Assignment 2

Social Network Analysis

Changelog

All important changes to the assignment specification and files will be listed here.

- `[06/04 18:32]` The following example is modified, {0} is added at rows 104 and 107 : Part 3 Simple Example (MS Excel file)
- `[01/04 14:00]` Assignment released

Aims

- To implement graph-based data analysis functions to mine a given social network
- To give you further practice with C and data structures (Graph ADT)

Admin

Marks contributes 19% towards your final mark (see Assessment section for more details)

Submit see the Submission section

Deadline 8pm on Friday of Week 10

Late penalty 1% off the maximum mark for each hour late. For example if an assignment worth 80% was submitted 15 hours late, the late penalty would have no effect. If the same assignment was submitted 24 hours late it would be awarded 76%, the maximum mark it can achieve at that time.

Introduction

The main focus of this assignment is to implement graph-based data analysis functions that could be used to identify influencers, followers and communities in a given social network.

Setting Up

Change into the directory you created for the assignment and run the following command:

```
$ unzip /web/cs2521/22T1/ass/ass2/downloads/files.zip
```

If you're working at home, download `files.zip` by clicking on the above link and then unzip the downloaded file.

This bundle of files includes the files you need to implement, as well as a few completed ADTs that you may use, some testing programs/scripts and sample graphs.

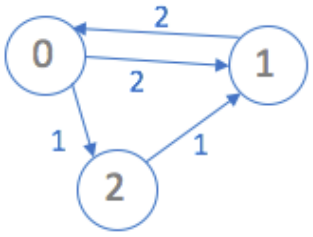
We have provided complete implementations of the Graph and Priority Queue ADTs. You may use these ADTs for any parts of the assignment as long as you do not modify them.

Part 1 - Dijkstra's Algorithm

Part 1 - Dijkstra's Algorithm

In order to discover influencers, we need to repeatedly find shortest paths between pairs of nodes. Your task is to implement a variant Dijkstra's algorithm to discover the shortest paths from a given source node to all other nodes in the graph. The algorithm has **one important additional feature**: if there are multiple shortest paths from a source node to another node, it keeps track of all of them by allowing each node to have multiple predecessors. In the code, this is achieved by each node having a linked list of predecessors (see `Dijkstra.h`). Each predecessor list must be in ascending order.

In the following example, while discovering shortest paths from node 0, we find that there are two possible shortest paths from node 0 to node 1 (`0 -> 1` and `0 -> 2 -> 1`), so node 1 has two possible predecessors: node 0 and node 2, as shown below.




```
Source node: 0
  Distances
    0: 0
    1: 2
    2: 1
  Predecessors
    0: NULL
    1: [0] -> [2] -> NULL
    2: [0] -> NULL

Source node: 1
  Distances
    0: 2
    1: 0
    2: 3
  Predecessors
    0: [1] -> NULL
    1: NULL
    2: [0] -> NULL

Source node: 2
  Distances
    0: 3
    1: 1
    2: 0
  Predecessors
    0: [1] -> NULL
    1: [2] -> NULL
    2: NULL
```

What you need to do:

Complete the file `Dijkstra.c` that implements all the functions declared in `Dijkstra.h`.

Part 2 - Centrality Measures for Social Network Analysis

Centrality measures play a very important role in analysing a social network. For example, nodes with higher betweenness often correspond to influencers in a social network. Your task is to implement two well-known centrality measures for a given directed weighted graph.

Closeness Centrality

The closeness centrality of a node x is calculated as the reciprocal of the sum of the lengths of the shortest paths between node x and all other nodes y ($y \neq x$) in the graph. Generally closeness is defined as below:

$$C(x) = \frac{1}{\sum_y d(y,x)}$$

where $d(y,x)$ is the shortest distance between vertices x and y.

However, considering we may have more than one connected components, **for this assignment** you need to use the **Wasserman and Faust formula** to calculate the closeness of a node in a directed graph as described below:

$$C_{WF}(u) = \frac{n-1}{N-1} * \frac{n-1}{\sum_{all\ v\ reachable\ from\ u} d(u,v)}$$

where $d(u, v)$ is the shortest-path distance in a directed graph from vertex u to v, n is the number of nodes reachable from u (which includes u itself), and N denotes the number of nodes in the graph.

