

	Pairwise path length in reference tree	Jaccard distance over extended gene set	WM distance over summary W2V	WM distance over gene symbols W2V	Cosine distance over over summary W2V	Cosine distance over over NCBI summary W2V	Cosine distance over gene symbols W2V	Cosine distance GO MF description W2V	Cosine distance GO CC description W2V	Cosine distance GO BP description W2V	Cosine distance over over summary W2V	Cosine distance over over NCBI summary W2V	WM distance over summary W2V	Jaccard distance over over summary W2V	WM distance over summary W2V	Pairwise path length in reference tree											
GO-distance (go_type=MF, measure=Wang, combine=BMA)	-0.008	0.449	0.334	0.332	0.317	0.315	-0.099	-0.074	-0.103	-0.091	-0.041	-0.072	0.348	0.319	0.218	0.111	0.078	0.111	0.117	0.105	0.267	0.197	0.332	0.372	0.446	0.264	1.0
GO-distance (go_type=CC, measure=Wang, combine=BMA)	-0.001	0.765	0.887	0.93	0.882	0.921	0.217	0.246	0.215	0.249	0.328	0.282	0.401	0.414	0.617	0.625	0.494	0.468	0.522	0.429	0.555	0.475	-0.109	0.865	-0.129	1.0	0.264
GO-distance (go_type=BP, measure=Wang, combine=BMA)	-0.002	-0.135	-0.103	-0.112	-0.078	-0.097	0.28	0.291	0.289	0.286	0.304	0.331	-0.283	-0.302	-0.124	0.095	-0.024	-0.345	-0.029	-0.125	-0.3	-0.265	0.793	-0.091	1.0	-0.129	0.446
Overlap distance over genes	-0.003	0.85	0.901	0.914	0.858	0.872	0.141	0.175	0.125	0.187	0.247	0.177	0.462	0.453	0.638	0.601	0.533	0.513	0.498	0.408	0.735	0.575	-0.054	1.0	-0.091	0.865	0.372
Minkowski distance (p=2) over genes	0.008	-0.039	-0.05	-0.064	-0.045	-0.063	0.134	0.149	0.134	0.138	0.168	0.176	-0.148	-0.193	-0.124	0.01	-0.064	-0.286	-0.064	-0.126	-0.201	-0.169	1.0	-0.054	0.793	-0.109	0.332
Minkowski distance (p=2) over gene trait frequency	-0.017	0.654	0.482	0.472	0.421	0.436	-0.251	-0.254	-0.268	-0.209	-0.235	-0.273	0.617	0.515	0.532	0.25	0.439	0.629	0.352	0.348	0.715	1.0	-0.169	0.575	-0.265	0.475	0.197
Minkowski distance (p=1) over genes	-0.009	0.652	0.538	0.548	0.477	0.502	-0.279	-0.266	-0.295	-0.252	-0.234	-0.297	0.605	0.571	0.591	0.293	0.408	0.703	0.381	0.388	1.0	0.715	-0.201	0.735	-0.3	0.555	0.267
Minkowski distance (p=1) over gene traits	-0.002	0.404	0.379	0.391	0.317	0.345	0.002	0.02	-0.001	0.014	0.035	0.008	0.203	0.197	0.503	0.319	0.528	0.509	0.299	1.0	0.388	0.348	-0.126	0.408	-0.125	0.429	0.105
Kappa distance over genes	0.005	0.457	0.522	0.531	0.473	0.488	0.247	0.295	0.261	0.227	0.314	0.283	0.098	0.054	0.487	0.695	0.493	0.461	1.0	0.299	0.381	0.352	-0.064	0.498	-0.029	0.522	0.117
Kappa distance over gene traits	-0.002	0.453	0.427	0.436	0.354	0.384	-0.252	-0.24	-0.253	-0.251	-0.235	-0.267	0.423	0.427	0.559	0.29	0.519	1.0	0.461	0.509	0.703	0.629	-0.286	0.513	-0.345	0.468	0.111
Jaccard distance over gene frequency	0.026	0.372	0.437	0.45	0.41	0.424	0.281	0.299	0.276	0.296	0.32	0.295	0.075	0.042	0.472	0.549	1.0	0.519	0.493	0.528	0.408	0.439	-0.064	0.533	-0.024	0.494	0.078
Random (uniform, (0,1))	0.003	0.466	0.588	0.603	0.567	0.578	0.579	0.604	0.568	0.6	0.629	0.593	-0.025	-0.091	0.492	1.0	0.549	0.29	0.695	0.319	0.293	0.25	0.01	0.601	0.095	0.625	0.111
