

	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	GO-distance (go_type=MF, measure=Wang, combine=BMA)	GO-distance (go_type=CC, measure=Wang, combine=BMA)	GO-distance (go_type=BP, measure=Wang, combine=BMA)	Overlap distance over genes	Overlap distance over gene traits	Minkowski distance (p=2) over genes	Minkowski distance (p=2) over gene traits	Minkowski distance (p=2) over gene trait frequency	Minkowski distance (p=1) over genes	Minkowski distance (p=1) over gene traits	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 traits	Cosine distance over gene trait frequency	Random (uniform, (0,1))
Pairwise path length in reference tree	1.0	0.312	0.358	0.267	0.064	0.231	0.22	0.109	0.096	0.142	0.151	0.158	0.19	0.464	0.544	0.205	0.146	0.132	0.205	0.132	0.205	0.443	0.373	0.426	0.385	0.334	-0.005
Jaccard distance over extended gene set	0.312	1.0	0.35	0.35	0.696	0.237	0.356	0.447	0.447	0.327	0.264	0.312	0.33	0.496	0.641	0.042	0.018	0.051	0.099	0.044	0.042	0.775	0.637	0.787	0.662	0.49	-0.003
WM distance over summary W2V	0.358	0.35	1.0	0.39	0.39	0.789	0.264	0.327	0.327	0.264	0.264	0.312	0.33	0.264	0.312	0.015	0.023	0.048	0.015	0.016	0.031	0.341	0.294	0.338	0.302	0.264	-0.009
WM distance over gene symbols W2V	0.267	0.35	0.39	1.0	0.39	0.789	0.264	0.327	0.327	0.264	0.264	0.312	0.33	0.535	0.615	0.054	0.059	0.069	0.091	0.092	0.049	0.771	0.685	0.776	0.69	0.602	-0.004
Cosine distance over over summary W2V	0.064	0.696	0.39	0.39	1.0	0.283	0.519	0.283	0.283	0.283	0.358	0.521	0.509	0.147	0.154	0.005	0.043	0.026	-0.034	0.009	0.033	0.183	0.175	0.182	0.177	0.162	-0.007
Cosine distance over over NCBI summary W2V	0.231	0.356	0.39	0.39	0.283	1.0	0.27	0.317	0.317	0.317	0.255	0.289	0.255	0.286	0.307	-0.074	-0.104	-0.081	-0.127	0.008	-0.074	0.325	0.311	0.316	0.316	0.285	0.0
Cosine distance over gene symbols W2V	0.22	0.356	0.35	0.35	0.27	0.27	1.0	0.609	0.609	0.609	0.589	0.519	0.556	0.389	0.369	-0.106	-0.163	-0.047	-0.107	-0.106	-0.106	0.386	0.417	0.389	0.421	0.485	-0.004
Cosine distance GO MF description W2V	0.109	0.447	0.447	0.447	0.317	0.317	0.609	1.0	0.609	0.609	0.589	0.519	0.556	0.389	0.369	-0.106	-0.163	-0.047	-0.107	-0.106	-0.106	0.386	0.417	0.389	0.421	0.485	-0.004
Cosine distance GO CC description W2V	0.096	0.447	0.447	0.447	0.317	0.317	0.609	0.609	1.0	0.609	0.589	0.519	0.556	0.389	0.369	-0.106	-0.163	-0.047	-0.107	-0.106	-0.106	0.386	0.417	0.389	0.421	0.485	-0.004
Cosine distance GO BP description W2V	0.142	0.356	0.356	0.356	0.27	0.27	0.492	0.492	0.492	1.0	0.196	0.19	0.488	0.196	0.19	-0.112	-0.169	-0.128	-0.11	-0.218	-0.229	0.171	0.173	0.187	0.185	0.247	-0.006
GO-distance (go_type=MF, measure=Wang, combine=BMA)	0.151	0.358	0.358	0.358	0.27	0.27	0.492	0.492	0.492	0.492	0.196	0.19	0.488	0.196	0.19	-0.112	-0.169	-0.128	-0.11	-0.218	-0.229	0.171	0.173	0.187	0.185	0.247	-0.006
GO-distance (go_type=CC, measure=Wang, combine=BMA)	0.158	0.358	0.358	0.358	0.27	0.27	0.492	0.492	0.492	0.492	0.196	0.19	0.488	0.196	0.19	-0.112	-0.169	-0.128	-0.11	-0.218	-0.229	0.171	0.173	0.187	0.185	0.247	-0.006
