

3.2.2 Detailed analysis

The following graphs give an overview of the results obtained in task 2. They will be discussed in more detail at the workshop.

We divided the evaluation of the results in three parts, first we will focus on the predictions of the GO terms, then predictions of the proteins and then how the complete prediction of proteins and their corresponding GO terms came out.

3.2.2.1 Prediction of GO terms

The results have been divided in 6 sections corresponding to the tasks (task 2.1 and task 2.2) and the three classes of the GO hierarchy (component, function and process). In each of these sections there are 4 diagrams.

The first two show the results by the number of predictions that have been made per individual GO term (this means that there are GO terms that appear very often in the results, i.e. they are more frequent, and others appear very seldom). "Predictions" refers to how many (individual) predictions have been made in each class and "correct" refers to how many of them are "high" according to the definition given above. The second diagram shows the "correct" predictions in relation to the total predictions of the previous diagram. For task 2.1 (where the GO terms were given and only the corresponding text had to be found) it seems that GO terms that appear very seldom (1 to 7) are poorly predicted and terms that appear with a certain frequency (8 and more times) are in 40 to 50% of the cases predicted correctly. In task 2.2 the terms appear in general with lower frequency (this is because the participants were "free" to predict the GO terms and the corresponding text so more different terms appear in total). For this task there is no obvious relation between how many times a specific GO term was predicted and the precision of the predictions.

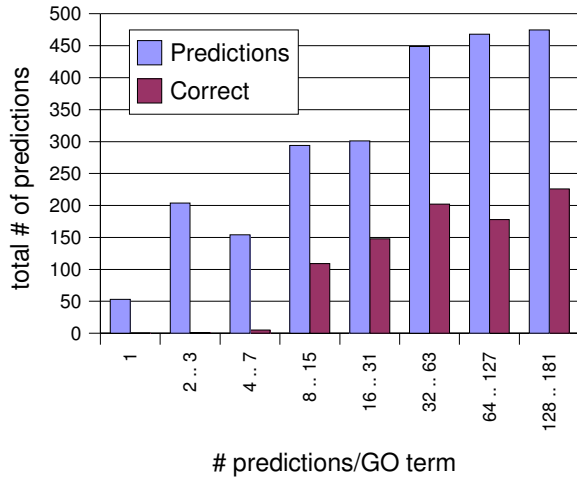
The third and fourth diagram show another view on the results. For each individual GO term, in how many % of the predictions it was predicted correctly. As in the previous diagrams absolute and relative numbers are shown. In general more than 50% of the terms are predicted with very low precision (50 to 70% in task 2.1 and 80 to 90% in task 2.2).

Some examples for GO terms with "good" predictions and "bad" predictions.

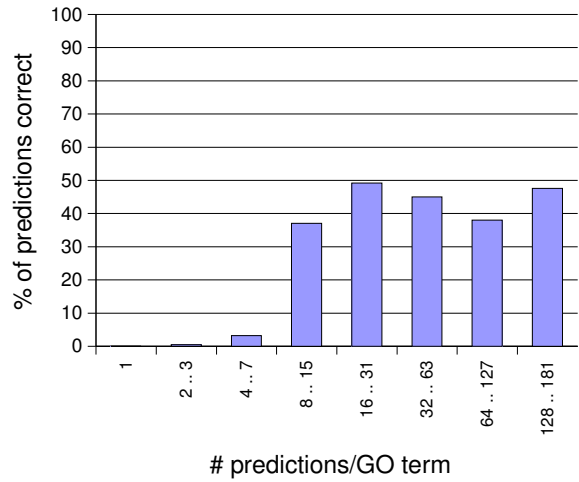
GO ID	GO Term	times predicted	correct predictions	%
GO component				
0030529	ribonucleoprotein complex	21	18	86
0016514	SWI/SNF complex	25	21	84
0005834	heterotrimeric G-protein complex	10	8	80
0045211	postsynaptic membrane	5	0	0
0005849	mRNA cleavage factor complex	6	0	0
0042827	platelet dense granule	7	0	0
GO function				
0016174	NADPH oxidase activity	9	9	100
0004709	MAP kinase kinase kinase activity	10	10	100
0004872	receptor activity	11	11	100
0008640	ubiquitin-like conjugating enzyme activity	6	0	0
0015407	monosaccharide-transporting ATPase activity	6	0	0

