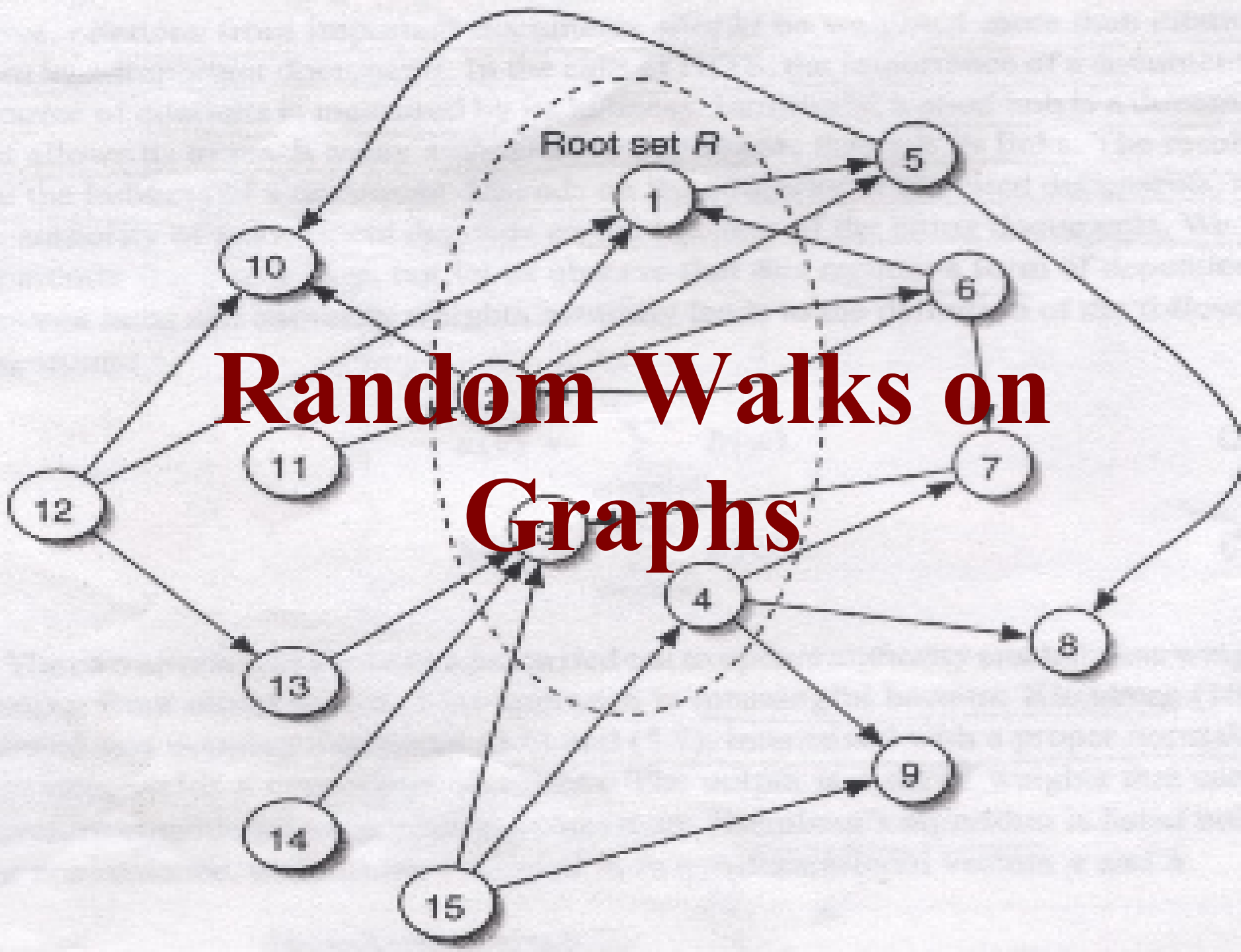


Random Walks on Graphs



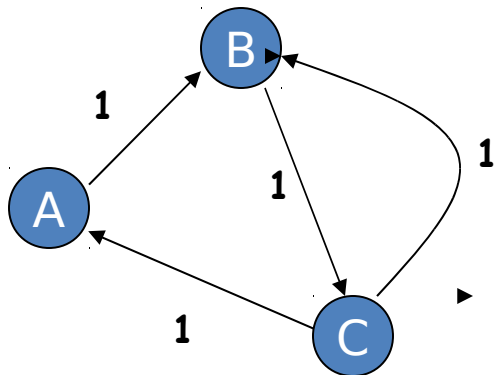
What is a Random Walk

- Given a graph and a starting point (node), we select a neighbor of it at random, and move to this neighbor;
- Then we select a neighbor of this node and move to it, and so on;
- The (random) sequence of nodes selected this way is a **random walk** on the graph

