



Notice that the algorithm cannot reach all desired values of clustering coefficients, because the network has to be scale-free. For example, a clustering coefficient of 1 implies that every couple of nodes are linked together ; such a network is obviously not scale-free.

## 2.1 Details about the algorithm

This algorithm is partially based on the algorithm by Di Camillo, Barbara, Gianna Toffolo, and Claudio Cobelli. "A gene network simulator to assess reverse engineering algorithms." Annals of the New York Academy of Sciences.

Let us call  $V$  the set of nodes to be connected in the graph  $G$  at the current iteration  $t$  and  $H$  the set of nodes to be connected at iteration  $t + 1$ .  $V$  is initialized as  $V = \{1, \dots, N\}$ , that is, with all the  $N$  nodes in  $G$ , whereas  $H$  is initialized as the empty set  $H$ . Nodes are then linked to each other through an iterative procedure, which consists of three main steps,