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LION(D, PPI, LP)
input:
        D: set of known disease proteins
        PPI: protein-protein interaction network
        LPI: lncRNA-protein interaction network
output:
        L: the set of ranked candidate lncRNAs

PPI_sub ← subgraph of PPI, all edges involving a protein in D
LPI_sub ← subgraph of LPI, all edges involving a protein in N

S ← disease subnetwork, the union of PPI_sub and LPI_sub
N ← number of nodes of S

$p^0$ ← vector with size N, initialized to all zeros                // probability vector for step 0
for each protein i in D do
        $p_i^0$ ← 1 / (number of elements in D)
end for
$p^k \leftarrow p^0$                                               // probability vector for step k
$r \leftarrow 0.5$                                                 // restart probability
W ← adjacency matrix of S, column normalized
$p^{k+1} \leftarrow (1 - r) * (W \bullet p^k) + r * p^0$           // probability vector for step k+1
while $\| p^{k+1} - p^k \|_{L1} > 10^{-6}$ do                      // main iteration
        $p^k \leftarrow p^{k+1}$
        $p^{k+1} \leftarrow (1 - r) * (W \bullet p^k) + r * p^0$
end while
L ← subset of $p^{k+1}$ representing all lncRNA nodes in S
return L
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