Spread of Tuberculosis

1. Is it possible that all cases stemmed from a single 'index' patient?  More formally, is there a node, n, such that there is a path from n to every other node in the graph with an active TB label?

To answer this question, we use a Breadth First Search. The input file will consist of the names of the people and the connections. The process is as follows:

**procedure** BFS(*G*,*v*) **is**

2 let *Q* be a queue

3 *Q*.push(*v*)

4 label *v* as discovered

5 **while** *Q* is not empty

6 *v* ← Q.pop()

7 **for all** edges from *v* to *w* **in** *G*.adjacentEdges(*v*) **do**

8 **if** *w* is not labeled as discovered

9 *Q*.push(*w*)

10 label *w* as discovered

From the list of all infected patients from the input file, each patient is paired with each other and BFS is applied to find whether there is a path from each of the patients. If there are paths for all pairs of patients, then the answer to the question is Yes, it is possible that all cases stemmed from a single index patient.

1. In order to best limit the continued spread, which uninfected people should be vaccinated?  This can be formalised as solving a min cut problem.  Let N(A) be the set of active TB nodes and N(O) be the set of all the other nodes.  Each edge in the minimum cut between these two sets will contain one person with known active TB and one person without.  The people without known active TB are candidates for vaccination.

To answer this question, we use a MinCut algorithm. This returns the lowest cost solution for all edges to be cut. The graph is a directed graph.

MinCutPhase(*G*, *w*):

*a* ← arbitrary vertex of *G*

*A* ← (*a*)

While *A* ≠ *V*

*v* ← vertex most tightly connected to *A*

*A* ← *A* U (*v*)

*s* and *t* are the last two vertices (in order) added to *A*

Return cut(*A-t*,*t*)