GO ID	GO Term	times predicted	correct predictions	%
0017028	protein stabilization activity	6	0	0
GO process				
0016079	synaptic vesicle exocytosis	5	5	100
0006354	RNA elongation	6	6	100
0016119	carotene metabolism	10	10	100
0000122	negative regulation of transcription from Pol II promoter	14	0	0
0019221	cytokine and chemokine mediated signaling pathway	15	0	0
0006874	calcium ion homeostasis	16	0	0

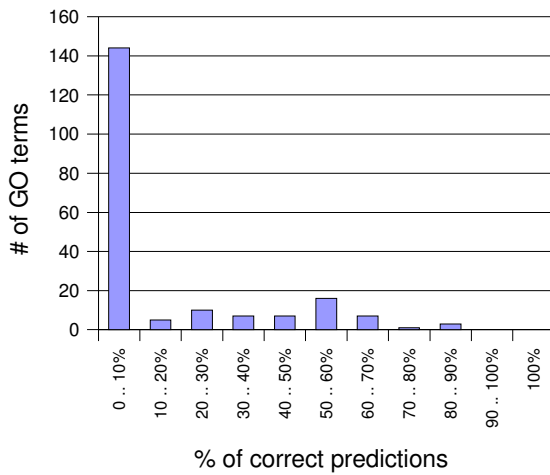
Task 2.1: GO component



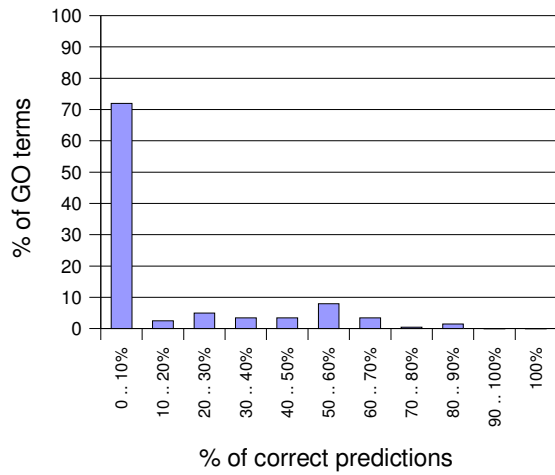
Task 2.1: GO component



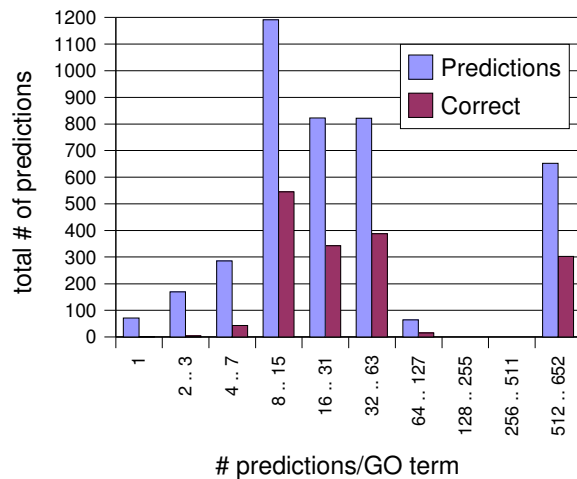
Task 2.1: GO component



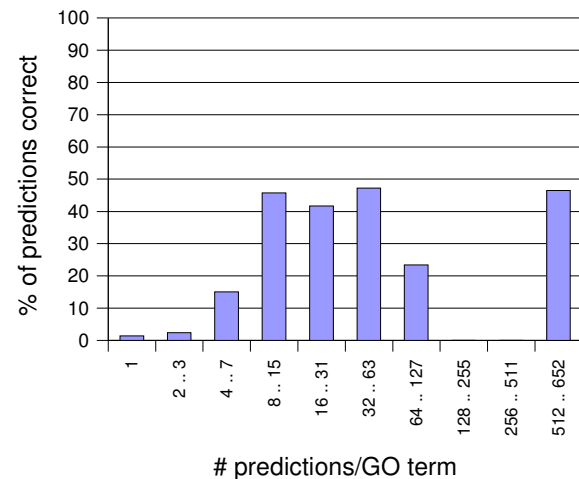
Task 2.1: GO component



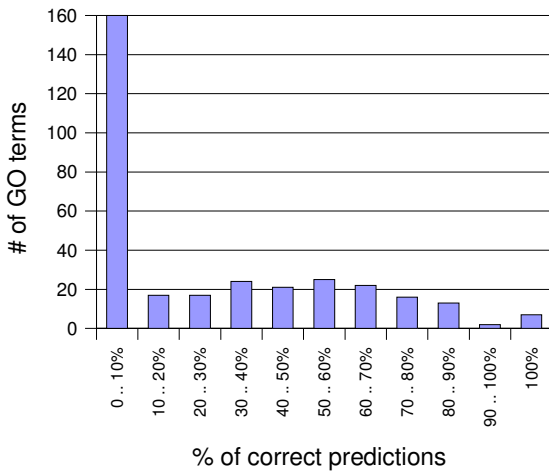
Task 2.1: GO function



