Additional file 6 - Evaluation of prediction method variants on reference and supported subsets for human, mouse, fly and yeast

The permissive accuracy (PA) and strict accuracy (SA) were calculated for all variants (DISCRETE, MERGED, COMMON and MAJORITY) for all interactions, and for interactions involving an integral membrane protein (M).

Human PPI sets	DISCRETE				MERGED				COMMON				MAJORITY			
	PA	SA	PA (M)	SA (M)	PA	SA	PA (M)	SA (M)	PA	SA	PA (M)	SA (M)	PA	SA	PA (M)	SA (M)
Reference	0.64	0.35	0.50	0.27	0.72	0.26	0.62	0.23	0.65	0.40	0.53	0.32	0.68	0.34	0.58	0.27
BPscore	0.84	0.56	0.76	0.46	0.86	0.55	0.79	0.42	0.85	0.57	0.77	0.47	0.86	0.55	0.79	0.43
Interologs	0.85	0.58	0.70	0.46	0.84	0.54	0.69	0.42	0.83	0.57	0.67	0.45	0.84	0.56	0.69	0.45
DDI	0.72	0.46	0.65	0.43	0.75	0.43	0.70	0.42	0.72	0.48	0.66	0.49	0.74	0.45	0.69	0.44
PMID	0.76	0.46	0.60	0.28	0.76	0.42	0.60	0.27	0.74	0.45	0.56	0.30	0.76	0.43	0.59	0.28
Method	0.74	0.38	0.61	0.29	0.76	0.37	0.63	0.27	0.73	0.41	0.58	0.32	0.75	0.38	0.62	0.29
DB	0.73	0.37	0.53	0.25	0.74	0.35	0.61	0.26	0.71	0.40	0.57	0.30	0.73	0.37	0.59	0.28
ALL	0.74	0.42	0.61	0.35	0.78	0.38	0.69	0.33	0.74	0.45	0.64	0.40	0.76	0.41	0.67	0.36
BIO	0.77	0.49	0.67	0.43	0.79	0.45	0.71	0.38	0.77	0.50	0.67	0.45	0.78	0.47	0.70	0.41
EVI	0.74	0.37	0.55	0.25	0.75	0.34	0.62	0.25	0.71	0.41	0.57	0.30	0.74	0.37	0.61	0.27

Mouse PPI sets	DISCRETE				MERGED				COMMON				MAJORITY			
	PA	SA	PA (M)	SA (M)	PA	SA	PA (M)	SA (M)	PA	SA	PA (M)	SA (M)	PA	SA	PA (M)	SA (M)
Reference	0.69	0.34	0.57	0.23	0.74	0.31	0.64	0.20	0.72	0.36	0.63	0.25	0.73	0.33	0.63	0.22
BPscore	0.86	0.56	0.73	0.25	0.86	0.53	0.72	0.19	0.86	0.54	0.71	0.22	0.86	0.54	0.72	0.22
Interologs	0.77	0.42	0.60	0.20	0.79	0.41	0.60	0.16	0.78	0.43	0.59	0.20	0.79	0.43	0.60	0.20
DDI	0.82	0.40	0.75	0.33	0.83	0.36	0.77	0.26	0.82	0.38	0.77	0.29	0.82	0.37	0.77	0.27
PMID	0.82	0.43	0.81	0.34	0.83	0.40	0.81	0.24	0.82	0.42	0.81	0.31	0.82	0.41	0.81	0.31
Method	0.68	0.37	0.52	0.20	0.71	0.34	0.62	0.19	0.71	0.39	0.62	0.27	0.70	0.36	0.59	0.23
DB	0.78	0.43	0.79	0.46	0.82	0.40	0.82	0.39	0.82	0.44	0.81	0.46	0.82	0.41	0.82	0.42
ALL	0.77	0.41	0.68	0.30	0.80	0.37	0.73	0.23	0.79	0.41	0.72	0.30	0.79	0.38	0.72	0.26
BIO	0.82	0.45	0.72	0.30	0.83	0.42	0.73	0.23	0.82	0.45	0.72	0.27	0.83	0.43	0.73	0.25
EVI	0.75	0.38	0.71	0.33	0.78	0.35	0.78	0.29	0.77	0.40	0.79	0.37	0.77	0.37	0.77	0.33

