



Using R to Create and Solve Assessment Problems for an Online Math for General Education Course



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INTRODUCTION

Perhaps one of the most difficult tasks for teachers is creating appropriate assessment problems to ask their students. Additionally, it may be more difficult to create a large library of questions in order to avoid cheating and provide students multiple attempts on a particular type of problem to deepen their understanding. I have used the mathematical program R to alleviate some of the struggles a teacher may face creating these problems. Specifically, I have written programs that create and solve problems involving apportionment and graph theory for the University of Central Oklahoma's *Math for General Education* online course. Within the programs is a problem creator that builds a question using randomized numbers and solves it using a specified algorithm.

ACKNOWLEDGEMENTS

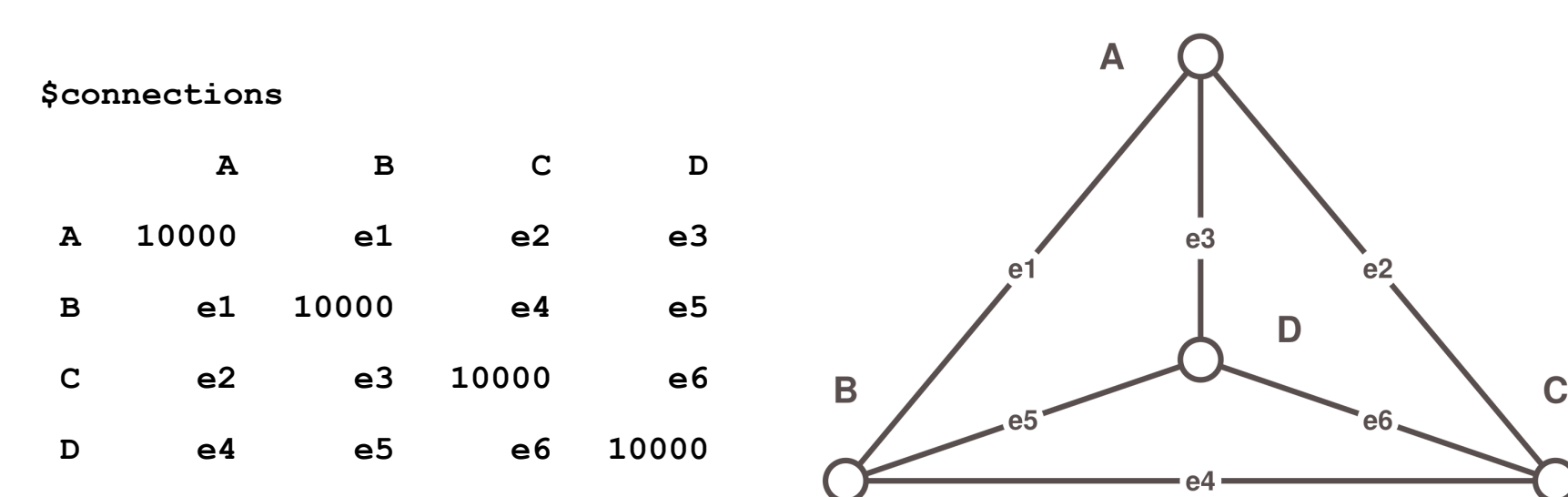
This project is based on work supported by a faculty on-campus grant from the Office of Research & Sponsored Programs, University of Central Oklahoma. Special thanks to Jonathan Yarborough and Dr. Sean Lavery for their help and support in R.

GRAPH THEORY

- The R code specifically creates and solves problems involving graphs with **Hamiltonian Circuits**.
 - Hamiltonian**: path visits every vertex once with no repeats.
 - Circuit**: path begins and ends at the same vertex.
- The **build.graph** function allows the user to choose the max potential edge value and path solving method.

```
build.graph <- function(max.value, method){...}
```
- The solving methods are: Nearest Neighbor Algorithm (**NNA**); Repeated Nearest Neighbor (**RNNA**); and the Sorted Edges Algorithm (**SEA**).
- Using a random 3-digit seed number and the sample command, edge weights are assigned randomly so that every problem created is unique.

```
set.seed(sample(100:999, 1))
n.edges <- 6
edges <- sample(1:max.value, n.edges)
```
- A "connections" matrix keeps track of the neighboring vertices, their connected edges, and the edge weights.



