

3.2.2.3 Complete predictions of proteins and corresponding GO terms

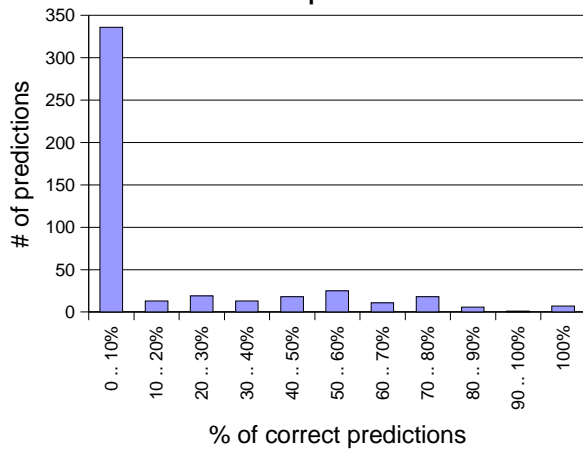
The results for the prediction of proteins and corresponding GO terms are presented in a similar way than in the previous sections. The diagrams show (for tasks 2.1 and 2.2 and for the three classes of GO terms), for each individual protein/GO term pair, what fraction of the predictions were “perfect” (i. e. both the protein and the GO term were marked with “high” by the evaluators).

The figures indicate that in task 2.1 (only the corresponding text for given GO terms had to be located in the documents) for about 60 to 70% of the protein/GO pairs the precision was low (0 to 10% of correct predictions) and in task 2.2 (the GO terms were not given but had also to be predicted) about 90% of the protein/GO pairs were predicted with low precision. This shows that task 2.2 was considerably more difficult than task 2.1.

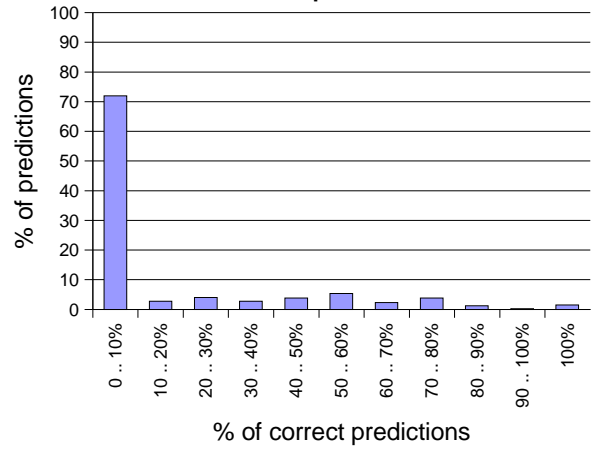
Some examples:

Accession number	Swiss-Prot/TREMBL description	GO ID	GO Term	times predicted	correct predictions	%
component						
Q8TDE4	PGC-1-related estrogen receptor alpha coactivator short isoform	0005634	nucleus	15	15	100
Q9NP80	Calcium-independent phospholipase A2	0005624	membrane fraction	14	14	100
Q9HBX6	Phosphoinositide-specific phospholipase C PLC-epsilon	0005624	membrane fraction	8	8	100
Q9UIR2	ATP sulfurylase/APS kinase isoform SK2	0005622	intracellular	13	0	0
Q9UBE0	Ubiquitin-like 1 activating enzyme E1A	0005634	nucleus	13	0	0
Q9Y566	SH3 and multiple ankyrin repeat domains protein 1	0005622	intracellular	13	0	0
function						
Q9BYG3	Nucleolar phosphoprotein Nopp34	0005515	protein binding	10	10	100
Q9NRQ7	Cholinephosphotransferase 1 alpha	0004142	diacylglycerol cholinephosphotransferase activity	4	4	100
Q9NRQ6	Cholinephosphotransferase 1 beta	0004142	diacylglycerol cholinephosphotransferase activity	4	4	100
Q9Y4G8	PDZ domain containing guanine nucleotide exchange factor 1	0005509	calcium ion binding	13	0	0
Q9Y231	Alpha-3-fucosyltransferase	0046920	alpha(1,3)-fucosyltransferase activity	16	0	0
Q9UBE0	Ubiquitin-like 1 activating enzyme E1A	0005515	protein binding	16	0	0
process						
Q96PH1	NADPH oxidase 5 gamma	0042554	superoxide release	5	5	100
O15520	Fibroblast growth factor-10 precursor	0050674	urothelial cell proliferation	4	4	100
Q9NRB3	Chondroitin 4-O-sulfotransferase 2	0030204	chondroitin sulfate metabolism	3	3	100
O75591	Type 1-like ryanodine receptor	0006928	cell motility	15	0	0
Q14686	Nuclear receptor coactivator 6	0006281	DNA repair	16	0	0
O15520	Fibroblast growth factor-10 precursor	0006950	response to stress	16	0	0

