

		Pairwise path length in reference tree																								
		Jaccard distance over extended gene set																								
		WM distance over gene symbols 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)																								
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		Overlap distance over genes																								
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		Random (uniform, (0,1))																								
	Pairwise path length in reference tree	0.025	0.398	0.296	0.383	0.182	0.306	-0.283	-0.256	-0.26	-0.281	-0.246	-0.256	0.458	0.495	0.209	0.134	0.161	0.3	0.093	0.274	0.268	0.276	0.381	0.294	1.0
	Jaccard distance over extended gene set	-0.032	0.66	0.813	0.733	0.324	0.171	-0.244	-0.225	-0.303	-0.226	-0.272	-0.363	0.351	0.373	0.819	0.667	0.672	0.528	0.458	0.459	0.546	0.545	0.817	1.0	0.294
	WM distance over gene symbols W2V	-0.058	0.664	0.826	0.761	0.433	0.322	-0.258	-0.233	-0.29	-0.243	-0.276	-0.347	0.427	0.445	0.788	0.679	0.684	0.635	0.565	0.541	0.756	0.706	1.0	0.817	0.381
	Cosine distance over over NCBI summary W2V	-0.006	0.481	0.556	0.332	0.266	0.018	-0.255	-0.282	-0.296	-0.242	-0.341	-0.367	0.348	0.269	0.644	0.574	0.566	0.812	0.564	0.549	0.769	1.0	0.706	0.545	0.276
	Cosine distance over gene symbols W2V	-0.02	0.642	0.606	0.349	0.329	0.016	-0.234	-0.251	-0.279	-0.217	-0.303	-0.345	0.368	0.267	0.658	0.614	0.666	0.73	0.515	0.63	1.0	0.769	0.756	0.546	0.268
	Cosine distance GO MF description W2V	-0.003	0.468	0.404	0.282	0.184	0.04	-0.13	-0.161	-0.152	-0.117	-0.224	-0.225	0.247	0.185	0.539	0.45	0.658	0.598	0.393	1.0	0.63	0.549	0.541	0.459	0.274
	Cosine distance GO CC description W2V	-0.066	0.321	0.528	0.249	0.344	-0.03	0.121	0.112	0.053	0.136	0.053	-0.007	-0.05	-0.071	0.624	0.715	0.544	0.524	1.0	0.393	0.515	0.564	0.565	0.458	0.093
	Cosine distance GO BP description W2V	-0.019	0.477	0.564	0.334	0.316	0.039	-0.156	-0.165	-0.194	-0.143	-0.211	-0.249	0.231	0.213	0.708	0.628	0.666	1.0	0.524	0.598	0.73	0.812	0.635	0.528	0.3
	GO-distance (go_type=MF, measure=Wang, combine=BMA)	-0.002	0.471	0.694	0.466	0.439	0.089	0.119	0.164	0.086	0.15	0.136	0.063	-0.07	0.06	0.89	0.875	1.0	0.666	0.544	0.658	0.666	0.566	0.684	0.672	0.161
	GO-distance (go_type=CC, measure=Wang, combine=BMA)	0.002	0.471	0.712	0.426	0.459	0.038	0.112	0.164	0.063	0.144	0.149	0.049	-0.104	0.018	0.89	1.0	0.875	0.628	0.715	0.45	0.614	0.574	0.679	0.667	0.134
	GO-distance (go_type=BP, measure=Wang, combine=BMA)	-0.022	0.587	0.803	0.548	0.463	0.097	-0.0	0.027	-0.052	0.031	-0.015	-0.096	0.061	0.152	1.0	0.89	0.89	0.708	0.624	0.539	0.658	0.644	0.788	0.819	0.209