The Wasserman and Faust formula is useful for graphs with more than one connected components. However, if a node is not connected to any other node (isolated), its closeness value C_{WF} should be 0.

Betweenness Centrality

The betweenness centrality of a node v is given by the expression:

$$g(v) = \sum_{s \neq v \neq t \neq s, \text{ and } t \text{ is reachable from } s} \frac{\sigma_{st}(v)}{\sigma_{st}}$$

where σ_{st} is the total number of shortest paths from node s to node t and $\sigma_{st}(v)$ is the number of those paths that pass through v.

What you need to do:

Complete the file `CentralityMeasures.c` that implements all the functions declared in `CentralityMeasures.h`. You are encouraged to use the Dijkstra API you implemented in Part 1. You may assume that all given graphs will contain at least three vertices.

For a more detailed explanation of closeness and betweenness centrality, please refer to: Explanations for Part 2

Part 3 - Discovering Community

Your task is to implement the Hierarchical Agglomerative Clustering (HAC) algorithm to discover communities in a given graph. In particular, you need to implement the Lance-Williams algorithm, as described below. In the lecture we will discuss how this algorithm works, and what you need to do to implement it. You may find the following resources useful for this part:

- Hierarchical Clustering (Wikipedia), for this assignment we are only interested in the "agglomerative" approach.
- Three videos by Victor Lavrenko, watch in order:
  - Agglomerative Clustering: how it works
  - Hierarchical Clustering 3: single-link vs. complete-link
  - Hierarchical Clustering 4: the **Lance-Williams algorithm**

You need to use the following (adapted) Lance-Williams HAC algorithm to derive a dendrogram:

- Calculate distances between each pair of vertices as described below.
- Create clusters for every vertex i, say c_i. Every vertex begins in its own cluster (but they will be merged later).
- Let $Dist(c_i, c_j)$ represent the distance between cluster c_i and c_j. Initially, it represents the distance between vertex i and j (since initially each vertex is in its own cluster).
- Until there is one cluster remaining:
  - Find the pair of clusters, c_i and c_j, with the smallest distance between them. If there are multiple alternatives, you can select any one of the pairs of closest clusters.
  - Remove the clusters c_i and c_j from the collection of clusters and add a new cluster c_{ij} (that contains all the vertices in c_i and c_j) to the collection of clusters.
  - Update the dendrogram to reflect the merging of c_i and c_j.
  - Calculate the distances $Dist(c_{ij}, c_k)$ between the newly added cluster c_{ij} and each other cluster c_k in the collection using the Lance-Williams formula using the selected method ('*Single linkage*' or '*Complete linkage*' - see below).
- Return the dendrogram

Distance Measure

For this assignment, we define the distance between a pair of vertices as follows: Let wt represent the maximum edge weight of all available weighted edges between a pair of vertices v and w. The distance d between vertices v and w is defined as $d = 1/wt$. If v and w are not connected by an edge, d is infinity (you may use `DBL_MAX` to represent infinity).

For example, if there is one directed link between v and w with weight wt, the distance between them is $1/wt$. If there are two links between v and w, we take the maximum of the two weights and the distance between them is $1/max(wt_{vw}, wt_{wv})$. Please note that in reality one can also consider alternative approaches, such as taking the average, minimum, etc. However, we need to pick one approach for this assignment and we will use the above distance measure.

Lance-Williams Formula

Lance-Williams Formula

The general Lance-Williams formula is:

$$Dist(c_{ij}, c_k) = \alpha_i * Dist(c_i, c_k) + \alpha_j * Dist(c_j, c_k) + \beta * Dist(c_i, c_j) + \gamma * abs(Dist(c_i, c_k) - Dist(c_j, c_k))$$

where α_i, α_j, β, and γ are determined by the chosen agglomerative criterion (i.e., single linkage, complete linkage, etc.).

However, given a specific agglomerative criterion, we can simplify the formula as follows:

For the *single linkage method*, the formula can be simplified to:

$$Dist(c_{ij}, c_k) = min(Dist(c_i, c_k), Dist(c_j, c_k))$$

For the *complete linkage method*, the formula can be simplified to:

$$Dist(c_{ij}, c_k) = max(Dist(c_i, c_k), Dist(c_j, c_k))$$

What you need to do:

Complete the file `LanceWilliamsHAC.c` that implements all the functions declared in `LanceWilliamsHAC.h`.

