Article Title

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ABSTRACT

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Keywords: Text Text Text Text Text Text Text Text

1 INTRODUCTION

Hello, how are we doing?

2 METHODS

2.1 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 respecitve ‘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.

2.2 Choosing the right evaluation metric

A plethora of different metric to evaluate the quality of functional annotation predictions is available using different approaches and there seems to be no clear standard yet. `TODO: THIS IS WEAK` Additionally,

Table 1. Number of removed annotations during cleanup.

Genome	Dataset	Obsolete Annotations	Duplicates
Brachypodium distachyon	GOMAP	696	43
Gossypium raimondii	GOMAP	184	0
Hordeum vulgarum	GoldStandard	0	4
Medicago truncatula A17	GOMAP	0	0
Medicago truncatula R108	GOMAP	0	0
Oryza sativa	GOMAP	111	2
	GoldStandard	38	556
	Gramene61-IEA	10	14
Phaseolus vulgaris	GOMAP	0	0
Sorghum bicolor	GOMAP	690	59
Triticum aestivum	GOMAP	285	0
	GoldStandard	0	10
	Gramene61-IEA	47	48
Vigna unguiculata	GOMAP	0	0
Zea mays B73.v3	GOMAP	1107	70
	GoldStandard	1	0
	Gramene49	94	2
	Phytozome	54	0
Zea mays B73.v4	GOMAP	752	83
	GoldStandard	55	174
	Gramene61-IEA	99	157
Zea mays Mo17	GOMAP	726	77
Zea mays PH207	GOMAP	798	76
Zea mays W22	GOMAP	754	82

each of the metrics has a different focus and lalala so choosing a metric for quality evaluation is not trivial. When we first published GOMAP (Wimalanathan et al., 2018), we used a modified version of the hierarchical evaluation metrics originally introduced in (Verspoor et al., 2006) because they were simple, clear, and part of an earlier attempt at unifying and standardizing GO annotation comparisons (Defoin-Platel et al., 2011). In the meantime, Plyusnin et al. (2018) have published an approach for evaluating different metrics showing substantial differences within the robustness of different approaches. `TODO DESCRIBE THEIR APPROACH` We have applied their method on the Gold Standards available to us to determine which evaluation metric is the most appropriate in our case. The results of this analysis can be seen in `TODO`.

We then evaluated our predictions and the other annotation sets using the best performing metrics as well as the one we previously used. `TODO`

