

	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	0.018	0.323	0.423	0.455	0.383	0.427	-0.194	-0.096	-0.188	-0.151	0.002	-0.091	0.563	0.602	0.303	0.238	0.299	0.191	0.15	0.22	0.388	0.144	0.114	0.434	0.196	0.302	0.413	1.0
Jaccard distance over extended gene set	-0.041	0.648	0.817	0.887	0.772	0.835	0.196	0.285	0.212	0.112	0.377	0.324	0.639	0.714	0.784	0.629	0.684	0.393	0.414	0.462	0.621	0.327	0.258	0.859	0.333	0.689	1.0	0.413
Dijkstra BMA PPI	-0.036	0.562	0.772	0.777	0.746	0.759	0.153	0.282	0.162	-0.012	0.354	0.243	0.624	0.697	0.643	0.49	0.575	0.362	0.417	0.466	0.53	0.215	0.226	0.727	0.278	1.0	0.689	0.302
WM distance over summary W2V	-0.031	0.301	0.302	0.335	0.28	0.329	0.101	0.105	0.131	0.048	0.129	0.167	0.196	0.251	0.348	0.33	0.491	0.255	0.253	0.393	0.347	0.221	0.853	0.379	1.0	0.278	0.333	0.196
WM distance over gene symbols W2V	-0.042	0.763	0.908	0.939	0.837	0.886	0.179	0.264	0.201	0.112	0.349	0.306	0.725	0.766	0.854	0.665	0.771	0.387	0.447	0.524	0.817	0.425	0.289	1.0	0.379	0.727	0.859	0.434
Cosine distance over over summary W2V	-0.002	0.203	0.206	0.229	0.185	0.213	0.118	0.107	0.123	0.042	0.102	0.127	0.084	0.128	0.295	0.37	0.47	0.298	0.319	0.461	0.311	0.299	1.0	0.289	0.853	0.226	0.258	0.114
Cosine distance over over NCBI summary W2V	-0.045	0.189	0.252	0.292	0.172	0.22	-0.145	-0.139	-0.129	-0.107	-0.127	-0.129	0.22	0.262	0.394	0.566	0.461	0.257	0.609	0.563	0.574	1.0	0.299	0.425	0.221	0.215	0.327	0.144
Cosine distance over gene symbols W2V	-0.046	0.565	0.63	0.634	0.494	0.541	-0.199	-0.17	-0.161	-0.152	-0.123	-0.122	0.603	0.619	0.757	0.691	0.755	0.352	0.555	0.672	1.0	0.574	0.311	0.817	0.347	0.53	0.621	0.388
Cosine distance GO MF description W2V	-0.037	0.357	0.403	0.418	0.305	0.327	-0.144	-0.133	-0.151	-0.138	-0.104	-0.141	0.327	0.385	0.62	0.716	0.837	0.381	0.672	1.0	0.672	0.563	0.461	0.524	0.393	0.466	0.462	0.22
Cosine distance GO CC description W2V	-0.041	0.207	0.341	0.36	0.249	0.269	-0.076	-0.038	-0.068	-0.1	-0.012	-0.048	0.204	0.3	0.517	0.872	0.631	0.231	1.0	0.672	0.555	0.609	0.319	0.447	0.253	0.417	0.414	0.15
Cosine distance GO BP description W2V	-0.029	0.396	0.433	0.418	0.391	0.369	-0.052	0.038	-0.076	-0.115	0.097	-0.031	0.436	0.398	0.491	0.383	0.37	1.0	0.231	0.381	0.352	0.257	0.298	0.387	0.255	0.362	0.393	0.191
GO-distance (go_type=MF, measure=Wang, combine=BMA)	-0.044	0.522	0.629	0.66	0.536	0.585	0.057	0.115	0.089	-0.036	0.16	0.14	0.443	0.531	0.833	0.792	1.0	0.37	0.631	0.837	0.755	0.461	0.47	0.771	0.491	0.575	0.684	0.299
GO-distance (go_type=CC, measure=Wang, combine=BMA)	-0.048	0.4	0.541	0.568	0.439	0.466	0.036	0.091	0.047	-0.023	0.131	0.093	0.345	0.425	0.76	1.0	0.792	0.383	0.872	0.716	0.691	0.566	0.37	0.665	0.33	0.49	0.629	0.238
GO-distance (go_type=BP, measure=Wang, combine=BMA)	-0.036	0.682	0.802	0.794	0.705	0.713	0.1	0.183	0.115	0.007	0.24	0.184	0.634	0.65	1.0	0.76	0.833	0.491	0.517	0.62	0.757	0.394	0.295	0.854	0.348	0.643	0.784	0.303