For a simple demonstration of the Lance-Williams algorithm, please refer to: Part 3 Simple Example (MS Excel file)

Note: Do not use the BSTree ADT for this task - the BSTree ADT is intended to be used by the testing program only.

Testing

We have provided some testing programs/scripts and sample graphs for you to get started. However, please note:

- You need to add more advanced test cases (graphs) to properly test your implementations.
- We will use more advanced test cases that are not included in the test cases provided to you when automarking your code.

Graphs

The sample graphs are in the `graphs/` directory. Each graph file consists of an integer representing the number of vertices, followed by a series of directed edges (one per line), where each edge is represented by three comma-separated values: (1) the source node, (2) the target node, (3) the edge weight. You can create your own graphs for testing by following this format.

Part 1

You can use the following commands to test your Dijkstra API. All graphs in the `graphs/` directory are applicable for testing this part.

```
$ make                              # compiles the program
$ ./testDijkstra graph-file         # tests with a specific graph, outputs to terminal
                                    # now manually compare with expected output in DijkstraTests/
$ ./testDijkstra graphs/1.in        # for example, tests with the graph in graphs/1.in
$ sh testDijkstra.sh graph-number   # runs a specific test
$ sh testDijkstra.sh 2              # for example, runs test for graph 2
$ sh testDijkstra.sh                # runs all provided tests
```

Part 2

You can use the following commands to test your CentralityMeasures API. All graphs in the `graphs/` directory are applicable for testing this part.

```
# compiles the program
$ make

# tests with a specific graph and centrality type, outputs to terminal
$ ./testCentralityMeasures graph-file centrality-type

# for example, tests with the graph in graphs/1.in
$ ./testCentralityMeasures graphs/1.in c     # closeness centrality
$ ./testCentralityMeasures graphs/1.in b     # betweenness centrality

# runs a specific test
$ sh testCentralityMeasures.sh graph-number centrality-type

# for example, runs test for graph 2
$ sh testCentralityMeasures.sh 2 c           # closeness centrality
$ sh testCentralityMeasures.sh 2 b           # betweenness centrality

# for example, runs all tests for graph 2
$ sh testCentralityMeasures.sh 2

# runs all provided tests
$ sh testCentralityMeasures.sh
```

Part 3

You can use the following commands to test your LanceWilliamsHAC API. The graphs applicable for testing Part 3 are: `graphs/1.in`, `graphs/2.in`, `graphs/3.in`, `graphs/4.in`.

```
$ make                                  # compiles the program
$ ./testLanceWilliamsHAC graph-file     # tests with a specific graph
$ sh testLanceWilliamsHAC.sh graph-number    # runs a specific test
$ sh testLanceWilliamsHAC.sh 2          # for example, runs test for graph 2
$ sh testLanceWilliamsHAC.sh            # runs all provided tests
```

Note that the `testLanceWilliamsHAC` program may produce different output to the `.out` files produced by the `testLanceWilliamsHAC.sh` script. This is because the testing script *sorts* all the lines of the output before writing it to the `.out` files. If your program produces debugging output then you should test with the `testLanceWilliamsHAC` program and not the testing script.

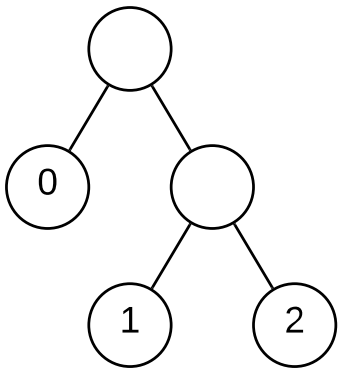
Note: We have only provided expected output for the single linkage method. You are expected to test and check the output for complete linkage yourself. (Hint: modify `testLanceWilliamsHAC.c` to test complete linkage.)