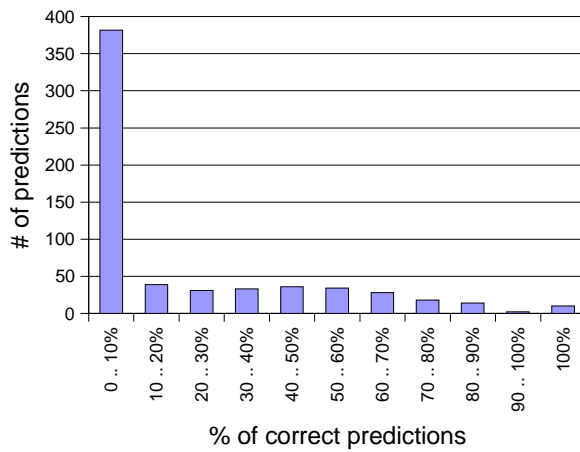
Task 2.1: protein-GO predictions
GO component



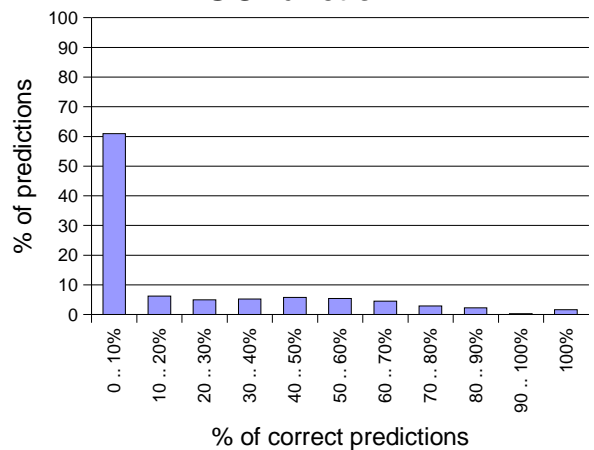
Task 2.1: protein-GO predictions
GO component



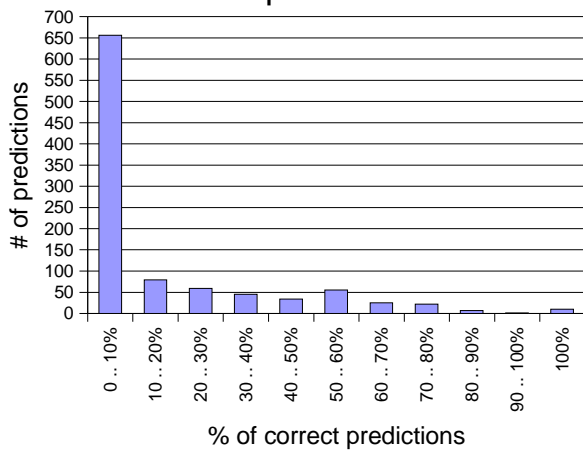
Task 2.1: protein-GO predictions
GO function



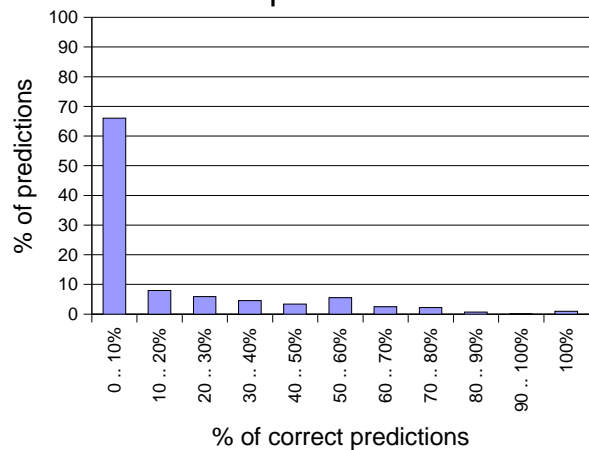
Task 2.1: protein-GO predictions
GO function



