

Table 1 - Basic information of prediction by various algorithms

This table shows the basic information of the results predicted by NPF, NC, Zhang, DCS, DSCP, PON and *GrAPFI*. MP is the number of proteins successfully matching at least one known function. PMP represents the number of proteins perfectly matching the known functions. MMP denotes the number of proteins completely mismatching the known functions. ZP is the number of proteins with zero-error prediction.

Methods	MP	PMP	MMP	ZP
NPF	1570	959	1290	1555
NC	1584	1105	1276	218
Zhang	810	685	2050	1115
DCS	1148	669	1712	669
DSCP	1298	760	1562	795
PON	574	257	2286	1443
<i>GrAPFI</i>	849	443	2011	1629

Table 2 – Basic information of selected target proteins

This table shows the basic information of three target proteins. The second column represents the number of its direct neighbors in the original PINs, while the third column is the number of domains it contains. The last column denotes the number of complexes involved.

Proteins	Degree	Number of domains	Number of complexes
YNL262W	13	2	1
YBR278W	9	0	1
YPR175W	9	1	1

Table 3 - Description of selected GO Terms

The underscored text represents the name of GO Term.

GO Term	Description
GO:0006272	<u>Leading strand elongation</u> , which is continuous as it proceeds in the same direction as the replication fork.
GO:0006273	<u>Lagging strand elongation</u> proceeds by discontinuous synthesis of short stretches of DNA, known as Okazaki fragments, from RNA primers; these fragments are then joined by DNA ligase.
GO:0006289	<u>Nucleotide excision</u> repair recognizes a wide range of substrates, including damage caused by UV irradiation and chemicals.
GO:0006298	The <u>mismatch repair system</u> promotes genomic fidelity by repairing base-base mismatches, insertion-deletion loops and heterologies generated during DNA replication and recombination.
GO:0006303	The <u>repair of a double-strand break</u> in DNA in which the two broken ends are re-joined with little or no sequence complementarity.
GO:0006348	<u>Chromatin silencing at telomere</u> means the repression of transcription of telomere DNA by altering the structure of chromatin.
GO:0007064	<u>Mitotic sister chromatid cohesion</u> . The cell cycle process in which the sister chromatids of a replicated chromosome are joined along the entire length of the chromosome.

Table 4 – The prediction results using ten-fold validation

Methods	Precision	Recall	F-measure
NPF	0.426	0.429	0.427
NC	0.125	0.461	0.196
Zhang	0.426	0.429	0.427
DCS	0.306	0.307	0.306
DSCP	0.354	0.356	0.355
PON	0.152	0.142	0.147
<i>GrAPFI</i>	0.233	0.223	0.228