

	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	Jaccard distance over summary W2V	Pairwise path length in reference tree	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 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 traits	Random (uniform, (0,1))
Pairwise path length in reference tree	1.0	0.231	0.247	0.227	0.279	0.227	0.247	0.231	1.0	0.231	0.247	0.227	0.279	0.227	0.247	0.231	1.0	0.231	0.247	0.227	0.279
Jaccard distance over extended gene set	0.483	1.0	0.647	1.0	0.455	0.748	0.334	0.47	0.647	1.0	0.231	0.247	0.227	0.279	0.227	0.247	0.231	1.0	0.231	0.247	0.227
Dijkstra BMA PPI	0.482	0.437	1.0	0.334	0.47	0.748	0.334	0.47	0.647	1.0	0.231	0.247	0.227	0.279	0.227	0.247	0.231	1.0	0.231	0.247	0.227
WM distance over summary W2V	0.401	0.34	0.375	1.0	0.334	0.47	0.334	0.47	0.647	1.0	0.231	0.247	0.227	0.279	0.227	0.247	0.231	1.0	0.231	0.247	0.227
WM distance over gene symbols W2V	0.555	0.512	0.854	0.511	0.826	0.221	0.254	0.32	0.273	0.39	0.469	0.462	0.614	0.622	0.526	0.741	0.591	0.509	0.542	0.753	0.756
Cosine distance over over summary W2V	0.31	0.243	0.266	0.235	0.206	0.066	0.088	0.068	0.089	0.156	0.123	0.24	0.157	0.273	0.113	0.408	0.289	0.183	0.316	0.425	0.404
Cosine distance over over NCBI summary W2V	0.291	0.233	0.524	0.238	0.503	-0.011	0.003	0.066	0.037	0.099	0.159	0.305	0.464	0.466	0.308	0.602	0.723	0.353	0.54	0.812	1.0
Cosine distance over gene symbols W2V	0.459	0.406	0.625	0.35	0.552	-0.13	-0.115	-0.116	-0.063	0.014	-0.006	0.492	0.637	0.317	0.207	0.599	0.52	0.332	0.425	1.0	0.812
Cosine distance GO MF description W2V	0.268	0.221	0.481	0.233	0.463	0.12	0.151	0.296	0.129	0.227	0.395	0.234	0.301	0.795	0.457	0.734	0.673	0.401	1.0	0.425	0.54
Cosine distance GO CC description W2V	0.365	0.308	0.508	0.302	0.433	0.037	0.085	0.113	0.045	0.18	0.209	0.342	0.361	0.467	0.719	0.395	0.429	1.0	0.401	0.332	0.353
Cosine distance GO BP description W2V	0.165	0.131	0.436	0.142	0.423	0.118	0.138	0.289	0.119	0.186	0.364	0.117	0.249	0.722	0.436	0.567	1.0	0.429	0.673	0.52	0.723
GO-distance (go_type=MF, measure=Wang, combine=BMA)	0.536	0.44	0.674	0.49	0.665	0.314	0.353	0.373	0.338	0.453	0.471	0.445	0.464	0.724	0.459	1.0	0.567	0.395	0.734	0.599	0.602
GO-distance (go_type=CC, measure=Wang, combine=BMA)	0.381	0.327	0.613	0.327	0.579	0.227	0.27	0.376	0.234	0.358	0.479	0.263	0.343	0.662	1.0	0.459	0.436	0.719	0.457	0.207	0.308
GO-distance (go_type=BP, measure=Wang, combine=BMA)	0.298	0.271	0.574	0.305	0.573	0.375	0.411	0.601	0.357	0.457	0.694	0.167	0.2	1.0	0.662	0.724	0.722	0.467	0.795	0.317	0.466
Overlap distance over genes	0.712	0.537	0.749	0.54	0.746	-0.243	-0.197	-0.193	-0.159	-0.02	-0.025	0.849	1.0	0.2	0.343	0.464	0.249	0.361	0.301	0.637	0.464
Overlap distance over gene traits	0.89	0.776	0.589	0.795	0.542	-0.16	-0.097	-0.268	-0.067	0.103	-0.135	1.0	0.849	0.167	0.263	0.445	0.117	0.342	0.234	0.492	0.305
Minkowski distance (p=2) over genes	0.132	0.216	0.504	0.314	0.591	0.811	0.826	0.961	0.77	0.812	1.0	-0.135	-0.025	0.694	0.479	0.471	0.364	0.209	0.395	-0.006	0.159
Minkowski distance (p=2) over gene trait frequency	0.422	0.42	0.429	0.555	0.477	0.924	0.944	0.789	0.943	1.0	0.812	0.103	-0.02	0.457	0.358	0.453	0.186	0.18	0.227	0.014	0.099
Minkowski distance (p=1) over genes	0.265	0.283	0.287	0.41	0.345	0.958	0.936	0.785	1.0	0.943	0.77	-0.067	-0.159	0.357	0.234	0.338	0.119	0.045	0.129	-0.063	0.037
Minkowski distance (p=1) over gene trait frequency	0.001	0.095	0.312	0.205	0.427	0.87	0.875	1.0	0.785	0.789	0.961	-0.268	-0.193	0.601	0.376	0.373	0.289	0.113	0.296	-0.116	0.066
Minkowski distance (p=1) over gene trait frequency	0.201	0.219	0.258	0.377	0.34	0.991	1.0	0.875	0.936	0.944	0.826	-0.097	-0.197	0.411	0.27	0.353	0.138	0.085	0.151	-0.115	0.003
Minkowski distance (p=1) over gene trait frequency	0.145	0.18	0.217	0.331	0.299	1.0	0.991	0.87	0.958	0.924	0.811	-0.16	-0.243	0.375	0.227	0.314	0.118	0.037	0.12	-0.13	-0.011
Kappa distance over genes	0.628	0.561	0.951	0.615	1.0	0.299	0.34	0.427	0.345	0.477	0.591	0.542	0.746	0.573	0.579	0.665	0.423	0.433	0.463	0.552	0.503
Kappa distance over gene traits	0.926	0.931	0.623	1.0	0.615	0.331	0.377	0.205	0.41	0.555	0.314	0.795	0.54	0.305	0.327	0.49	0.142	0.302	0.233	0.35	0.238
Jaccard distance over genes	0.688	0.636	1.0	0.623	0.951	0.217	0.258	0.312	0.287	0.429	0.504	0.589	0.749	0.574	0.613	0.674	0.436	0.508	0.481	0.625	0.524
Jaccard distance over gene traits	0.939	1.0	0.636	0.931	0.561	0.18	0.219	0.095	0.283	0.42	0.216	0.776	0.537	0.271	0.327	0.44	0.131	0.308	0.221	0.406	0.233
Cosine distance over gene trait frequency	1.0	0.939	0.688	0.926	0.628	0.145	0.201	0.001	0.265	0.422	0.132	0.89	0.712	0.298	0.381	0.536	0.165	0.365	0.268	0.459	0.291
Random (uniform, (0,1))	0.008	0.006	0.002	-0.024	-0.014	0.025	-0.034	-0.03	-0.009	-0.03	-0.03	-0.032	-0.008	-0.021	-0.003	0.011	-0.017	-0.02	-0.012	0.027	-0.005