

	Pairwise path length in reference tree	Jaccard distance over extended gene set	Dijkstra BMA PPI	WM distance over summary W2V	WM distance over gene symbols W2V	Cosine distance over NCBI summary W2V	Cosine distance over over summary W2V	Cosine distance GO MF description W2V	Cosine distance GO CC description W2V	Cosine distance GO BP description W2V	Cosine distance over genes	Cosine distance over gene traits	Overlap distance over genes	Overlap distance over gene traits	Minkowski distance (p=2) over genes	Minkowski distance (p=2) over gene trait frequency	Minkowski distance (p=1) over genes	Minkowski distance (p=1) over gene trait frequency	Kappa distance over genes	Kappa distance over gene traits	Jaccard distance over genes	Jaccard distance over gene trait frequency	Random (uniform, (0,1))					
Pairwise path length in reference tree	-0.005	0.334	0.385	0.426	0.373	0.443	-0.204	-0.205	-0.227	-0.146	-0.132	-0.205	0.464	0.544	0.19	0.158	0.151	0.142	0.096	0.109	0.231	0.22	0.064	0.358	0.267	0.333	0.312	1.0
Jaccard distance over extended gene set	-0.003	0.49	0.662	0.787	0.637	0.775	0.03	0.042	0.018	0.051	0.099	0.044	0.496	0.641	0.547	0.462	0.481	0.268	0.251	0.319	0.447	0.356	0.237	0.696	0.35	0.607	1.0	0.312
Dijkstra BMA PPI	-0.008	0.436	0.549	0.596	0.544	0.604	-0.057	-0.058	-0.135	-0.041	-0.02	-0.135	0.508	0.592	0.476	0.566	0.52	0.361	0.384	0.464	0.424	0.358	0.248	0.555	0.315	1.0	0.607	0.333
WM distance over summary W2V	-0.009	0.264	0.302	0.338	0.294	0.341	0.031	0.015	0.023	0.048	0.015	0.016	0.264	0.312	0.33	0.266	0.321	0.25	0.209	0.255	0.327	0.264	0.789	0.39	1.0	0.315	0.35	0.267
WM distance over gene symbols W2V	-0.004	0.602	0.69	0.776	0.685	0.771	0.049	0.054	0.059	0.069	0.091	0.092	0.535	0.615	0.614	0.509	0.521	0.358	0.356	0.349	0.798	0.519	0.283	1.0	0.39	0.555	0.696	0.358
Cosine distance over over summary W2V	-0.007	0.162	0.177	0.182	0.175	0.183	0.033	0.005	0.043	0.026	-0.034	0.009	0.147	0.154	0.26	0.255	0.289	0.255	0.247	0.267	0.317	0.27	1.0	0.283	0.789	0.248	0.237	0.064
Cosine distance over over NCBI summary W2V	0.0	0.285	0.316	0.316	0.311	0.325	-0.074	-0.104	0.015	-0.081	-0.127	0.008	0.286	0.307	0.392	0.493	0.463	0.397	0.441	0.432	0.609	1.0	0.27	0.519	0.264	0.358	0.356	0.22
Cosine distance over gene symbols W2V	-0.004	0.485	0.421	0.389	0.417	0.386	-0.106	-0.163	-0.047	-0.107	-0.214	-0.106	0.389	0.369	0.589	0.519	0.556	0.519	0.473	0.492	1.0	0.609	0.317	0.798	0.327	0.424	0.447	0.231
Cosine distance GO MF description W2V	-0.006	0.247	0.185	0.187	0.173	0.171	-0.112	-0.169	-0.128	-0.11	-0.218	-0.229	0.196	0.19	0.488	0.59	0.795	0.578	0.553	1.0	0.492	0.432	0.267	0.349	0.255	0.464	0.319	0.109
Cosine distance GO CC description W2V	-0.0	0.235	0.218	0.165	0.211	0.159	-0.076	-0.125	-0.016	-0.094	-0.201	-0.082	0.196	0.153	0.349	0.717	0.478	0.619	1.0	0.553	0.473	0.441	0.247	0.356	0.209	0.384	0.251	0.096
Cosine distance GO BP description W2V	-0.0	0.266	0.23	0.187	0.22	0.178	-0.121	-0.172	-0.086	-0.134	-0.231	-0.16	0.23	0.19	0.428	0.582	0.552	1.0	0.619	0.578	0.519	0.397	0.255	0.358	0.25	0.361	0.268	0.142
GO-distance (go_type=MF, measure=Wang, combine=BMA)	-0.006	0.324	0.314	0.339	0.303	0.327	0.008	-0.026	0.017	0.001	-0.062	-0.044	0.229	0.278	0.716	0.72	1.0	0.552	0.478	0.795	0.556	0.463	0.289	0.521	0.321	0.52	0.481	0.151
