

TBD

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Methods

Clean up

All functional annotation sets were cleaned up the following way (using definitions from the Gene Ontology version 2019-07-01):

1. Any annotations where the GO accession was marked as obsolete were removed.
2. Some terms in the GO have ‘alternative ids’. When naively removing duplicates, two entries will not be recognized as duplicates if they have different accessions pointing to the same GO term. Therefore, all GO accessions were changed to their respective ‘main id’ and the dataset was again scanned for duplicates.

Table 1 provides information on the number of annotations that were removed this way from each dataset. All further analyses were performed on the cleaned datasets since we assume the user will only be interested in still valid and non-redundant functional annotations.

Results

... a quantitative comparison of the datasets in Table.

Table 1: Number of removed annotations during cleanup.

Genome	Dataset	Obsolete Annotations	Duplicates
Triticum_aestivum	GOMAP	285	0
Hordeum_vulgarum	GOMAP	101	0
Glycine_max	GOMAP	203	0
Arachis_hypogaea	GOMAP	0	0
Zea_mays.PH207	GOMAP	798	76
Zea_mays.Mo17	GOMAP	726	77
Phaseolus_vulgaris	GOMAP	0	0
Vigna_unguiculata	GOMAP	0	0
Medicago_truncatula.R108	GOMAP	0	0
Zea_mays.B73.v3	GOMAP	1107	70
Zea_mays.W22	GOMAP	754	82
Medicago_truncatula.A17	GOMAP	0	0
Zea_mays.B73.v4	GOMAP	752	83
Oryza_sativa	GoldStandard	38	556
	GOMAP	111	2

Table 2: Quantitative metrics of the cleaned functional annotation sets. C, F, P, and A refer to the aspects of the GO: Cellular Component, Biological Function, Molecular Process, and Any/All.

Genome	Genes	Dataset	Annotations ^a				Annotated Genes [%] ^b				Median Ann. per G. ^c			
			C	F	P	A	C	F	P	A	C	F	P	A
Arachis_hypogaea		GOMAP	153433	132944	493799	780176	576.67	568.55	671.23	671.24	2	2	6	10
Glycine_max		GOMAP	129215	113827	417555	660597	460.20	470.34	528.71	528.72	2	2	6	11
Hordeum_vulgarum		GOMAP	88130	80282	272823	441235	352.37	364.70	397.33	397.34	2	2	5	10
Medicago_truncatula.A17		GOMAP	107362	99719	364065	571146	423.25	437.36	504.43	504.44	2	2	6	10
Medicago_truncatula.R108		GOMAP	112343	108031	382322	602696	403.32	502.20	557.06	557.06	1	2	5	9
Oryza_sativa		GOMAP	72780	64685	248700	386165	286.19	298.53	358.24	358.25	2	2	6	9
		GoldStandard	7730	11060	19378	38176	57.25	73.83	90.31	113.87	1	1	1	3
Phaseolus_vulgaris	100	GOMAP	72005	64583	229630	366218	259.34	255.39	274.32	274.33	2	2	6	11
Triticum_aestivum		GOMAP	267741	218623	785960	1272324	956.04	981.87	1078.90	1078.91	2	2	6	10
Vigna_unguiculata		GOMAP	75867	68313	243278	387458	271.73	271.24	297.72	297.73	2	2	6	11
Zea_mays.B73.v3		GOMAP	135211	87420	291251	513882	348.66	380.73	394.68	394.69	3	2	6	11
Zea_mays.B73.v4		GOMAP	88827	82251	278719	449797	367.17	373.37	393.23	393.24	2	2	6	10
Zea_mays.Mo17		GOMAP	87567	79214	277787	444568	336.18	351.05	386.19	386.20	2	2	6	10
Zea_mays.PH207		GOMAP	90617	85500	288677	464794	351.70	367.62	405.56	405.57	2	2	6	10
Zea_mays.W22		GOMAP	95390	85039	289780	470209	369.87	376.85	406.89	406.90	2	2	6	10

^a How many annotations in the C, F, and P aspect does this dataset contain? A = How many in total? $A = C + F + P$ ^b How many genes in the genome have at least one GO term from the C, F, P aspect annotated to them? A = How many at least one from any aspect? ($A = C \cup F \cup P$)^c Take a typical gene that is present in the annotation set. How many annotations does it have in each aspect? A = How many in total? Ask your favorite statistician why $A \neq C + F + P$