NEAREST NEIGHBOR ALGORITHM

- Given a starting vertex and the connections matrix, the **nearest.neighbor** function finds the "best" Hamiltonian Circuit by going to the neighboring vertices whose edge weight is the smallest (i.e. the "nearest neighbor"). It will only visit that neighbor if that vertex has not yet been visited.

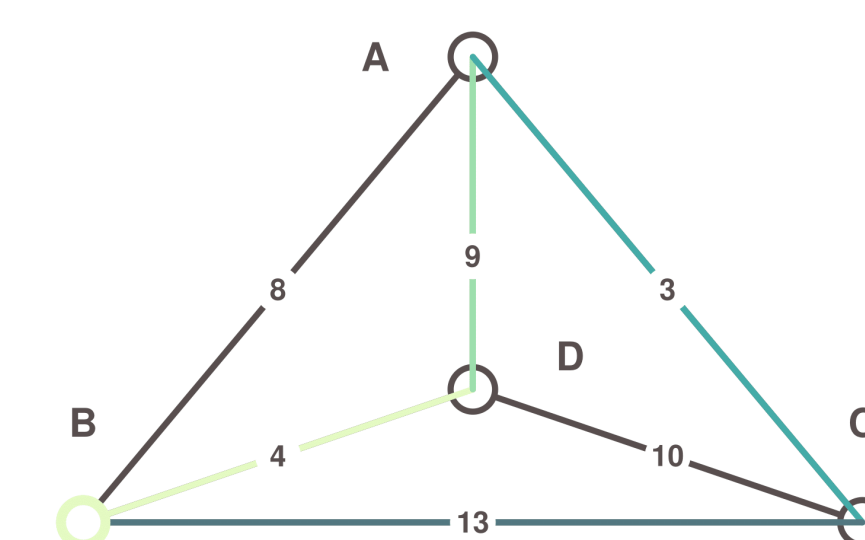
```
nearest.neighbor <- function(vertex, connections){...}
```
- A stack of vertices is created that will eventually become the "best" path. The **stack** is initialized as the **vertex** passed from the **build.graph** function. A **total.weight** value of the path is also initialized.

```
stack <- c(vertex)
total.weight <- 0
```
- The neighborhood of the last vertex in the **stack** is checked for its "best" neighbor (the one with the smallest edge weight). If the "best" neighbor is already in the **stack** (has been visited), then the next "best" neighbor is used.
- The stack is updated with the new vertex and the **total.weight** value is updated with the new edge weight.
- The code will run until all of the vertices have been visited and the path returns to the starting vertex.

```
$starting.vertex
[1] "B"

$path
[1] "B" "D" "A" "C" "B"

$total.weight
[1] 29
```