An example

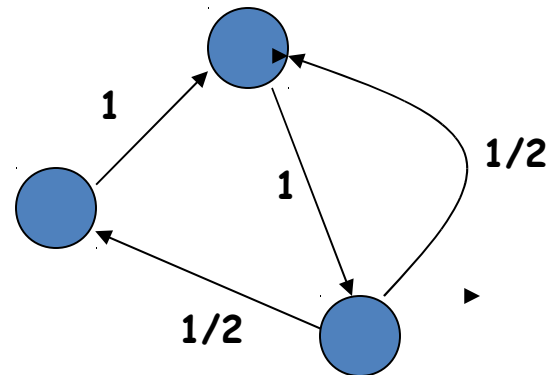
0	1	0
0	0	1
1	1	0

Adjacency matrix W

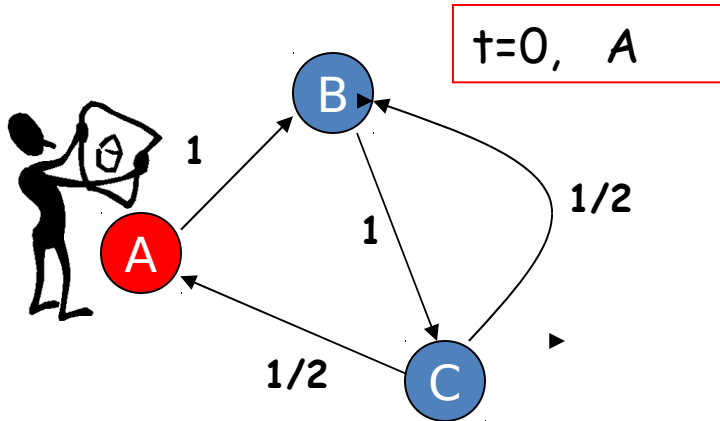


0	1	0
0	0	1
1/2	1/2	0

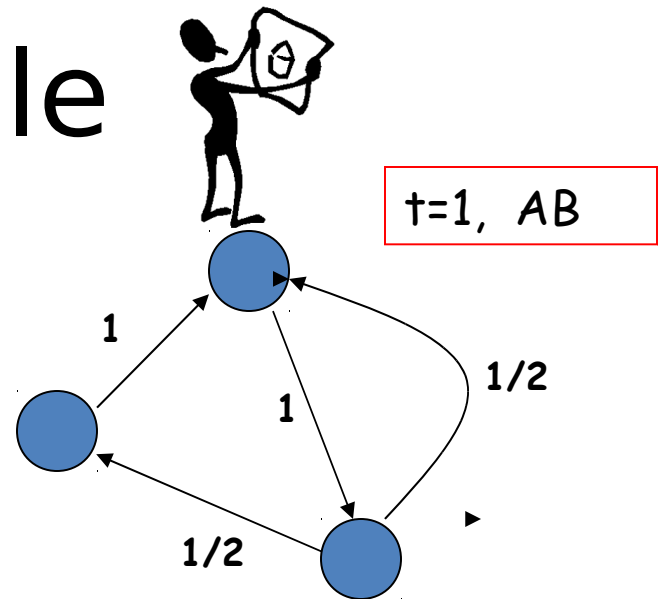
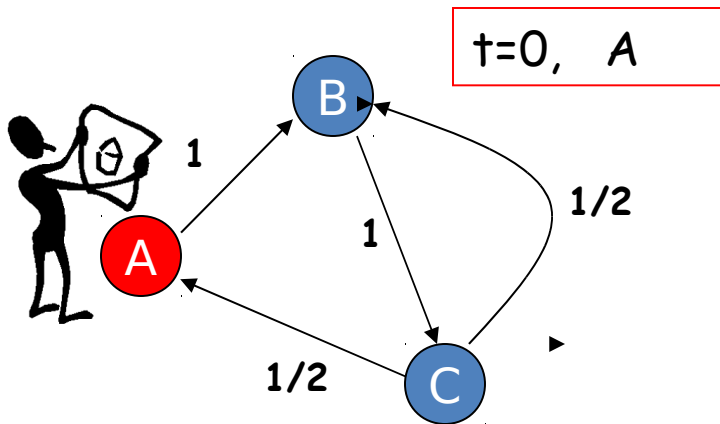
Transition matrix Q