GO-distance (go_type=BP, measure=Wang, combine=BMA)	0.19	0.358	0.358	0.358	0.27	0.27	0.492	0.492	0.492	0.492	0.196	0.19	0.488	0.196	0.19	-0.112	-0.169	-0.128	-0.11	-0.218	-0.229	0.171	0.173	0.187	0.185	0.247	-0.006
Overlap distance over genes	0.464	0.641	0.39	0.39	0.283	0.519	0.283	0.283	0.283	0.283	0.358	0.521	0.509	0.147	0.154	0.005	0.043	0.026	-0.034	0.009	0.033	0.183	0.175	0.182	0.177	0.162	-0.007
Overlap distance over gene traits	0.544	0.641	0.39	0.39	0.696	0.237	0.356	0.447	0.447	0.327	0.264	0.312	0.33	0.496	0.641	0.042	0.018	0.051	0.099	0.044	0.042	0.775	0.637	0.787	0.662	0.49	-0.003
Minkowski distance (p=2) over genes	0.19	0.158	0.158	0.158	0.237	0.356	0.447	0.447	0.327	0.264	0.264	0.312	0.33	0.264	0.312	0.015	0.023	0.048	0.015	0.016	0.031	0.341	0.294	0.338	0.302	0.264	-0.009
Minkowski distance (p=2) over gene traits	0.158	0.151	0.151	0.151	0.237	0.356	0.447	0.447	0.327	0.264	0.264	0.312	0.33	0.264	0.312	0.015	0.023	0.048	0.015	0.016	0.031	0.341	0.294	0.338	0.302	0.264	-0.009
Minkowski distance (p=2) over gene trait frequency	0.151	0.142	0.142	0.142	0.237	0.356	0.447	0.447	0.327	0.264	0.264	0.312	0.33	0.264	0.312	0.015	0.023	0.048	0.015	0.016	0.031	0.341	0.294	0.338	0.302	0.264	-0.009
Minkowski distance (p=1) over genes	0.142	0.109	0.109	0.109	0.237	0.356	0.447	0.447	0.327	0.264	0.264	0.312	0.33	0.264	0.312	0.015	0.023	0.048	0.015	0.016	0.031	0.341	0.294	0.338	0.302	0.264	-0.009
Minkowski distance (p=1) over gene traits	0.142	0.109	0.109	0.109	0.237	0.356	0.447	0.447	0.327	0.264	0.264	0.312	0.33	0.264	0.312	0.015	0.023	0.048	0.015	0.016	0.031	0.341	0.294	0.338	0.302	0.264	-0.009
Minkowski distance (p=1) over gene trait frequency	0.142	0.109	0.109	0.109	0.237	0.356	0.447	0.447	0.327	0.264	0.264	0.312	0.33	0.264	0.312	0.015	0.023	0.048	0.015	0.016	0.031	0.341	0.294	0.338	0.302	0.264	-0.009
Kappa distance over genes	0.109	0.096	0.096	0.096	0.237	0.356	0.447	0.447	0.327	0.264	0.264	0.312	0.33	0.264	0.312	0.015	0.023	0.048	0.015	0.016	0.031	0.341	0.294	0.338	0.302	0.264	-0.009
Kappa distance over gene traits	0.109	0.096	0.096	0.096	0.237	0.356	0.447	0.447	0.327	0.264	0.264	0.312	0.33	0.264	0.312	0.015	0.023	0.048	0.015	0.016	0.031	0.341	0.294	0.338	0.302	0.264	-0.009
Jaccard distance over genes	0.096	0.096	0.096	0.096	0.237	0.356	0.447	0.447	0.327	0.264	0.264	0.312	0.33	0.264	0.312	0.015	0.023	0.048	0.015	0.016	0.031	0.341	0.294	0.338	0.302	0.264	-0.009
Jaccard distance over gene traits	0.096	0.096	0.096	0.096	0.237	0.356	0.447	0.447	0.327	0.264	0.264	0.312	0.33	0.264	0.312	0.015	0.023	0.048	0.015	0.016	0.031	0.341	0.294	0.338	0.302	0.264	-0.009
Cosine distance over gene trait frequency	0.142	0.356	0.356	0.356	0.27	0.27	0.492	0.492	0.492	1.0	0.196	0.19	0.488	0.196	0.19	-0.112	-0.169	-0.128	-0.11	-0.218	-0.229	0.171	0.173	0.187	0.185	0.247	-0.006
Random (uniform, (0,1))	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	0.312	1.0