SORTED EDGES ALGORITHM

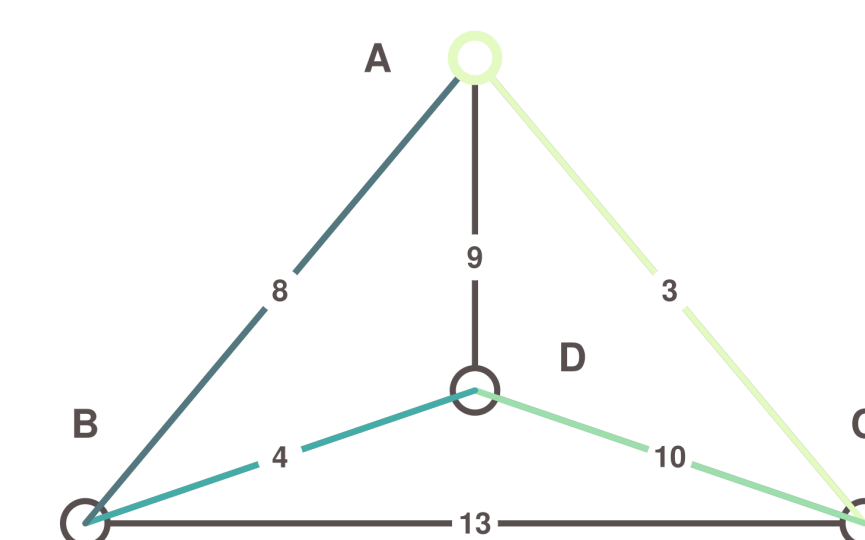
- Given the list of vertices and the connections matrix, the **sorted.edges** function finds the "best" Hamiltonian Circuit by selecting the smallest unused edge in the graph. It will not use an edge if it creates a circuit that does not contain all vertices or gives a vertex of degree 3.

```
sorted.edges <- function(vertices, connections){...}
```
- Two vectors, **OutputFirst** and **OutputLast**, are initialized to hold the vertices of the "best" edges. The edge weights are compared against each other before the "best" one is chosen. One vertex of the "best" edge is placed in **OutputFirst** and the other vertex in **OutputLast**.
- The code will run until all of the vertices have been visited and the circuit is complete.

```
> OutputFirst
[1] "A" "B" "A" "C"
> OutputLast
[1] "C" "D" "B" "D"
```
- The first edge's vertices are placed on a stack. The path is then organized based off the last vertex in the stack using the matching vertices in the vectors, **OutputFirst** and **OutputLast**. The total weight of the path is also calculated.

```
$path
[1] "A" "C" "D" "B" "A"

$total.weight
[1] 25
```



APPORTIONMENT

- Apportionment determines how to divide a fixed number of things among groups of different sizes (e.g. representative seats and populations).
- The **build.apportionment** function allows the user to choose the number of populations needing apportioned and the apportionment solving method.

```
build.apportionment <- function(n.places, method){...}
```
- Solving methods: Hamilton, Jefferson, and Huntington-Hill.
- Using a random 3-digit seed number and the sample command, the number of seats and population sizes are assigned randomly so that every problem created is unique.

```
set.seed(sample(100:999, 1))
n.seats <- sample(50:100, 1)
populations <- sample(seq(from = 25000, to = 100000,
by = 500), n.places)
```

```
divisor <- pop.top["Total", "Population"] / n.seats
```

- A population matrix tracks information for all methods.

	Population	Quota	Lower.Quota	Geometric.Mean	Initial	Final	(Extra for Hamilton)
A	P1	NA	NA	NA	NA	NA	NA
B	P2	NA	NA	NA	NA	NA	NA
C	P3	NA	NA	NA	NA	NA	NA
D	P4	NA	NA	NA	NA	NA	NA
E	P5	NA	NA	NA	NA	NA	NA
Total	PopTotal	NA	NA	NA	NA	NA	NA

HAMILTON'S METHOD

- The **hamilton** function uses the population table, divisor, number of seats, and number of populations to determine the allocation of the seats.

```
hamilton <- function(pop.top, div, n.seats, n.places){...}
```
- The floor of the quotas is computed for each population and placed in the **initial** column of the population table. The lower quotas are then summed.

```
low.quota <- floor(quota)
pop.top[i, "Initial"] <- low.quota
pop.top["Total", "Initial"]
<- sum(pop.top[c(1:n.places), "Initial"])
```
- If the initial total is not equal to the number of seats needing apportioned, then the extra seats are allotted to the populations based off their quota's decimal values.
- The **(Extra for Hamilton)** column contains the truncated decimals for each population quota. The maximum decimal value is determined and its population receives +1 seat. The max value is then changed to -1 to signify the decimals have been used. This code will run until the number of seats is met.