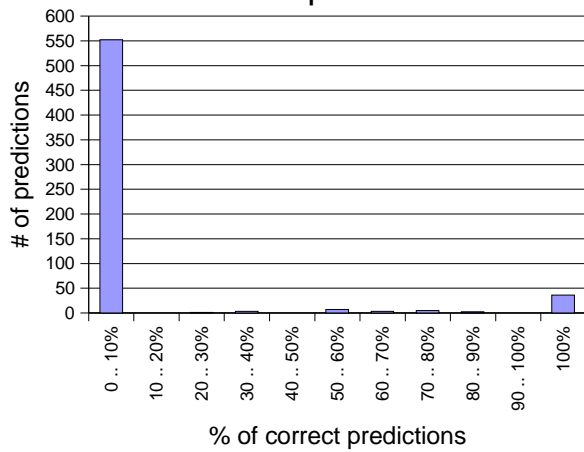
Task 2.1: protein-GO predictions
GO process



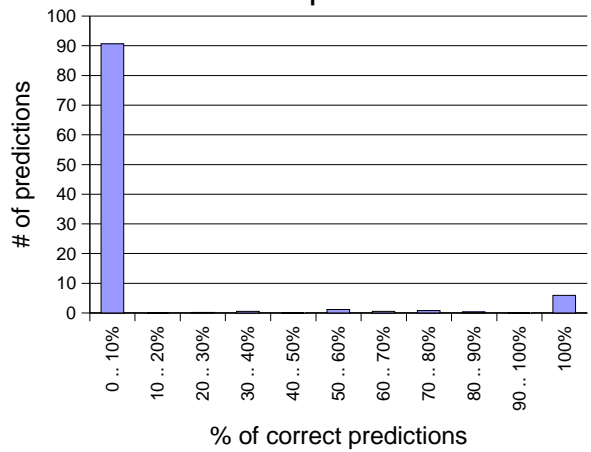
Task 2.1: protein-GO predictions
GO process



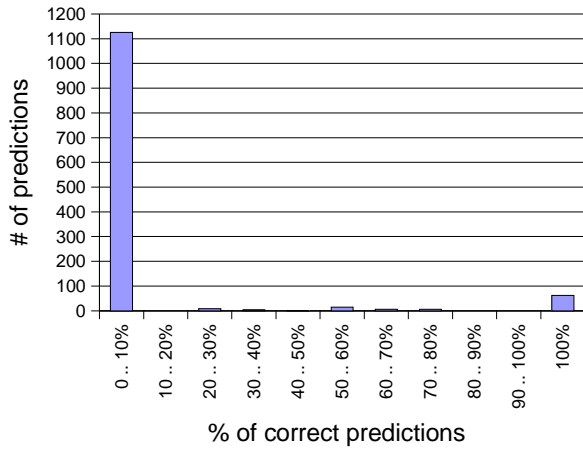
Task 2.2: protein-GO predictions
GO component



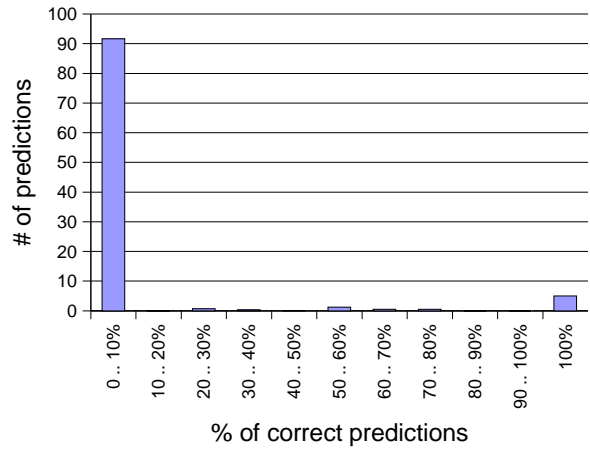
Task 2.2: protein-GO predictions
GO component



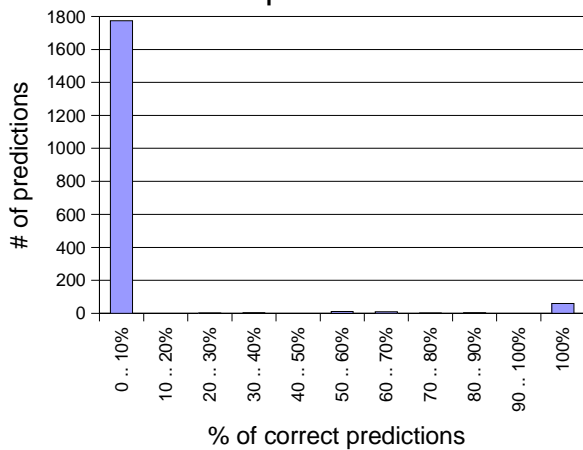
Task 2.2: protein-GO predictions
GO function



Task 2.2: protein-GO predictions
GO function



Task 2.2: protein-GO predictions
GO process



Task 2.2: protein-GO predictions
GO process

