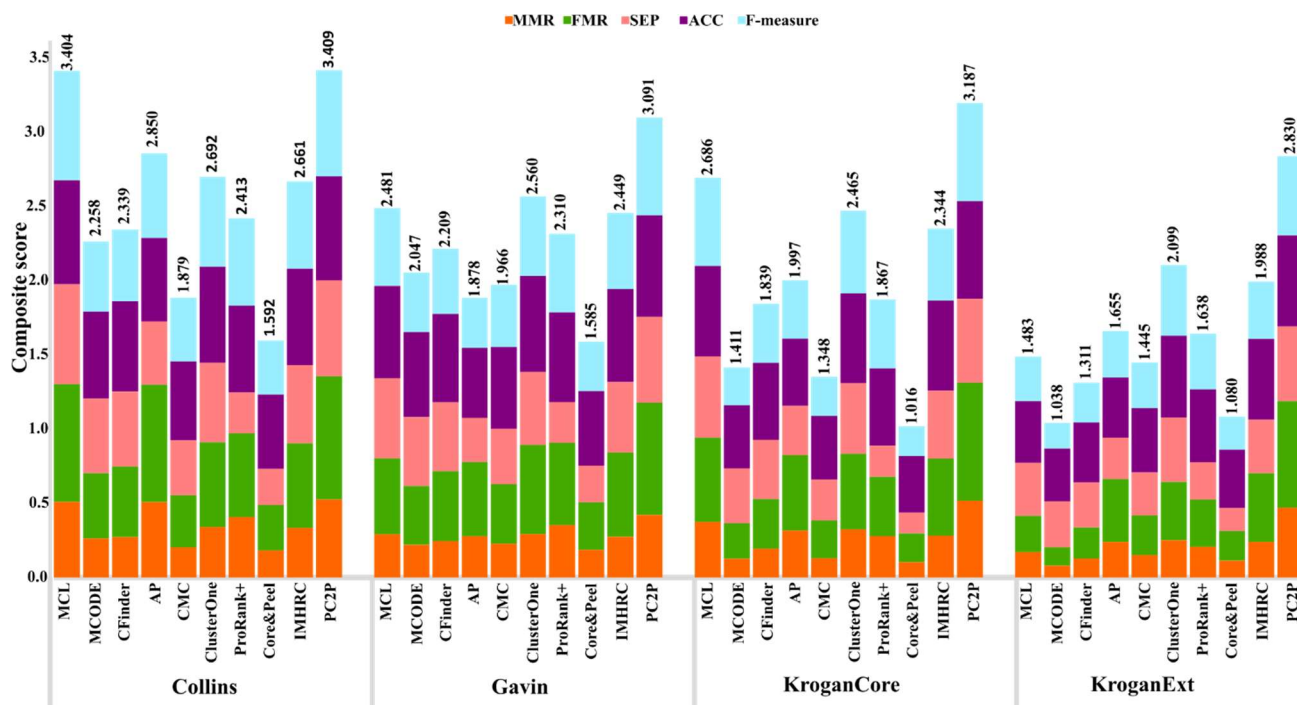


H



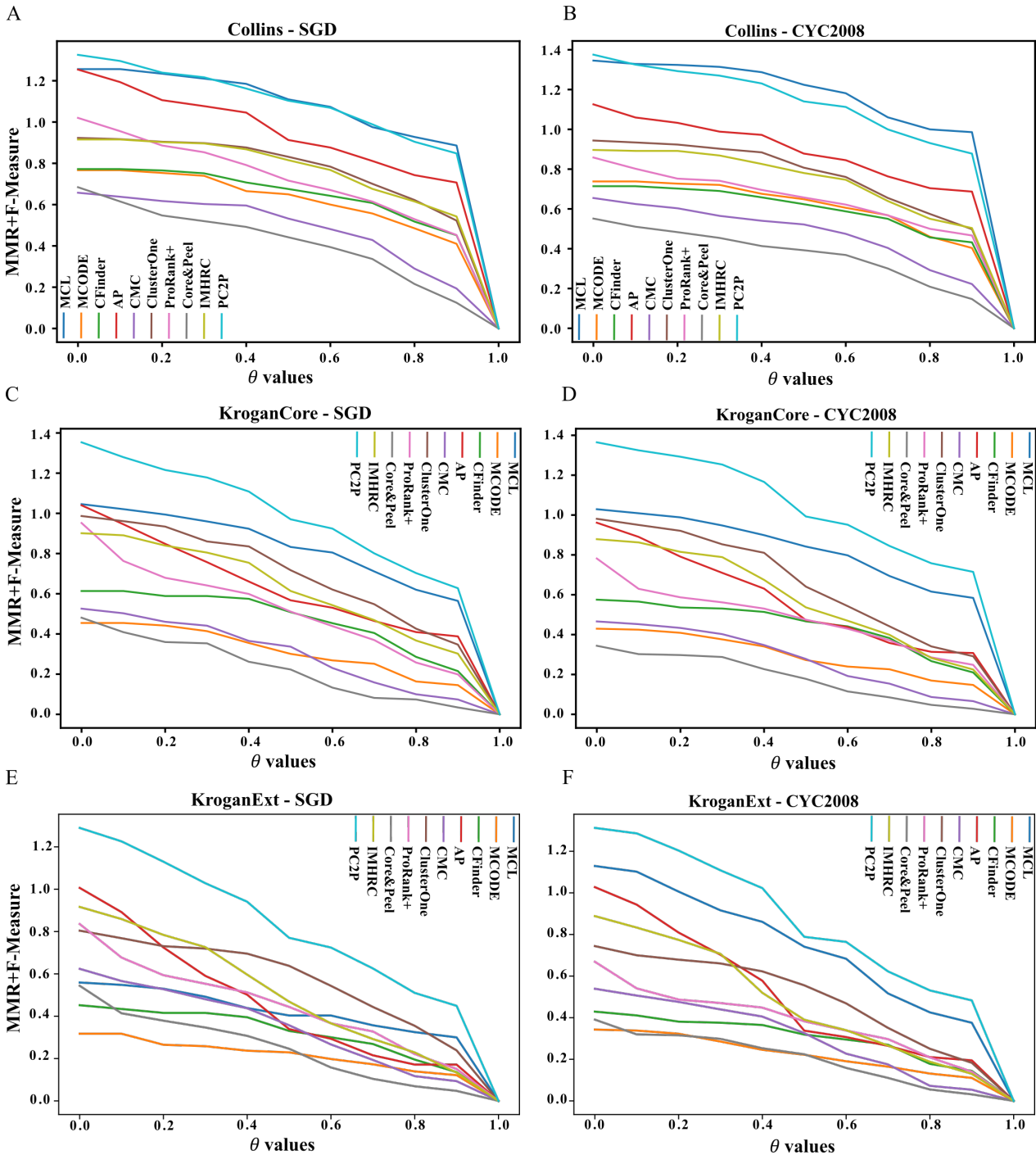


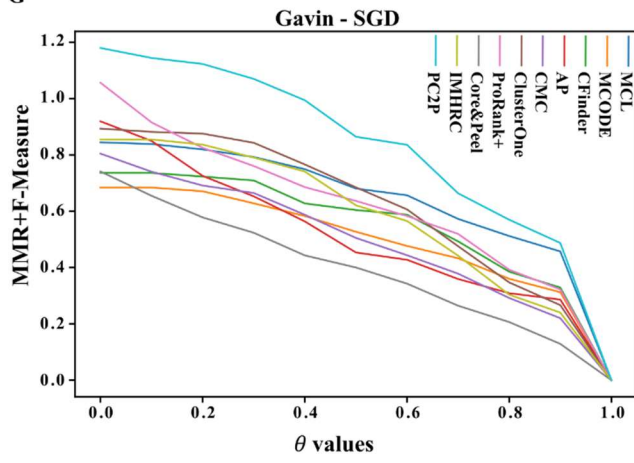
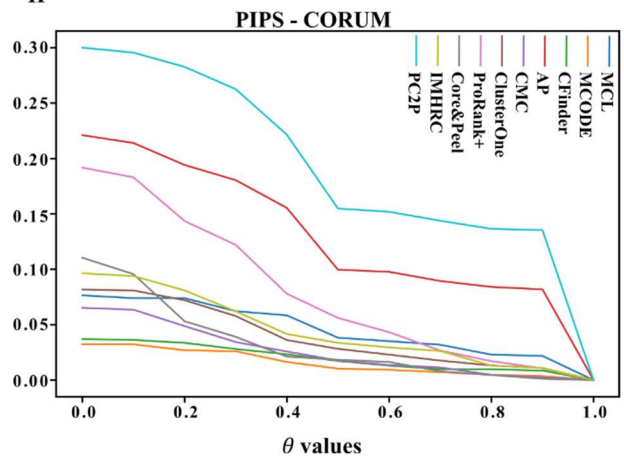
**Supplementary Figure 2. Comparative analysis of approaches for prediction of protein complexes in yeast.** The comparative analyses is conducted with respect to a composite score combining five performance measures, maximum matching ratio (MMR), fraction match (FMR), separation (SEP), accuracy (ACC), and F-measure. Eight approaches, ordered by the year of publication, are compared on four PPI networks in yeast with respect to SGD gold standard. PC2P outperforms all approaches on three of the networks.





**Supplementary Figure 3. Summation of MMR and F-measure+ of approaches for prediction of protein complexes.** The sum of MMR and F-measure+ is conducted over the range of from 0 to 1. Ten approaches, ordered by the year of publication, are compared on (A-B) Collins, (C-D) KroganCore, (E-F) KroganExt, and (G-H) Gavin and PIPS in yeast and human respectively. PCP2 outperforms all approaches except in Collins.



**G****H**

**Supplementary Figure 4. Distribution of clusters size.** The distribution of clusters size from ten approaches are compared on (A) Collins, (B) Gavin, (C) KroganCore, (D) KroganExt, (E) PIPS, and (F) STRING PPI networks. Distribution of cluster size of PC2P does not differ with respect to the compared approaches: For all algorithms, except ClusterOne, Core&Peel, and IMHRC, the cluster size distributions are monotonically decreasing by increasing the size of clusters.

