

Pairwise path length in reference tree Jaccard distance over extended gene set 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))

0.018 -0.029 -0.052 0.038 -0.076-0.115 0.097 -0.031 0.436 0.785 0.759 -0.115 0.036 -0.115-0.108 0.154 0.01