Pairwise path length in reference tree	0.002	0.547	0.596	0.612	0.538	0.572	-0.02	0.002	-0.02	-0.001	0.027	-0.002	0.403	0.391	1.0	0.492	0.472	0.559	0.487	0.503	0.591	0.532	-0.124	0.638	-0.124	0.617	0.218
Jaccard distance over extended gene set	-0.028	0.569	0.399	0.439	0.405	0.479	-0.601	-0.601	-0.603	-0.551	-0.538	-0.574	0.969	1.0	0.391	-0.091	0.042	0.427	0.054	0.197	0.571	0.515	-0.193	0.453	-0.302	0.414	0.319
WM distance over summary W2V	-0.053	0.602	0.42	0.431	0.436	0.461	-0.553	-0.548	-0.567	-0.503	-0.476	-0.537	1.0	0.969	0.403	-0.025	0.075	0.423	0.098	0.203	0.605	0.617	-0.148	0.462	-0.283	0.401	0.348
WM distance over gene symbols W2V	0.018	0.005	0.223	0.248	0.315	0.304	0.971	0.976	0.979	0.952	0.973	1.0	-0.537	-0.574	-0.002	0.593	0.295	-0.267	0.283	0.008	-0.297	-0.273	0.176	0.177	0.331	0.282	-0.072
Cosine distance over over summary W2V	0.015	0.118	0.306	0.313	0.387	0.351	0.952	0.976	0.94	0.942	1.0	0.973	-0.476	-0.538	0.027	0.629	0.32	-0.235	0.314	0.035	-0.234	-0.235	0.168	0.247	0.304	0.328	-0.041
Cosine distance over over NCBI summary W2V	0.012	0.037	0.21	0.22	0.305	0.278	0.977	0.951	0.953	1.0	0.942	0.952	-0.503	-0.551	-0.001	0.6	0.296	-0.251	0.227	0.014	-0.252	-0.209	0.138	0.187	0.286	0.249	-0.091
Cosine distance over gene symbols W2V	0.018	-0.046	0.166	0.187	0.255	0.241	0.991	0.981	1.0	0.953	0.94	0.979	-0.567	-0.603	-0.02	0.568	0.276	-0.253	0.261	-0.001	-0.295	-0.268	0.134	0.125	0.289	0.215	-0.103
Cosine distance GO MF description W2V	0.018	0.033	0.23	0.235	0.303	0.269	0.986	1.0	0.981	0.951	0.976	0.976	-0.548	-0.601	0.002	0.604	0.299	-0.24	0.295	0.02	-0.266	-0.254	0.149	0.175	0.291	0.246	-0.074
Cosine distance GO CC description W2V	0.017	-0.013	0.183	0.193	0.274	0.245	1.0	0.986	0.991	0.977	0.952	0.971	-0.553	-0.601	-0.02	0.579	0.281	-0.252	0.247	0.002	-0.279	-0.251	0.134	0.141	0.28	0.217	-0.099
Cosine distance GO BP description W2V	0.0	0.797	0.921	0.961	0.967	1.0	0.245	0.269	0.241	0.278	0.351	0.304	0.461	0.479	0.572	0.578	0.424	0.384	0.488	0.345	0.502	0.436	-0.063	0.872	-0.097	0.921	0.315
Overlap distance over genes	0.003	0.827	0.95	0.946	1.0	0.967	0.274	0.303	0.255	0.305	0.387	0.315	0.436	0.405	0.538	0.567	0.41	0.354	0.473	0.317	0.477	0.421	-0.045	0.858	-0.078	0.882	0.317
Overlap distance over gene traits	0.002	0.857	0.981	1.0	0.946	0.961	0.193	0.235	0.187	0.22	0.313	0.248	0.431	0.439	0.612	0.603	0.45	0.436	0.531	0.391	0.548	0.472	-0.064	0.914	-0.112	0.93	0.332
Minkowski distance (p=2) over genes	0.001	0.891	1.0	0.981	0.95	0.921	0.183	0.23	0.166	0.21	0.306	0.223	0.42	0.399	0.596	0.588	0.437	0.427	0.522	0.379	0.538	0.482	-0.05	0.901	-0.103	0.887	0.334
Minkowski distance (p=2) over gene trait frequency	-0.021	1.0	0.891	0.857	0.827	0.797	-0.013	0.033	-0.046	0.037	0.118	0.005	0.602	0.569	0.547	0.466	0.372	0.453	0.457	0.404	0.652	0.654	-0.039	0.85	-0.135	0.765	0.449
Minkowski distance (p=1) over genes	1.0	-0.021	0.001	0.002	0.003	0.0	0.017	0.018	0.018	0.012	0.015	0.018	-0.053	-0.028	0.002	0.003	0.026	-0.002	0.005	-0.002	-0.009	-0.017	0.008	-0.003	-0.002	-0.001	-0.008
Minkowski distance (p=1) over gene traits																											