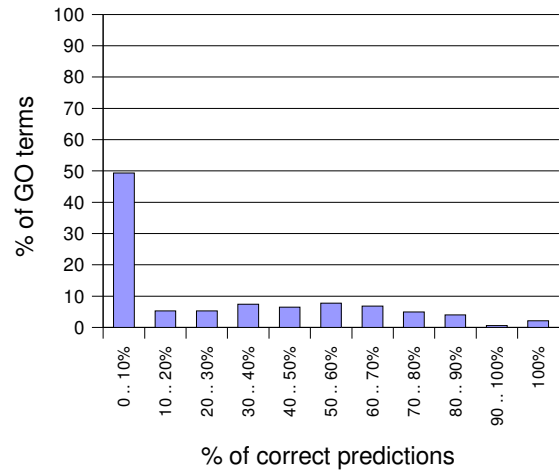
Task 2.1: GO function



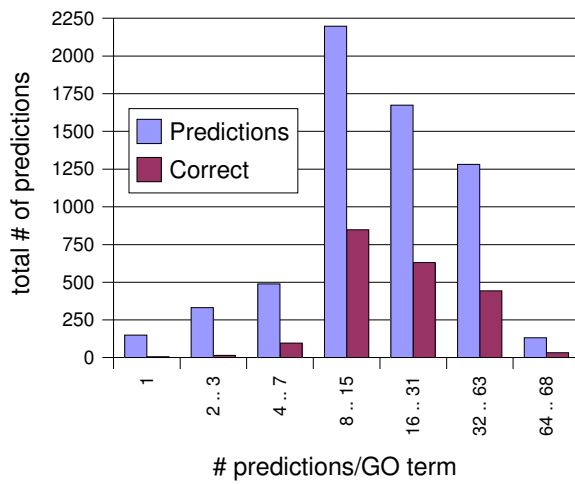
Task 2.1: GO function



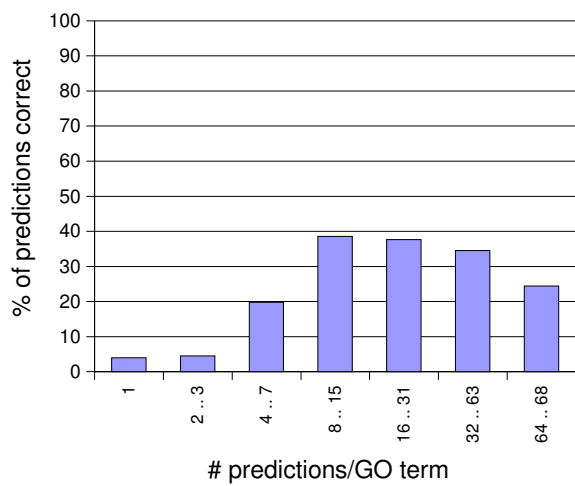
Task 2.1: GO function



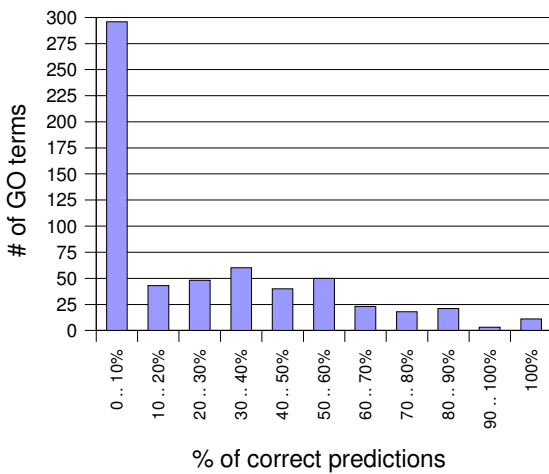
Task 2.1: GO process



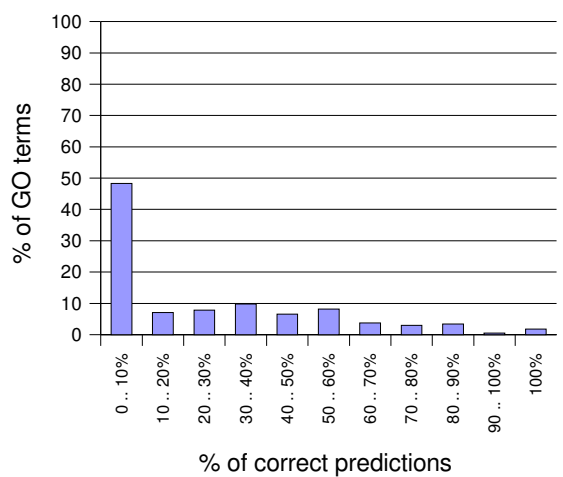
Task 2.1: GO process



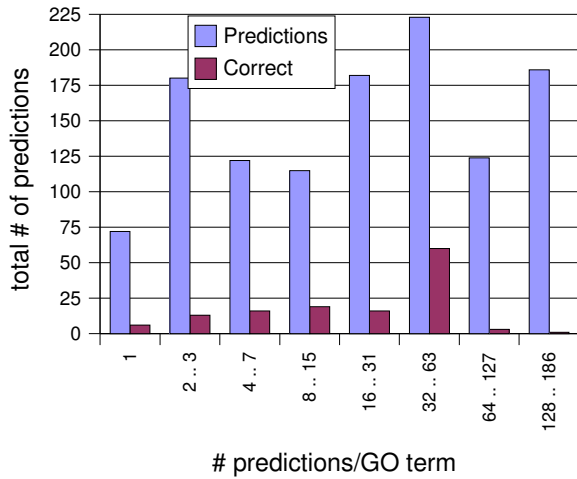
Task 2.1: GO process