	Population	Quota	Initial	Final	(Extra for Hamilton)
A	31000	9.513228	9	10	-1.00000000
B	78500	24.089947	24	24	0.08994709
C	40000	12.275132	12	12	0.27513228
D	77000	23.629630	23	24	-1.00000000
E	57000	17.492063	17	17	0.49206349
Total	283500	NA	85	87	NA

JEFFERSON'S METHOD

- The **jefferson** function uses the population table, divisor, number of seats, number of populations, and a modified divisor list to determine the allocation of seats.

```
jefferson <- function(pop.top, div, n.seats, n.places,
mod.div.list){...}
```
- The floor of the quotas is computed for each population and placed in the **initial** column of the population table and then summed.
- If the initial total is less than the number of seats needed, then the divisor is reduced and the quotas and allocations are recalculated. If the initial total is greater than the number of seats needed, then the divisor is increased. The new divisors are kept track of in the **mod.div.list** until a working divisor is found.
- The **range.jefferson** and **test.jefferson** functions determine the range of working divisors for Jefferson's method. The divisors being tested are tracked in a list with the first working divisor as one bound of the range and the last working divisor as the other bound. Each bound has an error of being <1 away from the actual divisor boundary because the divisors are checked in increments of 1.

	Population	Quota	Initial
A	31000	9.513228	9
B	78500	24.089947	24
C	40000	12.649441	12
D	77000	24.350174	24
E	57000	18.025453	18
Total	283500	NA	87
	Population	Quota	Initial
A	31000	9.513228	9
B	78500	24.089947	24
C	40000	12.275132	12
D	77000	23.629630	23
E	57000	17.492063	17
Total	283500	NA	85

	Population	Quota	Initial
A	31000	9.803317	9
B	78500	24.824528	24
C	40000	12.649441	12
D	77000	24.350174	24
E	57000	18.025453	18
Total	283500	NA	87
	Population	Quota	Initial
A	31000	9.513228	9
B	78500	24.089947	24
C	40000	12.275132	12
D	77000	23.629630	23
E	57000	17.492063	17
Total	283500	NA	85

HUNTINGTON-HILL METHOD

- The **huntington.hill** function uses the population table, divisor, number of seats, number of populations, and a modified divisor list to determine the allocation of seats.

```
huntington.hill <- function(pop.top, div, n.seats,
n.places, mod.div.list){...}
```
- The floor of the quotas, n , is computed for each population and placed in the **Lower.Quota** column of the population table. The geometric mean, $\sqrt{n(n+1)}$, is calculated and placed in the **Geometric.Mean** column of the population table.
- If the quota is larger than the geometric mean, then the quota is rounded up. If it is smaller, then it is rounded down. The resulting quotas are the initial allocation of the seats.
- If the initial total is less than the number of seats needed, then the divisor is reduced. If the initial total is greater than the number of seats needed, then the divisor is increased. Quotas and allocations are then recalculated.
- The **range.huntington.hill** and **test.huntington.hill** functions determine the range of working divisors for Huntington-Hill. If the original divisor works, "it's fine".

	Population	Quota	Lower.Quota	Geometric.Mean	Initial
A	31000	9.513228	9	9.486833	10
B	78500	24.089947	24	24.494897	24
C	40000	12.275132	12	12.489996	12
D	77000	23.629630	23	23.494680	24
E	57000	17.492063	17	17.492856	17
Total	283500	NA	NA	NA	87
	Population	Quota	Lower.Quota	Geometric.Mean	Initial
A	31000	9.513228	9	9.486833	10
B	78500	24.089947	24	24.494897	24
C	40000	12.275132	12	12.489996	12
D	77000	23.629630	23	23.494680	24
E	57000	17.492063	17	17.492856	17
Total	283500	NA	NA	NA	87