How to interpret the output of `testLanceWilliamsHAC.sh`

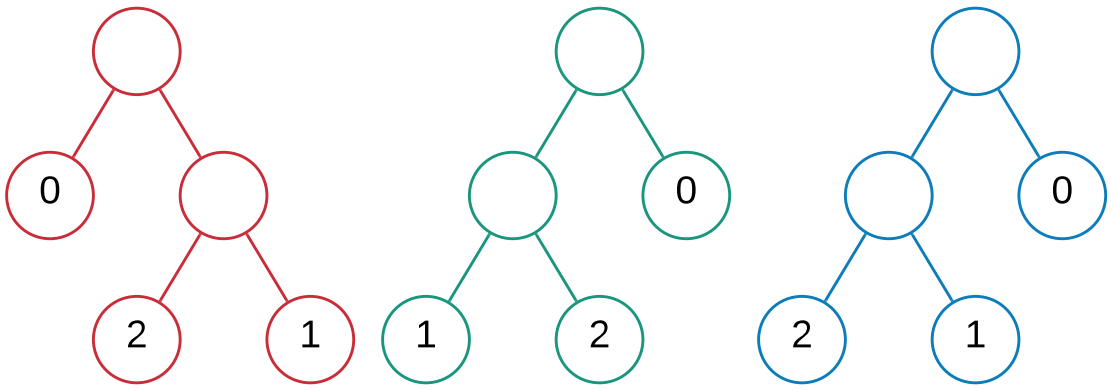
The testing script produces output like this in the `.out` files:

```
0: {0, 1, 2}
1: {0} (leaf)
1: {1, 2}
2: {1} (leaf)
2: {2} (leaf)
```

Each line of the output describes a node in the dendrogram. The number to the left of the colon is the level that the node appears on (the level of the root node is 0). The set to the right of the colon lists the vertices that are contained within that sub-dendrogram (sub-tree). Leaf nodes are indicated by `(leaf)` at the end of the line. The above output corresponds to the dendrogram:



However, since the order of the lines does not matter, it can also correspond to any of these dendrograms:



Note that all of these dendrograms are essentially the same - in all of them, vertex 0 is on level 1, vertices 1 and 2 are on level 2, there is a cluster containing the vertices 1 and 2, and there is a cluster containing all the vertices. It doesn't matter which one of these dendrograms you produce - the testing script sorts the output lines, so all correct dendrograms will result in the same output.

Assumptions/Clarifications/Notes

- In a graph, vertices are numbered 0 to $N - 1$, where N is the number of vertices.
- All edge weights will be positive.
- Graphs will not contain parallel edges or self-loop edges.
- All input graphs will be valid.
- You may not `#include` any additional libraries, as all the libraries you require are already included.
- You are not required to use the priority queue ADT, but it is expected to make Task 1 easier.
- You can assume that the graphs used to test complete linkage in Part 3 will be complete. That is, there will always be at least one edge between every pair of nodes.

Frequently Asked Questions

- **Are we allowed to create our own functions?** Of course...
- **Are we allowed to create our `#define`s and structs?** Yes.
- **Are we allowed to change the signatures of the given functions?** No. If you change these, your code won't compile and we won't be able to test it.
- **What is the difference between a "node" and a "vertex"?** Nodes and vertices are the same thing.
- **How do we return an array?** To return a new array from a function, the array must be `malloc`'d. Otherwise, the array will go out of scope (i.e., no longer exist) once the function returns.
- **What errors do we need to handle?** You should handle common errors such as `NULL` returned from `malloc` by printing an error message to `stderr` and terminating the program. You are not required to handle other errors.
- **The explanation of Part 3 in the Excel file has sets as indices for the dist and dendrogram arrays.** Those aren't indices - they're clusters. When you implement your solution, you will need to find a way to associate each cluster with an array index.

Submission

You need to submit the following files:

- Dijkstra.c
- CentralityMeasures.c
- LanceWilliamsHAC.c

You must submit all of these files, even if you did not complete all of the tasks. No supporting files are permitted in this assignment. This means all your code must be in these three files.

You can submit via the command line using the `give` command:

```
$ give cs2521 ass2 Dijkstra.c CentralityMeasures.c LanceWilliamsHAC.c
```

or you can submit via WebCMS. You may not submit any other files. You can submit multiple times. Only your last submission will be marked. You can check the files you have submitted here.

WARNING:

After you submit, you **must** check that your submission was successful by going to your submissions page. Check that the timestamp is correct. If your submission does not appear under Last Submission or the timestamp is not correct, then resubmit.

Compilation

You must ensure that your final submission compiles on CSE machines. Submitting non-compiling code leads to extra administrative overhead and will result in a 10% penalty.