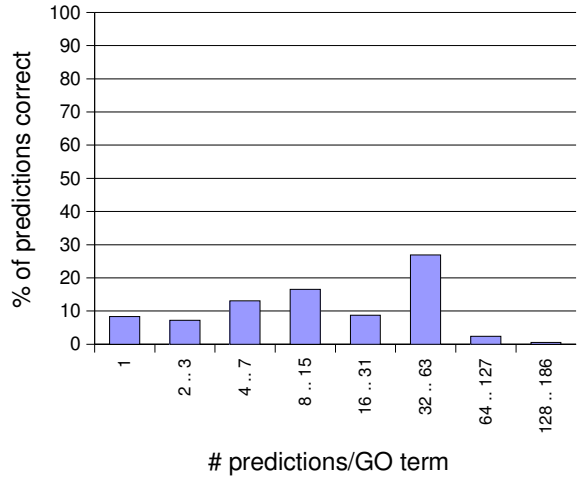
Task 2.1: GO process



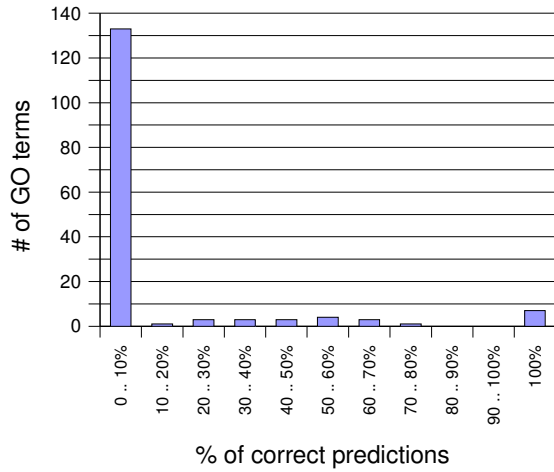
Task 2.2: GO component



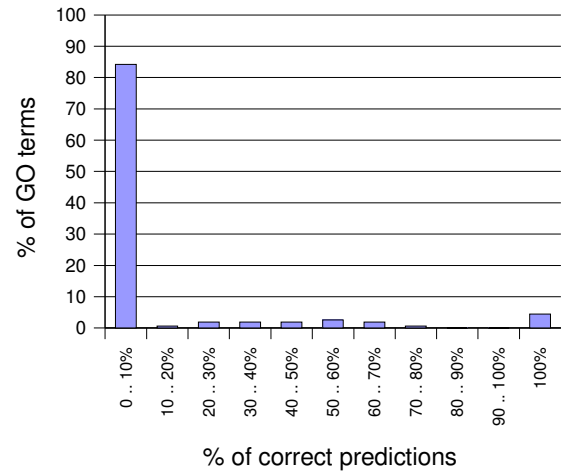
Task 2.2: GO component



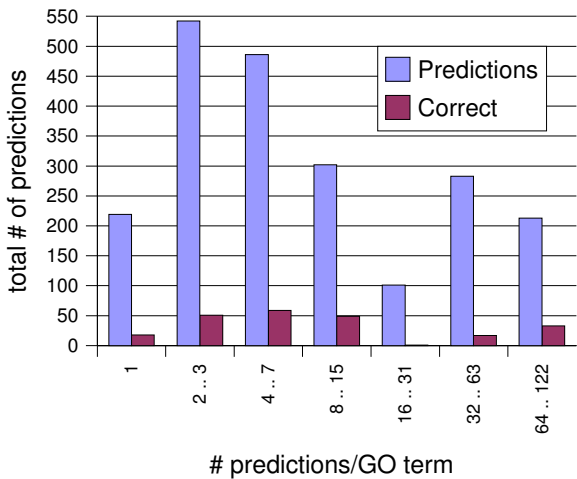
Task 2.2: GO component



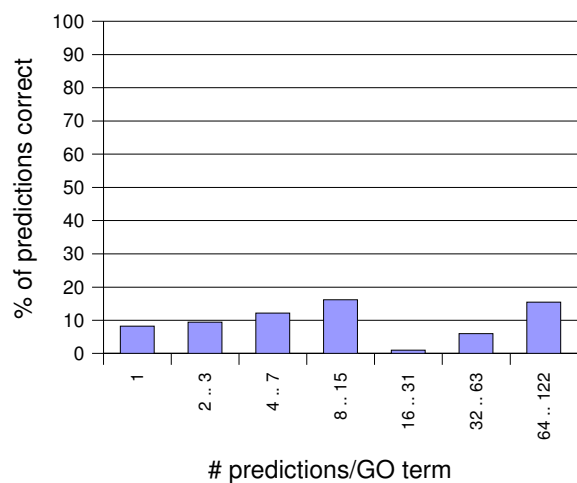
Task 2.2: GO component



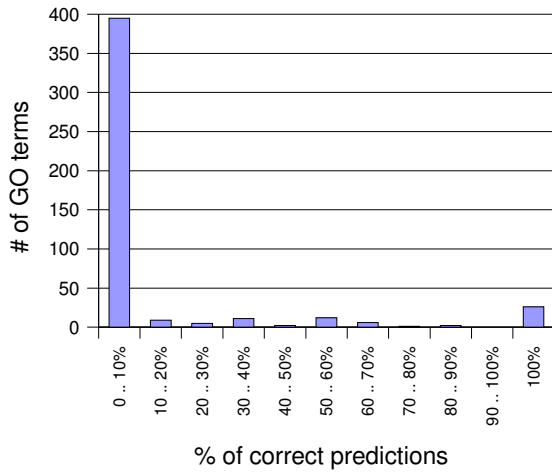
