

| | Pairwise path length in reference tree | Jaccard distance over extended gene set | Dijkstra BMA PPI | WM distance over over gene symbols W2V | Jaccard distance over over gene symbols W2V | Pairwise path length in reference tree | 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=1) over genes | Minkowski distance (p=1) over gene traits | 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 | 0.025 | 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 | 0.206 | 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 | 0.441 | 1.0 | 0.294 |
| Dijkstra BMA PPI | -0.031 | 0.425 | 0.382 | 0.329 | 0.17 | 0.158 | -0.615 | -0.665 | -0.632 | -0.617 | -0.7 | -0.703 | 0.727 | 0.501 | 0.153 | -0.125 | -0.083 | 0.307 | 0.225 | 0.292 | 0.325 | 0.433 | 0.478 | 1.0 | 0.441 | 0.206 |
| 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 | 0.478 | 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 | 0.433 | 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 | 0.325 | 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 | 0.292 | 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 | 0.225 | 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 | 0.307 | 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 | -0.083 | 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 | -0.125 | 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 | 0.153 | 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 | 0.501 | 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 | 0.727 | 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 | -0.703 | -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 | -0.7 | -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 | -0.617 | -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 | -0.632 | -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 | -0.665 | -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 | -0.615 | -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 | 0.158 | 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 | 0.17 | 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 | 0.329 | 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 | 0.382 | 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 | 0.425 | 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 | -0.031 | -0.032 | 0.025 |