Algorithm for measuring term similarities across ontologies.

**ALGORITHM:** Algorithm for measuring term similarities across ontologies.

**Input:** term set $T_1 = \{t_{1,1}, t_{1,2}, \ldots, t_{1,n}\}$, ‘IS_A’ relationships of $T_1$, term set $T_2 = \{t_{2,1}, t_{2,2}, \ldots, t_{2,m}\}$, ‘IS_A’ relationships of $T_2$, gene set $G = \{g_1, g_2, \ldots, g_v\}$, term-gene pairs set $TG = \{(t_1, g_1), (t_1, g_2), \ldots, (t_m, g_k)\}$, weights of gene-gene pair $\{w_{g1,2}, w_{g1,3}, \ldots, w_{gp}\}$.

**Output:** The similarity of all the term pairs.

1. For each term-gene pair $(t_i, g_j)$ in $TG$
2. Calculate weights of each pair $(w(t_i, g_j))$ using equation 1.
3. For each term-gene pair $(t_i, g_j)$ in $TG$
4. Normalize weights of each pair $(nw(t_i, g_j))$ using equation 2.
5. For each term $t_i$ in $T_1$ or $T_2$
6. Calculate weights of each pair $(w(t_i))$ using equation 3.
7. For each term $t_i$ in $T_1$ or $T_2$
8. Normalize weights of each pair $(nw(t_i))$ using equation 4.
9. For each gene-gene pair $(g_i, g_j)$ in $T_1$ or $T_2$
10. Normalize weights of each pair $(w(g_i, g_j))$ using equation 5.
11. For each term $t_i$ in $T_1$ or $T_2$
12. Calculate the vector of each term ($WV_t$) using ITM probe.
13. For each $t_i$ in $T_1$
14. For each $t_j$ in $T_2$
15. Calculate the similarity of $t_i$ and $t_j$ ($Sim(t_i, t_j)$) using equation 7&8
16. add $Sim(t_i, t_j)$ to $Sim(T_1, T_2)$.
17. return $Sim(T_1, T_2)$. 