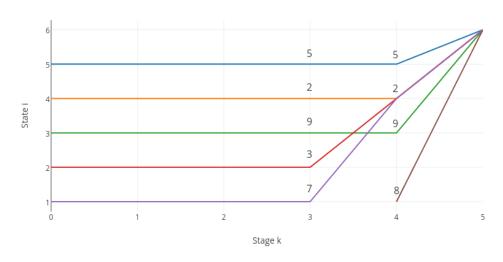
Problemset 2

Daniel Bestard Delgado, Michael Cameron, Hans-Peter Höllwirth, Akhil Lohia March 2, 2017

1 Shortest Path via DP





Using the DP algorithm as discussed in class we find the above graph. Hence the shortest path from each node to node 6 is as follows:

From node 1: 7

From node 2: 3

From node 3: 9 From node 4: 2 From node 5: 5

2 Shortest Path via Label Correcting Methods

In order to find the shortest path of the directed graph provided in this exercise we need to apply two algorithms that come from the general framework label correcting methods. Before going into detail it is necessary to provide some notation from this general framework:

- *i*: denotes the node.
- j: denotes the child of i.
- g_i : length of the shortest path found so far.
- $d_i + a_{ij}$: length of the shortest path to i found so far followed by arc (i, j).
- *UPPER*: length of the shortest path from the source to the target found so far. It is set to *infty* as long as the target has not been found.
- *OPEN*: contains nodes that are currently active, which means that it is possible their inclusion for the shortest path. Initially it contains the source.

The label correcting algorithm takes the following steps:

- 1. Remove node i from OPEN and for each child j of i, execute step 2.
- 2. If $d_i + a_{ij} < min\{d_j, UPPER\}$, set $d_j = d_i + a_{ij}$ and set i to be the parent of j. In addition,
 - (a) If $j \neq t$, place j in OPEN if it is not already in OPEN.
 - (b) If j = t, set UPPER to be the new value $d_i + a_{ij}$ of d_t
- 3. If OPEN is empty, terminate; else go to step 1.

One of the algorithms that is part of the label correction methods is the **Bellman-Ford** algorithm. In this algorithm the node is always removed from the top of OPEN and each node entering OPEN is placed at the bottom of OPEN. The following table displays the results of this algorithm for each iteration. Note that in the third column there is a number in parenthesis for each path, which corresponds to its length.

Iter.	Exiting OPEN	OPEN at the end of iter.	UPPER
0	-	1	∞
1	1	1-3(1),1-2(2)	∞
2	1-2	1-2-4(3), 1-2-3(3), 1-3(1)	2
3	1-3	1-3-4(4),1-3-2(2),1-2-4(3),1-2-3(3)	2
4	1-2-3	1-3-4(4),1-3-2(2),1-2-4(3)	2
5	1-2-4	1-3-4(4),1-3-2(2)	2
6	1-3-2	1-3-4(4)	2
7	1-3-4	Ø	2

Just to clarify, note that in the second iteration we reach the target through the path 1-2-5. The length of this path is 2. Given that j = t we set UPPER to be the new value of d_t as part b) of the algorithm specifies. The UPPER variable does not get updated anymore because we do not find any other path that goes from the source to the target that has length smaller than 2. Therefore, the shortest path is 1-2-5.

The other algorithm that belongs to the label correction methods is called **Dijkstra's algorithm**. It is very similar to the previous one, but at each iteration it removes from OPEN a node with the minimum value of the label instead of removing the right (top) most node of OPEN. The results of the algorithms are:

Iter.	Exiting OPEN	OPEN at the end of iter.	UPPER
0	-	1	∞
1	1	1-3(1),1-2(2)	∞
2	1-3	1-2(2),1-3-2(2),1-3-4(4)	∞
3	1-2	1-2-3(3),1-3-2(2),1-3-4(4)	2
4	1-3-2	1-2-3(3),1-3-4(4)	2
5	1-2-3	1-3-4(4)	2
6	1-3-4	Ø	2

Again the shortest path is 1-2-5 for the same reasoning as before. Therefore, both algorithms reach the same outcome in this case.

3 Clustering

4 Path Bottleneck Problem

- s: denotes the origin node.
- t: denotes the terminal node.
- α_{ij} : length from node i to node j.

- b_i : size of bottleneck in the minimum bottleneck path from s to i.
- pi: parent of node i.
- *UPPER*: size of bottleneck in the minimum bottleneck path from s to t. It is set to *infty* as long as the target has not been found.
- *OPEN*: contains nodes that are currently active, which means that it is possible their inclusion for the bottle neck path. Initially it contains the source.

The label correcting algorithm takes the following steps:

- 1. Remove node i from OPEN and for each child j of i, execute step 2.
- 2. If $min\{b_i, \alpha_{ij}\} < min\{d_j, UPPER\}$, set $b_j = min\{b_i, \alpha_{ij}\}$, and set i to be the parent of j. In addition,
 - (a) If $j \neq t$, place j in OPEN if it is not already in OPEN.
 - (b) If j = t, set UPPER to be the new value $d_i + a_{ij}$ of d_t
- 3. If OPEN is empty, terminate; else go to step 1.