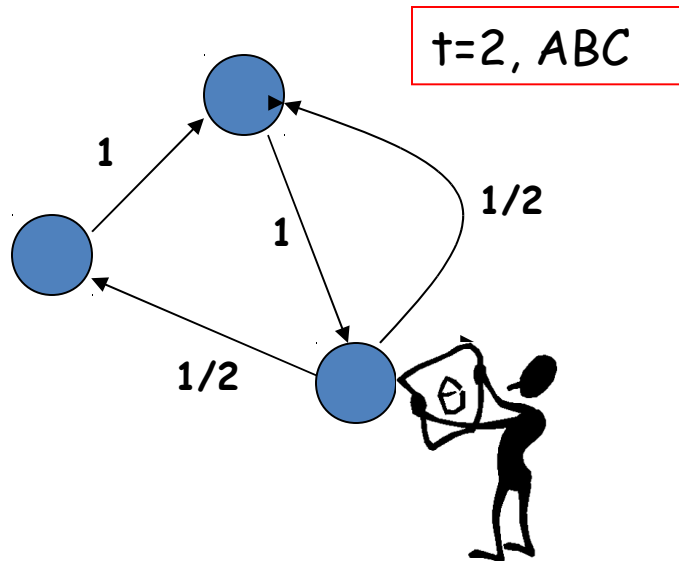
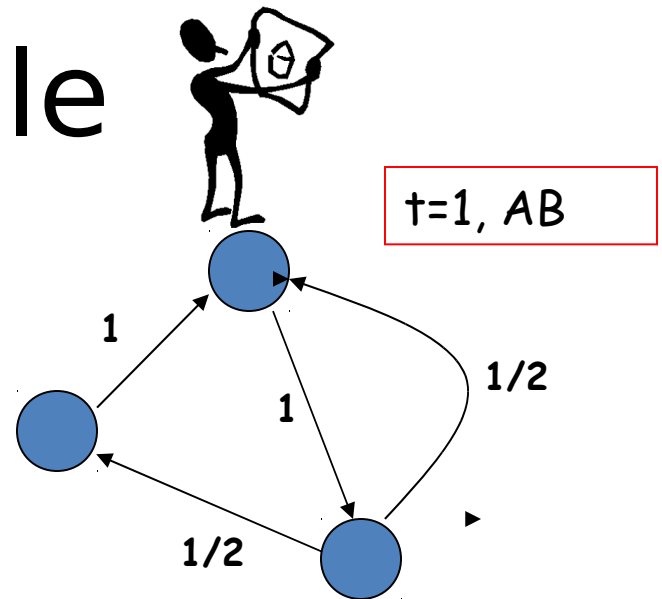
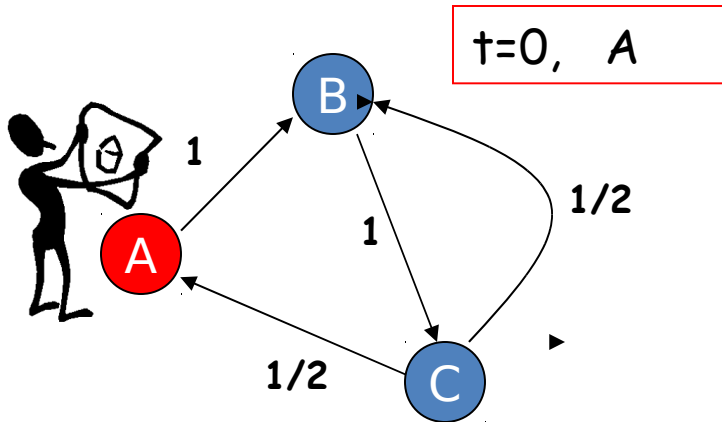
An example