3 RESULTS

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

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

			Genes Annotated[%][a]				Annotations[b]				Median Ann. per G.[c]			
Genome	Genes	Dataset	CC	BF	MP	A	CC	BF	MP	A	CC	BF	MP	A
Arachis hypogaea	67,124	GOMAP	85.91	84.70	100.00	**100.00**	153,433	132,944	493,799	**780,176**	2	2	6	**10**
Brachypodium distachyon	100	GOMAP	27,923.00	29,292.00	34,309.00	**34,310.00**	75,877	69,709	255,807	**401,393**	2	2	6	**10**
Glycine max	52,872	GOMAP	87.04	88.96	100.00	**100.00**	129,215	113,827	417,555	**660,597**	2	2	6	**11**
Gossypium raimondii	100	GOMAP	34,908.00	34,651.00	37,504.00	**37,505.00**	96,793	85,511	307,921	**490,225**	2	2	6	**11**
Hordeum vulgarum	39,734	GOMAP	88.68	91.79	100.00	**100.00**	88,130	80,282	272,823	**441,235**	2	2	5	**10**
		GoldStandard	0.02	0.05	0.05	**0.07**	7	23	45	**75**	0	1	1	**2**
Medicago truncatula A17	50,444	GOMAP	83.90	86.70	100.00	**100.00**	107,362	99,719	364,065	**571,146**	2	2	6	**10**
Medicago truncatula R108	55,706	GOMAP	72.40	90.15	100.00	**100.00**	112,343	108,031	382,322	**602,696**	1	2	5	**9**
Oryza sativa	35,825	GOMAP	79.89	83.33	100.00	**100.00**	72,780	64,685	248,700	**386,165**	2	2	6	**9**
		GoldStandard	15.98	20.61	25.21	**31.79**	7,730	11,060	19,378	**38,176**	1	1	1	**3**
		Gramene61-IEA	30.07	43.37	46.63	**59.86**	14,633	32,787	39,105	**86,529**	1	1	1	**3**
Phaseolus vulgaris	27,433	GOMAP	94.54	93.10	100.00	**100.00**	72,005	64,583	229,630	**366,218**	2	2	6	**11**
Sorghum bicolor	100	GOMAP	28,154.00	29,353.00	34,128.00	**34,129.00**	76,689	70,190	259,413	**406,292**	2	2	6	**10**
Triticum aestivum	107,891	GOMAP	88.61	91.01	100.00	**100.00**	267,741	218,623	785,960	**1,272,324**	2	2	6	**10**
		GoldStandard	0.89	0.57	1.54	**1.73**	1,590	923	4,807	**7,323**	1	0	2	**3**
		Gramene61-IEA	26.74	55.24	48.72	**70.24**	38,975	109,319	109,518	**257,832**	0	1	1	**2**
Vigna unguiculata	29,773	GOMAP	91.27	91.10	100.00	**100.00**	75,867	68,313	243,278	**387,458**	2	2	6	**11**
Zea mays B73.v3	100	GOMAP	34,866.00	38,073.00	39,468.00	**39,469.00**	135,211	87,420	291,251	**513,882**	3	2	6	**11**
		GoldStandard	1,548.00	60.00	151.00	**1,634.00**	1,565	65	299	**1,929**	1	0	0	**1**
		Gramene49	11,834.00	17,991.00	15,800.00	**21,926.00**	20,072	31,056	30,089	**81,217**	1	1	1	**3**
		Phytozome	4,524.00	13,728.00	11,365.00	**16,132.00**	4,787	19,044	13,100	**36,931**	0	1	1	**2**
Zea mays B73.v4		GOMAP	36,717.00	37,337.00	39,323.00	**39,324.00**	88,827	82,251	278,719	**449,797**	2	2	6	**10**
		GoldStandard	8,349.00	10,067.00	12,120.00	**14,971.00**	11,510	15,019	25,737	**52,428**	1	1	1	**3**
		Gramene61-IEA	14,774.00	22,064.00	23,965.00	**29,152.00**	20,265	47,657	58,110	**126,525**	1	1	2	**3**
Zea mays Mo17		GOMAP	33,618.00	35,105.00	38,619.00	**38,620.00**	87,567	79,214	277,787	**444,568**	2	2	6	**10**
Zea mays PH207		GOMAP	35,170.00	36,762.00	40,556.00	**40,557.00**	90,617	85,500	288,677	**464,794**	2	2	6	**10**
Zea mays W22		GOMAP	36,987.00	37,685.00	40,689.00	**40,690.00**	95,390	85,039	289,780	**470,209**	2	2	6	**10**

[a] How many genes in the genome have at least one GO term from the CC, BF, MP aspect annotated to them? A = How many at least one from any aspect? ($A = CC \cup BF \cup MP$)
[b] How many annotations in the CC, BF, and MP aspect does this dataset contain? A = How many in total? $A = CC + BF + MP$
[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 $A \neq CC + BF + MP$

Table 3. Quality evaluation of the used GO annotation sets.

Genome	Dataset	SimGIC2 score	TC AUCPCR score
Hordeum vulgarum	GOMAP	0.158996	0.000477
Oryza sativa	GOMAP	0.253680	0.204084
	Gramene61-IEA	0.330437	0.193740
Triticum aestivum	GOMAP	0.218996	0.010039
	Gramene61-IEA	0.175564	0.005397
Zea mays B73.v3	GOMAP	0.052182	0.012709
	Gramene49	0.091475	0.019127
	Phytozome	0.028721	0.004498
Zea mays B73.v4	GOMAP	0.257543	0.196845
	Gramene61-IEA	0.328777	0.188584

3.1 Quality Evaluation

`TODO` If it turns out that our predictions are good with hF but bad with more approriate metrics, explanation would be that score thresholds for the prediction tools used in the GOMAP pipeline have been chosen to maximize this hF value. It now seems reasonable to re-adjust these thresholds to maximize a different metric which will likely result in a drop in hF score but increase in other metrics. Again emphasizes the importance of choosing the right evaluation metric.

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