Overlap distance over genes	-0.031	0.67	0.792	0.813	0.765	0.813	-0.133	0.029	-0.12	-0.135	0.156	0.022	0.924	1.0	0.65	0.425	0.531	0.398	0.3	0.385	0.619	0.262	0.128	0.766	0.251	0.697	0.714	0.602
Overlap distance over gene traits	-0.032	0.742	0.799	0.762	0.785	0.759	-0.115	0.036	-0.115	-0.108	0.154	0.01	1.0	0.924	0.634	0.345	0.443	0.436	0.204	0.327	0.603	0.22	0.084	0.725	0.196	0.624	0.639	0.563
Minkowski distance (p=2) over genes	0.032	0.296	0.359	0.408	0.507	0.52	0.913	0.929	0.967	0.643	0.908	1.0	0.01	0.022	0.184	0.093	0.14	-0.031	-0.048	-0.141	-0.122	-0.129	0.127	0.306	0.167	0.243	0.324	-0.091
Minkowski distance (p=2) over gene traits	0.042	0.37	0.486	0.489	0.622	0.579	0.859	0.968	0.838	0.517	1.0	0.908	0.154	0.156	0.24	0.131	0.16	0.097	-0.012	-0.104	-0.123	-0.127	0.102	0.349	0.129	0.354	0.377	0.002
Minkowski distance (p=2) over gene trait frequency	0.046	0.35	0.146	0.162	0.242	0.238	0.795	0.555	0.66	1.0	0.517	0.643	-0.108	-0.135	0.007	-0.023	-0.036	-0.115	-0.1	-0.138	-0.152	-0.107	0.042	0.112	0.048	-0.012	0.112	-0.151
Minkowski distance (p=1) over genes	0.038	0.2	0.242	0.278	0.395	0.397	0.944	0.915	1.0	0.66	0.838	0.967	-0.115	-0.12	0.115	0.047	0.089	-0.076	-0.068	-0.151	-0.161	-0.129	0.123	0.201	0.131	0.162	0.212	-0.188
Minkowski distance (p=1) over gene traits	0.046	0.279	0.381	0.384	0.533	0.488	0.926	1.0	0.915	0.555	0.968	0.929	0.036	0.029	0.183	0.091	0.115	0.038	-0.038	-0.133	-0.17	-0.139	0.107	0.264	0.105	0.282	0.285	-0.096
Minkowski distance (p=1) over gene trait frequency	0.052	0.271	0.258	0.268	0.405	0.37	1.0	0.926	0.944	0.795	0.859	0.913	-0.115	-0.133	0.1	0.036	0.057	-0.052	-0.076	-0.144	-0.199	-0.145	0.118	0.179	0.101	0.153	0.196	-0.194
Kappa distance over genes	-0.015	0.77	0.922	0.967	0.954	1.0	0.37	0.488	0.397	0.238	0.579	0.52	0.759	0.813	0.713	0.466	0.585	0.369	0.269	0.327	0.541	0.22	0.213	0.886	0.329	0.759	0.835	0.427
Kappa distance over gene traits	0.005	0.808	0.955	0.923	1.0	0.954	0.405	0.533	0.395	0.242	0.622	0.507	0.785	0.765	0.705	0.439	0.536	0.391	0.249	0.305	0.494	0.172	0.185	0.837	0.28	0.746	0.772	0.383
Jaccard distance over genes	-0.032	0.786	0.956	1.0	0.923	0.967	0.268	0.384	0.278	0.162	0.489	0.408	0.762	0.813	0.794	0.568	0.66	0.418	0.36	0.418	0.634	0.292	0.229	0.939	0.335	0.777	0.887	0.455
Jaccard distance over gene traits	-0.014	0.839	1.0	0.956	0.955	0.922	0.258	0.381	0.242	0.146	0.486	0.359	0.799	0.792	0.802	0.541	0.629	0.433	0.341	0.403	0.63	0.252	0.206	0.908	0.302	0.772	0.817	0.423
Cosine distance over gene trait frequency	-0.003	1.0	0.839	0.786	0.808	0.77	0.271	0.279	0.2	0.35	0.37	0.296	0.742	0.67	0.682	0.4	0.522	0.396	0.207	0.357	0.565	0.189	0.203	0.763	0.301	0.562	0.648	0.323
Random (uniform, (0,1))	1.0	-0.003	-0.014	-0.032	0.005	-0.015	0.052	0.046	0.038	0.046	0.042	0.032	-0.032	-0.031	-0.036	-0.048	-0.044	-0.029	-0.041	-0.037	-0.046	-0.045	-0.002	-0.042	-0.031	-0.036	-0.041	0.018