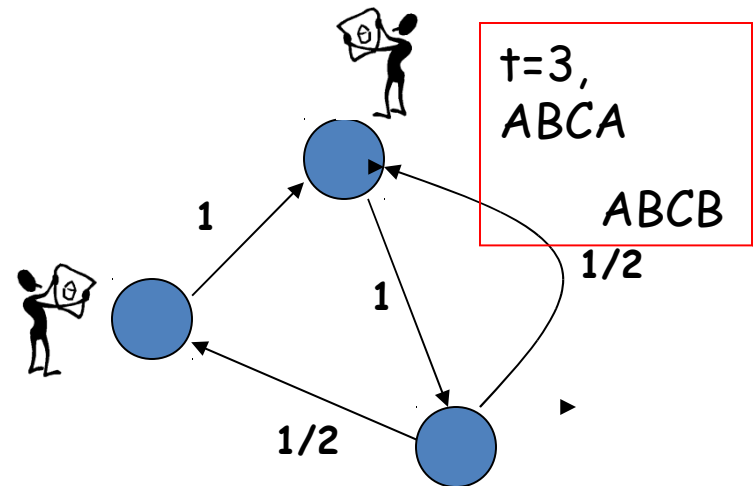
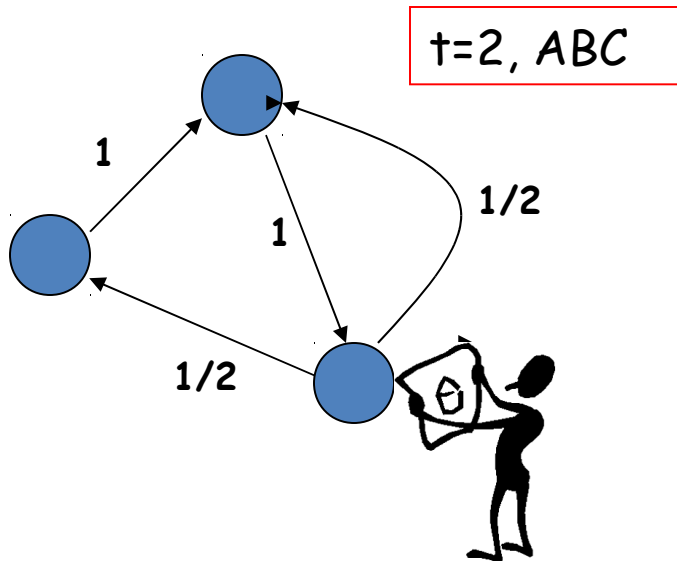
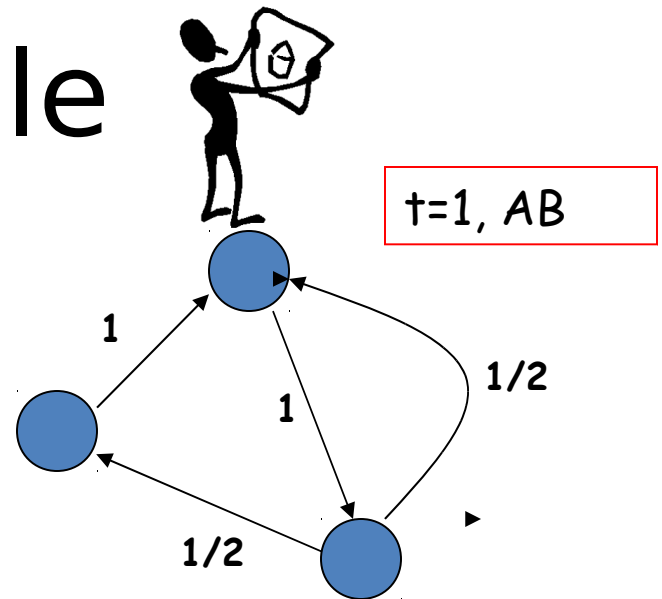
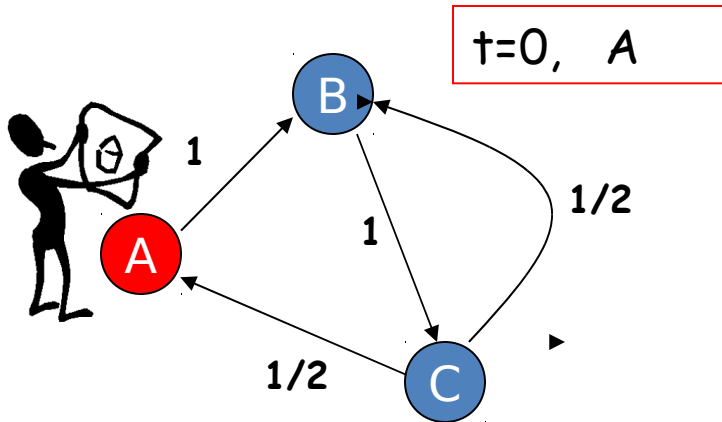
An example



