	Random (uniform, (0,1))	Cosine distance over gene trait frequency	Jaccard distance over gene traits	Jaccard distance over genes	Kappa distance over gene traits	Kappa distance over genes	Minkowski distance (p=1) over gene trait frequency	Minkowski distance (p=1) over gene traits	Minkowski distance (p=1) over genes	Minkowski distance (p=2) over gene trait frequency	Minkowski distance (p=2) over gene traits	Minkowski distance (p=2) over genes	Overlap distance over gene traits	Overlap distance over genes	GO-distance (go_type=BP, measure=Wang, combine=BMA)	GO-distance (go_type=CC, measure=Wang, combine=BMA)	GO-distance (go_type=MF, measure=Wang, combine=BMA)	Cosine distance GO BP description W2V	Cosine distance GO CC description W2V	Cosine distance GO MF description W2V	Cosine distance over gene symbols W2V	Cosine distance over over NCBI summary W2V	Cosine distance over over summary W2V	WM distance over gene symbols W2V	WM distance over summary W2V	Jaccard distance over extended gene set	Pairwise path length in reference tree
Pairwise path length in reference tree	-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
Jaccard distance over extended gene set	-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
WM distance over summary W2V	-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
WM distance over gene symbols W2V	-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
Cosine distance over over summary W2V	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
Cosine distance over over NCBI summary W2V	-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
Cosine distance over gene symbols W2V	-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
Cosine distance GO MF description W2V	-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
Cosine distance GO CC description W2V	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
Cosine distance GO BP description W2V	-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
GO-distance (go_type=MF, measure=Wang, combine=BMA)	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
GO-distance (go_type=CC, measure=Wang, combine=BMA)	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
GO-distance (go_type=BP, measure=Wang, combine=BMA)	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
Overlap distance over genes	-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
Overlap distance over gene traits	-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
Minkowski distance (p=2) over genes	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
Minkowski distance (p=2) over gene traits	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
Minkowski distance (p=2) over gene trait frequency	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
Minkowski distance (p=1) over genes	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
Minkowski distance (p=1) over gene traits	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
Minkowski distance (p=1) over gene trait frequency	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
Kappa distance over genes	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
Kappa distance over gene traits	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
Jaccard distance over genes	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
Jaccard distance over gene traits	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
Cosine distance 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
Random (uniform, (0,1))	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