	Overlap distance over genes	0.004	0.466	0.275	0.551	-0.008	0.425	-0.736	-0.655	-0.671	-0.734	-0.606	-0.639	0.755	1.0	0.152	0.018	0.06	0.213	-0.071	0.185	0.267	0.269	0.445	0.373	0.495
	Overlap distance over gene traits	-0.017	0.582	0.311	0.407	0.033	0.235	-0.742	-0.767	-0.726	-0.748	-0.793	-0.781	1.0	0.755	0.061	-0.104	-0.07	0.231	-0.05	0.247	0.368	0.348	0.427	0.351	0.458
	Minkowski distance (p=2) over genes	-0.021	-0.502	-0.161	-0.19	0.325	0.142	0.928	0.969	0.971	0.93	0.97	1.0	-0.781	-0.639	-0.096	0.049	0.063	-0.249	-0.007	-0.225	-0.345	-0.367	-0.347	-0.363	-0.256
	Minkowski distance (p=2) over gene traits	-0.019	-0.428	-0.059	-0.112	0.366	0.138	0.907	0.979	0.919	0.902	1.0	0.97	-0.793	-0.606	-0.015	0.149	0.136	-0.211	0.053	-0.224	-0.303	-0.341	-0.276	-0.272	-0.246
	Minkowski distance (p=2) over gene trait frequency	-0.019	-0.348	-0.034	-0.192	0.371	0.014	0.994	0.959	0.971	1.0	0.902	0.93	-0.748	-0.734	0.031	0.144	0.15	-0.143	0.136	-0.117	-0.217	-0.242	-0.243	-0.226	-0.281
	Minkowski distance (p=1) over genes	-0.034	-0.431	-0.103	-0.173	0.371	0.135	0.97	0.964	1.0	0.971	0.919	0.971	-0.726	-0.671	-0.052	0.063	0.086	-0.194	0.053	-0.152	-0.279	-0.296	-0.29	-0.303	-0.26
	Minkowski distance (p=1) over gene traits	-0.029	-0.384	-0.012	-0.105	0.396	0.117	0.966	1.0	0.964	0.959	0.979	0.969	-0.767	-0.655	0.027	0.164	0.164	-0.165	0.112	-0.161	-0.251	-0.282	-0.233	-0.225	-0.256
	Minkowski distance (p=1) over gene trait frequency	-0.02	-0.369	-0.046	-0.192	0.373	0.035	1.0	0.966	0.97	0.994	0.907	0.928	-0.742	-0.736	-0.0	0.112	0.119	-0.156	0.121	-0.13	-0.234	-0.255	-0.258	-0.244	-0.283
	Kappa distance over genes	-0.1	0.137	0.285	0.652	0.564	1.0	0.035	0.117	0.135	0.014	0.138	0.142	0.235	0.425	0.097	0.038	0.089	0.039	-0.03	0.04	0.016	0.018	0.322	0.171	0.306
	Kappa distance over gene traits	-0.064	0.323	0.679	0.428	1.0	0.564	0.373	0.396	0.371	0.371	0.366	0.325	0.033	-0.008	0.463	0.459	0.439	0.316	0.344	0.184	0.329	0.266	0.433	0.324	0.182
	Jaccard distance over genes	-0.083	0.511	0.751	1.0	0.428	0.652	-0.192	-0.105	-0.173	-0.192	-0.112	-0.19	0.407	0.551	0.548	0.426	0.466	0.334	0.249	0.282	0.349	0.332	0.761	0.733	0.383
	Jaccard distance over gene traits	-0.054	0.658	1.0	0.751	0.679	0.285	-0.046	-0.012	-0.103	-0.034	-0.059	-0.161	0.311	0.275	0.803	0.712	0.694	0.564	0.528	0.404	0.606	0.556	0.826	0.813	0.296
	Cosine distance over gene trait frequency	-0.029	1.0	0.658	0.511	0.323	0.137	-0.369	-0.384	-0.431	-0.348	-0.428	-0.502	0.582	0.466	0.587	0.471	0.471	0.477	0.321	0.468	0.642	0.481	0.664	0.66	0.398
	Random (uniform, (0,1))	1.0	-0.029	-0.054	-0.083	-0.064	-0.1	-0.02	-0.029	-0.034	-0.019	-0.019	-0.021	-0.017	0.004	-0.022	0.002	-0.002	-0.019	-0.066	-0.003	-0.02	-0.006	-0.058	-0.032	0.025