Every time you make a submission, a dryrun test will be run on your code to check that it compiles. Please ensure that your final submission successfully compiles, even for parts that you have not completed.

Assessment Criteria

This assignment will contribute 20% to your final mark.

Correctness

80% of the marks for this assignment will be based on the correctness of your code, and will be based on autotesting. We will test your program using the same testing programs that we have given you (`testDijkstra`, `testCentralityMeasures` and `testLanceWilliamsHAC`), but we will use different graphs from those provided to you.

Marks for correctness will be distributed as follows:

Part 1	Dijkstra's algorithm	30% of the correctness mark
Part 2	Closeness centrality	20% of the correctness mark
	Betweenness centrality	30% of the correctness mark
Part 3	Discovering community	20% of the correctness mark

Efficiency

There is no strict efficiency requirement, but tests that take too long to run (i.e., 5 real time seconds on a single execution of one of the testing programs without `valgrind`) will be terminated automatically and you will receive 0 for the test. The graphs we use during testing will be about the same size as those provided to you.

Memory errors/leaks

Additionally, you must ensure that your code does not contain memory errors or leaks, as code that contains memory errors is unsafe and it is bad practice to leave memory leaks in your program. Note that our tests will always free the memory associated with the returned arrays/structures from your functions by calling `freeNodeData` or `free`. See the test programs for more details.

Submissions that contain memory errors or leaks will receive a penalty of 10% of the correctness mark, deducted from the attained mark. Specifically, there will be a separate memory error/leak check for each part, and the penalty will be 10% of the marks for that part. You can check for memory errors and leaks with `valgrind`. For example:

```
$ valgrind -q --leak-check=full ./testDijkstra graph-file > /dev/null
```

A program that contains no memory errors or leaks will produce no output from this command. You can learn more about memory errors and leaks in the Debugging with GDB and Valgrind lab exercise.

Note that you should not run `valgrind` on `testDijkstra.sh` or any other files ending with `.sh`. `valgrind` can only be run on C executables.

Style

20% of the marks for this assignment will come from hand marking of the readability of the code you have written. These marks will be awarded on the basis of clarity, commenting, elegance and style. The following is an indicative list of characteristics that will be assessed, though your program will be assessed wholistically so other characteristics may be assessed too (see the style guide for more details):

- Consistent and sensible indentation and spacing
- Using blank lines and whitespace
- Using functions to avoid repeating code
- Decomposing code into functions and not having overly long functions
- Using comments effectively and not leaving planning or debugging comments

The course staff may vary the assessment scheme after inspecting the assignment submissions but it will remain broadly similar to the description above.

Originality of Work

This is an individual assignment. The work you submit must be your own work and only your work apart from the exceptions below. Joint work is not permitted. At no point should a student read or have a copy of another student's assignment code.

You may use any amount of code from the lectures and labs of the **current iteration** of this course. You must clearly attribute the source of this code in a comment.

You may use small amounts (< 10 lines) of general purpose code (not specific to the assignment) obtained from sites such as Stack Overflow or other publicly available resources. You must clearly attribute the source of this code in a comment.

You are not permitted to request help with the assignment apart from in the course forum, help sessions or from course lecturers or tutors.

Do not provide or show your assignment work to any other person (including by posting it publicly on the forum) apart from the teaching staff of COMP2521. When posting on the course forum, teaching staff will be able to view the assignment code you have recently submitted with give.

The work you submit must otherwise be entirely your own work. Submission of work partially or completely derived from any other person or jointly written with any other person is not permitted. The penalties for such an offence may include negative marks, automatic failure of the course and possibly other academic discipline. Assignment submissions will be examined both automatically and manually for such issues.

Relevant scholarship authorities will be informed if students holding scholarships are involved in an incident of plagiarism or other misconduct. If you knowingly provide or show your assignment work to another person for any reason, and work derived from it is submitted, then you may be penalised, even if the work was submitted without your knowledge or consent. This may apply even if your work is submitted by a third party unknown to you.

COMP2521 22T1: Data Structures and Algorithms is brought to you by

the School of Computer Science and Engineering

at the University of New South Wales, Sydney.

For all enquiries, please email the class account at cs2521@cse.unsw.edu.au

CRICOS Provider 00098G