GO-distance (go_type=CC, measure=Wang, combine=BMA)	-0.005	0.346	0.366	0.35	0.356	0.338	0.011	-0.024	0.025	0.003	-0.074	-0.023	0.262	0.292	0.659	1.0	0.72	0.582	0.717	0.59	0.519	0.493	0.255	0.509	0.266	0.566	0.462	0.158
GO-distance (go_type=BP, measure=Wang, combine=BMA)	-0.005	0.464	0.426	0.444	0.42	0.439	0.02	-0.006	0.021	0.021	-0.019	-0.009	0.381	0.382	1.0	0.659	0.716	0.428	0.349	0.488	0.589	0.392	0.26	0.614	0.33	0.476	0.547	0.19
Overlap distance over genes	-0.008	0.576	0.675	0.779	0.676	0.818	-0.267	-0.209	-0.283	-0.196	-0.058	-0.175	0.769	1.0	0.382	0.292	0.278	0.19	0.153	0.19	0.369	0.307	0.154	0.615	0.312	0.592	0.641	0.544
Overlap distance over gene traits	-0.006	0.7	0.731	0.603	0.765	0.629	-0.315	-0.294	-0.298	-0.289	-0.22	-0.259	1.0	0.769	0.381	0.262	0.229	0.23	0.196	0.196	0.389	0.286	0.147	0.535	0.264	0.508	0.496	0.464
Minkowski distance (p=2) over genes	0.007	-0.096	0.06	0.14	0.094	0.175	0.779	0.831	0.919	0.704	0.779	1.0	-0.259	-0.175	-0.009	-0.023	-0.044	-0.16	-0.082	-0.229	-0.106	0.008	0.009	0.092	0.016	-0.135	0.044	-0.205
Minkowski distance (p=2) over gene traits	0.001	0.0	0.139	0.232	0.176	0.257	0.824	0.924	0.698	0.814	1.0	0.779	-0.22	-0.058	0.019	-0.074	-0.062	-0.231	-0.201	-0.218	-0.214	-0.127	-0.034	0.091	0.015	-0.02	0.099	-0.132
Minkowski distance (p=2) over gene trait frequency	0.002	0.024	0.06	0.12	0.094	0.14	0.928	0.9	0.774	1.0	0.814	0.704	-0.289	-0.196	0.021	0.003	0.001	-0.134	-0.094	-0.11	-0.107	-0.081	0.026	0.069	0.048	-0.041	0.051	-0.146
Minkowski distance (p=1) over genes	0.009	-0.095	0.022	0.06	0.06	0.089	0.891	0.868	1.0	0.774	0.698	0.919	-0.298	-0.283	0.021	0.025	0.017	-0.086	-0.016	-0.128	-0.047	0.015	0.043	0.059	0.023	-0.135	0.018	-0.227
Minkowski distance (p=1) over gene traits	0.004	-0.055	0.068	0.127	0.116	0.153	0.97	1.0	0.868	0.9	0.924	0.831	-0.294	-0.209	-0.006	-0.024	-0.026	-0.172	-0.125	-0.169	-0.163	-0.104	0.005	0.054	0.015	-0.058	0.042	-0.205
Minkowski distance (p=1) over gene trait frequency	0.005	-0.054	0.039	0.083	0.081	0.104	1.0	0.97	0.891	0.928	0.824	0.779	-0.315	-0.267	0.02	0.011	0.008	-0.121	-0.076	-0.112	-0.106	-0.074	0.033	0.049	0.031	-0.057	0.03	-0.204
Kappa distance over genes	-0.004	0.601	0.816	0.984	0.812	1.0	0.104	0.153	0.089	0.14	0.257	0.175	0.629	0.818	0.439	0.338	0.327	0.178	0.159	0.171	0.386	0.325	0.183	0.771	0.341	0.604	0.775	0.443
Kappa distance over gene traits	-0.003	0.758	0.983	0.797	1.0	0.812	0.081	0.116	0.06	0.094	0.176	0.094	0.765	0.676	0.42	0.356	0.303	0.22	0.211	0.173	0.417	0.311	0.175	0.685	0.294	0.544	0.637	0.373
Jaccard distance over genes	-0.004	0.593	0.816	1.0	0.797	0.984	0.083	0.127	0.06	0.12	0.232	0.14	0.603	0.779	0.444	0.35	0.339	0.187	0.165	0.187	0.389	0.316	0.182	0.776	0.338	0.596	0.787	0.426
Jaccard distance over gene traits	-0.003	0.738	1.0	0.816	0.983	0.816	0.039	0.068	0.022	0.06	0.139	0.06	0.731	0.675	0.426	0.366	0.314	0.23	0.218	0.185	0.421	0.316	0.177	0.69	0.302	0.549	0.662	0.385
Cosine distance over gene trait frequency	-0.007	1.0	0.738	0.593	0.758	0.601	-0.054	-0.055	-0.095	0.024	0.0	-0.096	0.7	0.576	0.464	0.346	0.324	0.266	0.235	0.247	0.485	0.285	0.162	0.602	0.264	0.436	0.49	0.334
Random (uniform, (0,1))	1.0	-0.007	-0.003	-0.004	-0.003	-0.004	0.005	0.004	0.009	0.002	0.001	0.007	-0.006	-0.008	-0.005	-0.005	-0.006	-0.0	-0.0	-0.006	-0.004	0.0	-0.007	-0.004	-0.009	-0.008	-0.003	-0.005