Task 2.2: GO function



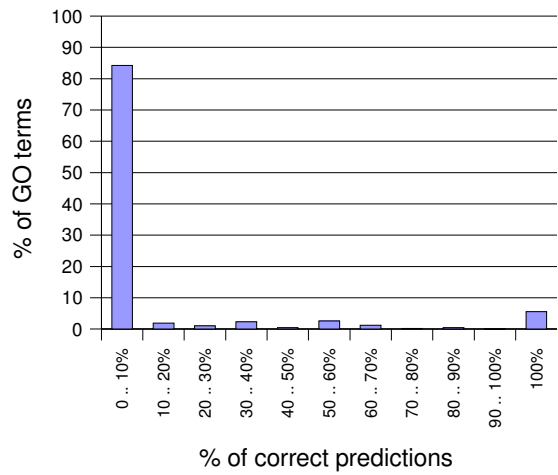
Task 2.2: GO function



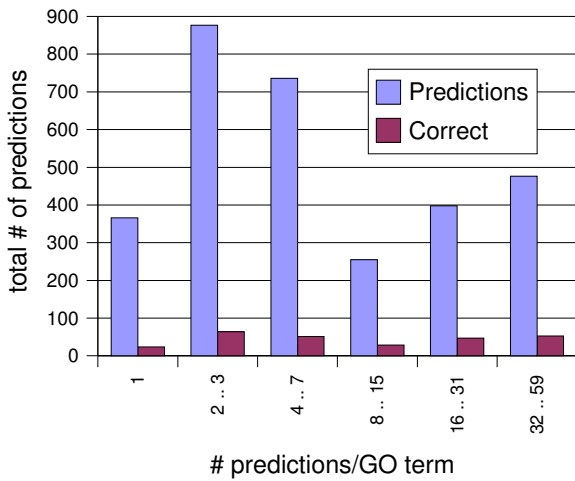
Task 2.2: GO function



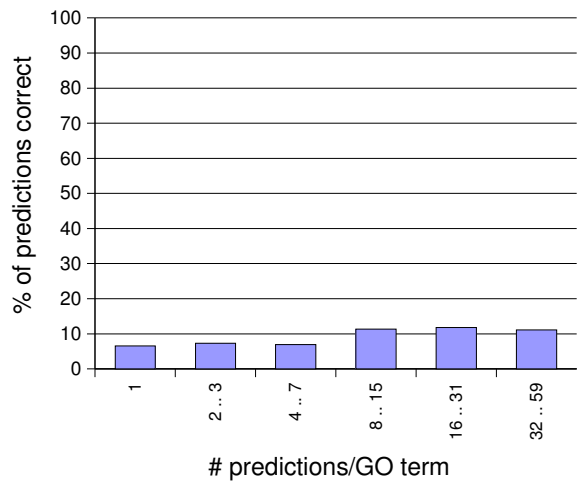
Task 2.2: GO function



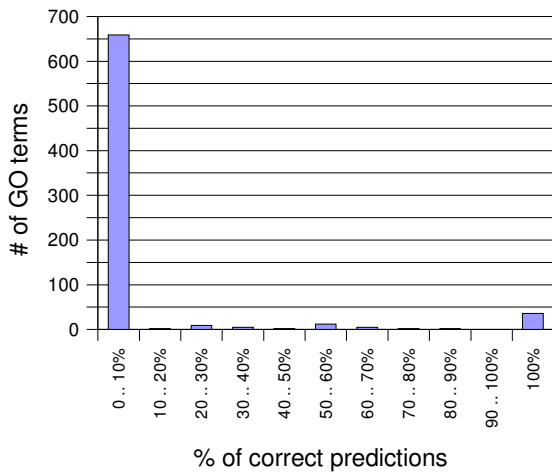
Task 2.2: GO process



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Task 2.2: GO process



Task 2.2: GO process