5 TSP Computational Assignment

Appendix - R Code

```
# Compute distance matrix
distance.matrix <- function(data) {</pre>
    # use high dummy value for distance to itself
    dm <- matrix(10000, N, N)</pre>
    for (i in 1:N) {
        for (j in 1:N) {
             if (i != j)
                 # Euclidian distance
                 dm[i,j] <- round(sqrt((data[i,2] - data[j,2])**2 +</pre>
                                        (data[i,3] - data[j,3])**2),3)
        }
    }
    return(dm)
}
dm <- distance.matrix(data)</pre>
# Compute path length
path.length <- function(dm, path) {</pre>
    length <- 0
    N <- length(path)
    # walk through path and add up distance
    for (i in 2:N) {
        length <- length + dm[path[i-1],path[i]]</pre>
    }
    # add distance back to origin
    length <- length + dm[path[N],path[1]]</pre>
    return(length)
}
# Plot path
plot.path <- function(data, path) {</pre>
    N <- length(path)
    # plot cities
    par( mar=c(0.5,0.5,0.5,0.5), mfrow=c(1,1))
    plot(-data[,3:2], type='p', pch=16, cex=0.5, asp=1, xaxt='n', yaxt='n')
    # plot path through cities
    for (i in 2:N) {
        segments(-data[path[i-1],3], -data[path[i-1],2],
                  -data[path[i],3], -data[path[i],2], col="red")
```

```
segments(-data[path[N],3], -data[path[N],2],
              -data[path[1],3], -data[path[1],2], col="red")
}
# Nearest neighbor algorithm
nn.path <- function(dm) {</pre>
    visited <- rep(0,N)</pre>
    path \leftarrow rep(0,N)
    # starting point
    city <- 1
    visited[city] <- TRUE</pre>
    path[1] <- 1
    # repeatedly visit nearest not-yet visited neighbor
    for (i in 2:N) {
        leg <- min(dm[city, !visited])</pre>
         # find index of nearest city and add it to path
        potentials <- which(dm[city,] == leg)</pre>
         for (j in 1:length(potentials)) {
             if (!visited[potentials[j]]) {
                 city <- potentials[j]</pre>
                 visited[city] <- TRUE</pre>
                 path[i] <- city</pre>
                 break
             }
        }
    }
    return(path)
# Insertion Heuristics
insertion.path <- function(dm) {</pre>
    visited <- rep(0,N)</pre>
    # start with initial subtour
    visited[1] <- visited[2] <- visited[3] <- TRUE</pre>
    path <-c(1,2,3,1)
    while (0 %in% visited){
         # find closest unvisited city to subtour
        leg <- min(dm[!!visited, !visited])</pre>
         # find index of closest unvisited city
        potentials <- which(dm[,] == leg, arr.ind=TRUE)</pre>
        for (k in 1:nrow(potentials)) {
```

if (!!visited[potentials[k,1]] & !visited[potentials[k,2]]) {

```
city <- as.numeric(potentials[k,2])</pre>
                 visited[city] <- TRUE</pre>
                 break
            }
        }
        # find shortest detour to new city
        detour <- list(len=1000000, from=0, to=0)
        for (i in 1:(length(path)-1)) {
             pot.detour.len <- dm[path[i],city] + dm[path[i+1],city] - dm[path[i],path[i+1]]</pre>
             if (pot.detour.len < detour$len) {</pre>
                 detour$len <- pot.detour.len</pre>
                 detour$from <- i
                 detour$to <- i+1
             }
        }
        # add detour to new path
        path <- c(path[1:detour$from], city, path[detour$to:length(path)])</pre>
    return(path[1:N])
}
```

```
# 2-opt path improvement
two.opt.path <- function(dm, path) {</pre>
    path <- c(path, path[1])</pre>
    N <- length(path)</pre>
    changes <- TRUE
    # keep updating path until it is 2-opt path
    while (changes) {
        changes <- FALSE
        for (i in 1:(N-3)) {
             for (j in (i+2):(N-1)) {
                 # if alternative path is segment is shorter than current segment
                 curr.len <- dm[path[i],path[i+1]] + dm[path[j], path[j+1]]</pre>
                 new.len <- dm[path[i],path[j]] + dm[path[i+1],path[j+1]]</pre>
                 if (new.len < curr.len) {</pre>
                      # swap positions
                     path[(i+1):j] <- path[j:(i+1)]</pre>
                     changes <- TRUE
                 }
            }
        }
    }
    return(path[1:(N-1)])
```

```
# ------
# Run path computations and plot solutions
```

```
# compute distance matrix
dm <- distance.matrix(data)</pre>
# compute nearest neighbor path
path.nn <- nn.path(dm)</pre>
path.length(dm, path.nn)
plot.path(data, path.nn)
# compute insertion heuristics path
path.insert <- insertion.path(dm)</pre>
path.length(dm, path.insert)
plot.path(data, path.insert)
# compute 2-opt improved nearest neighbor path
path.nn.2opt <- two.opt.path(dm, path.nn)</pre>
path.length(dm, path.nn.2opt)
plot.path(data, path.nn.2opt)
# compute 2-opt improved insertion heuristics path
path.insert.2opt <- two.opt.path(dm, path.insert)</pre>
path.length(dm, path.insert.2opt)
plot.path(data, path.insert.2opt)
```