

	R-HSA-8982491	R-HSA-1474290	R-HSA-373755	R-HSA-422475	immune_only
Pairwise path length in reference tree	1.0	1.0	1.0	1.0	1.0
Jaccard distance over extended gene set	0.244	0.195	0.3	0.178	0.215
Dijkstra BMA PPI	0.226	0.084	0.332	0.216	0.143
WM distance over summary W2V	0.182	0.362	0.162	0.203	NaN
WM distance over gene symbols W2V	0.266	0.349	0.367	0.21	0.335
Cosine distance over over summary W2V	0.174	0.351	0.102	0.06	NaN
Cosine distance over over NCBI summary W2V	0.161	0.251	0.318	0.228	0.267
Cosine distance over gene symbols W2V	0.39	0.277	0.382	0.196	0.278
Cosine distance GO MF description W2V	0.263	0.175	0.255	0.111	0.28
Cosine distance GO CC description W2V	0.135	0.192	0.239	0.114	0.079
Cosine distance GO BP description W2V	0.105	0.174	0.339	0.183	0.291
GO-distance (go_type=MF, measure=Wang, combine=BMA)	0.438	0.122	0.25	0.136	0.14
GO-distance (go_type=CC, measure=Wang, combine=BMA)	0.078	0.124	0.234	0.143	0.118
GO-distance (go_type=BP, measure=Wang, combine=BMA)	0.144	0.217	0.222	0.144	0.172
Overlap distance over genes	0.428	0.253	0.554	0.408	0.614
Overlap distance over gene traits	0.583	0.304	0.501	0.259	0.449
Minkowski distance (p=2) over genes	-0.09	0.012	-0.042	-0.09	-0.201
Minkowski distance (p=2) over gene traits	-0.019	0.023	-0.033	-0.084	-0.192
Minkowski distance (p=2) over gene trait frequency	-0.08	-0.011	-0.106	-0.038	-0.241
Minkowski distance (p=1) over genes	-0.09	0.012	-0.042	-0.09	-0.201
Minkowski distance (p=1) over gene traits	-0.019	0.023	-0.033	-0.084	-0.192
Minkowski distance (p=1) over gene trait frequency	-0.054	-0.001	-0.08	-0.074	-0.228
Kappa distance over genes	0.27	0.337	0.442	0.201	0.458
Kappa distance over gene traits	0.418	0.317	0.371	0.133	0.099
Jaccard distance over genes	0.316	0.319	0.503	0.4	0.604
Jaccard distance over gene traits	0.468	0.296	0.359	0.162	0.213
Cosine distance over gene trait frequency	0.555	0.434	0.264	0.209	0.388
Random (uniform, (0,1))	0.04	-0.008	0.019	-0.004	0.022