

	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 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	0.042	0.483	0.348	0.307	0.366	0.273	-0.157	-0.113	-0.168	-0.138	-0.023	-0.1	0.583	0.485	0.177	0.078	0.455	0.036	0.141	0.232	0.34	0.14	0.183	0.279	0.227	0.247	0.231	1.0
Jaccard distance over extended gene set	-0.006	0.473	0.459	0.845	0.459	0.793	0.241	0.275	0.369	0.276	0.386	0.529	0.379	0.509	0.714	0.551	0.711	0.538	0.474	0.58	0.575	0.567	0.314	0.827	0.47	0.647	1.0	0.231
Dijkstra BMA PPI	0.027	0.482	0.437	0.718	0.432	0.72	0.191	0.214	0.267	0.229	0.314	0.367	0.388	0.585	0.545	0.454	0.744	0.552	0.411	0.546	0.67	0.594	0.236	0.748	0.334	1.0	0.647	0.247
WM distance over summary W2V	0.042	0.401	0.34	0.375	0.334	0.323	0.219	0.242	0.265	0.246	0.32	0.352	0.263	0.146	0.492	0.224	0.54	0.336	0.201	0.446	0.332	0.295	0.772	0.455	1.0	0.334	0.47	0.227
WM distance over gene symbols W2V	0.002	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	0.402	1.0	0.455	0.748	0.827	0.279
Cosine distance over over summary W2V	0.022	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	1.0	0.402	0.772	0.236	0.314	0.183
Cosine distance over over NCBI summary W2V	-0.005	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	0.404	0.756	0.295	0.594	0.567	0.14
Cosine distance over gene symbols W2V	0.027	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	0.425	0.753	0.332	0.67	0.575	0.34
Cosine distance GO MF description W2V	-0.012	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	0.316	0.542	0.446	0.546	0.58	0.232
Cosine distance GO CC description W2V	-0.02	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	0.183	0.509	0.201	0.411	0.474	0.141
Cosine distance GO BP description W2V	-0.017	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	0.289	0.591	0.336	0.552	0.538	0.036
GO-distance (go_type=MF, measure=Wang, combine=BMA)	0.011	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	0.408	0.741	0.54	0.744	0.711	0.455
GO-distance (go_type=CC, measure=Wang, combine=BMA)	-0.003	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	0.113	0.526	0.224	0.454	0.551	0.078
GO-distance (go_type=BP, measure=Wang, combine=BMA)	-0.021	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	0.273	0.622	0.492	0.545	0.714	0.177
Overlap distance over genes	-0.008	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	0.157	0.614	0.146	0.585	0.509	0.485
Overlap distance over gene traits	-0.032	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	0.24	0.462	0.263	0.388	0.379	0.583
Minkowski distance (p=2) over genes	-0.03	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	0.123	0.469	0.352	0.367	0.529	-0.1
Minkowski distance (p=2) over gene traits	-0.03	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	0.156	0.39	0.32	0.314	0.386	-0.023
Minkowski distance (p=2) over gene trait frequency	-0.009	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	0.089	0.273	0.246	0.229	0.276	-0.138
Minkowski distance (p=1) over genes	-0.03	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	0.068	0.32	0.265	0.267	0.369	-0.168
Minkowski distance (p=1) over gene traits	-0.034	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	0.088	0.254	0.242	0.214	0.275	-0.113
Minkowski distance (p=1) over gene trait frequency	-0.025	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	0.066	0.221	0.219	0.191	0.241	-0.157
Kappa distance over genes	-0.014	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	0.206	0.826	0.323	0.72	0.793	0.273
Kappa distance over gene traits	-0.024	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	0.235	0.511	0.334	0.432	0.459	0.366
Jaccard distance over genes	0.002	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	0.266	0.854	0.375	0.718	0.845	0.307
Jaccard distance over gene traits	0.006	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	0.243	0.512	0.34	0.437	0.459	0.348
Cosine distance over gene trait frequency	0.008	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	0.31	0.555	0.401	0.482	0.473	0.483
Random (uniform, (0,1))	1.0	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	0.022	0.002	0.042	0.027	-0.006	0.042