Fly	DISCRETE				MERGED				COMMON				MAJORITY			
PPI sets	PA	SA	PA (M)	SA (M)	PA	SA	PA (M)	SA (M)	PA	SA	PA (M)	SA (M)	PA	SA	PA (M)	SA (M)
Reference	0.57	0.32	0.50	0.22	0.65	0.28	0.61	0.20	0.61	0.38	0.59	0.30	0.62	0.32	0.58	0.23
BPscore	0.97	0.65	0.78	0.21	0.98	0.63	0.80	0.20	0.98	0.68	0.79	0.30	0.98	0.64	0.80	0.20
Interologs	0.91	0.64	-	-	0.91	0.62	-	-	0.91	0.65	-	-	0.91	0.62	-	-
DDI	0.94	0.65	0.89	0.39	0.95	0.62	0.93	0.40	0.94	0.66	0.87	0.40	0.95	0.65	0.93	0.40
PMID	0.91	0.57	0.76	0.12	0.93	0.51	0.85	0.06	0.92	0.60	0.75	0.17	0.93	0.56	0.85	0.06
Method	0.89	0.48	0.34	-	0.88	0.41	0.34	-	0.86	0.48	0.34	-	0.88	0.45	0.34	-
DB	0.47	0.27	0.29	0.21	0.56	0.27	0.39	0.28	0.51	0.33	0.38	0.35	0.53	0.29	0.35	0.29
ALL	0.56	0.32	0.41	0.18	0.65	0.30	0.53	0.21	0.61	0.38	0.52	0.27	0.62	0.33	0.49	0.21
BIO	0.93	0.60	0.75	0.20	0.95	0.57	0.85	0.21	0.94	0.63	0.84	0.28	0.94	0.60	0.82	0.21
EVI	0.51	0.28	0.33	0.17	0.60	0.27	0.43	0.20	0.55	0.34	0.42	0.25	0.57	0.30	0.40	0.20

Yeast	DISCRETE				MERGED				COMMON				MAJORITY			
PPI sets	PA	SA	PA (M)	SA (M)	PA	SA	PA (M)	SA (M)	PA	SA	PA (M)	SA (M)	PA	SA	PA (M)	SA (M)
Reference	0.60	0.34	0.45	0.23	0.77	0.15	0.58	0.10	0.59	0.36	0.36	0.23	0.67	0.35	0.46	0.23
BPscore	0.94	0.69	0.89	0.58	0.95	0.53	0.92	0.50	0.94	0.69	0.91	0.65	0.94	0.65	0.91	0.59
Interologs	0.91	0.61	1.00	0.71	0.93	0.60	1.00	0.71	0.93	0.63	1.00	0.71	0.93	0.61	1.00	0.71
DDI	0.83	0.56	0.84	0.56	0.89	0.51	0.91	0.53	0.88	0.60	0.87	0.60	0.88	0.55	0.90	0.57
PMID	0.86	0.58	0.84	0.55	0.90	0.50	0.86	0.46	0.89	0.62	0.86	0.55	0.89	0.57	0.86	0.52
Method	0.81	0.53	0.63	0.35	0.87	0.36	0.68	0.23	0.84	0.55	0.65	0.34	0.84	0.49	0.64	0.31
DB	0.62	0.36	0.43	0.22	0.74	0.19	0.48	0.13	0.60	0.36	0.36	0.20	0.67	0.34	0.42	0.18
ALL	0.66	0.40	0.51	0.29	0.77	0.21	0.56	0.17	0.64	0.40	0.44	0.28	0.71	0.39	0.50	0.25
BIO	0.92	0.66	0.88	0.57	0.94	0.50	0.92	0.50	0.93	0.67	0.90	0.64	0.93	0.62	0.90	0.58
EVI	0.63	0.37	0.44	0.23	0.75	0.20	0.49	0.14	0.61	0.37	0.37	0.21	0.67	0.35	0.43	0.19

ALL: Union of all subsets (BPscore ∪ Interologs ∪ DDI ∪ PMID ∪ Method ∪ DB)

BIO: Union of sequence-feature-based subsets (BPscore ∪ Interologs ∪ DDI)

EVI: Union of PPI detection processes based subsets (PMID ∪ Method ∪ DB)

M: Interactions involving an integral membrane protein