An example



An example



Random Walk algorithm

Input:

- the adjacency matrix \mathbf{W} of a graph $G=\langle V,E\rangle$
- A subset of nodes V_C having property C

- Initialization of nodes:

if $v \in V_C$ then $p^0_v = 1 / |V_C|$ else $p^0_v = 0$

- Set transition matrix: $\mathbf{Q} = \mathbf{D}^{-1}\mathbf{W}$

where \mathbf{D} is a diagonal matrix with $d_{ii} = \sum_j w_{ij}$

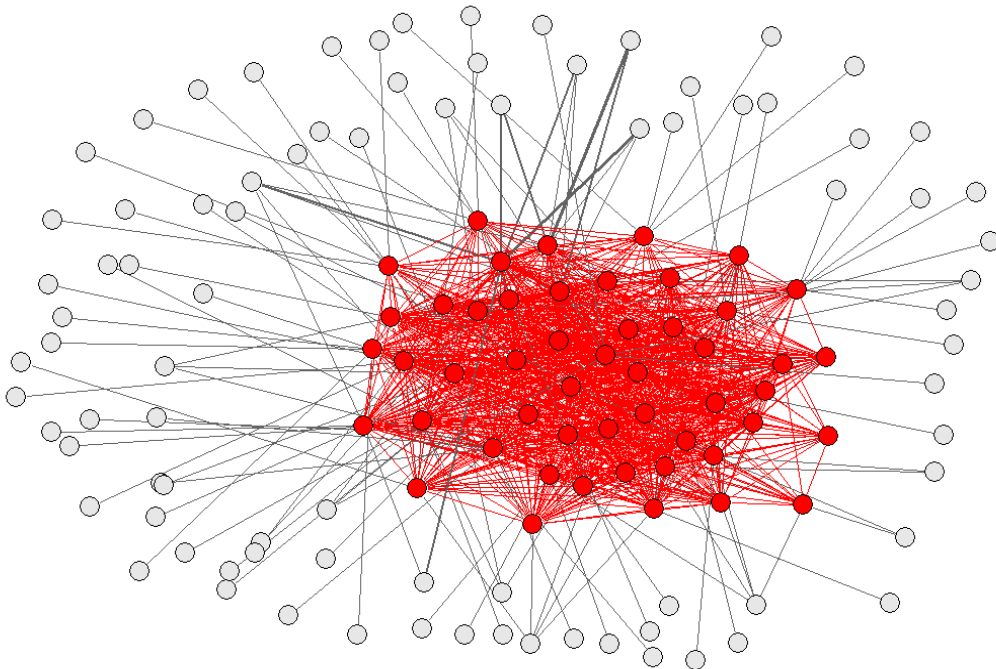
- Iteratively update until convergence or until $t=k$

$$\mathbf{p}^t = \mathbf{Q}^T \mathbf{p}^{t-1}$$

Output: \mathbf{p}^t

Random walking algorithm to rank genes w.r.t to a functional class C

- Having a set V of genes, a subset V_C of genes are “a priori” known to belong to a given functional class C (i.e. a Gene Ontology class)
- Can we rank the other genes in the set $V \setminus V_C$ w.r.t their likelihood to belong to V_C ?



Random walk
algorithm