CAlgogen CGraphe size: integer genome: list::boolean mutationRate: double nbNodes: integer crossingRate: double init () generationNb: integer double fit2distri() igraph: list:: Cgraph double clustering() fgraph: list:: CGraph double smallWorld() ___init__() double fitness() list::double fitness() void genome2adj() void mutation() void graphPrint() void crossina() void genomodif(CGraphe) void iPopCreation() double robustness() void fPopChamt() boolean disassortativity() list:: CGraph best Graph ()