Social Network - Assignment #1

Aurora Sterpellone - Gür Piren

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1 Introduction

Through this file, we will reveal the number and nature of the partnerships between heroes, villains, and neutral characters across the Marvel Universe. While doing so, we will try to answer a number of questions that were raised as part of the first homework assignment for the Social Network Analysis.

1.1 Acknowledgements

The AI was utilized as a complementary tool to have a better grasp of the concepts and questions across the file. Our interpretations of some of the results were secured through AI perspective. Although we sticked to the in-class exercises and files, some of the plots were created using the AI support.

1.2 Libraries

```r
library(igraph)
library(stringr)
library(dplyr)
library(ggraph) # ultimately, might not use it. check at the end
library(tidygraph) # ultimately, might not use it. check at the end
library(ggrepel)
library(extrafont)
library(tibble)
library(fmsb)
library(GGally)
library(tidyr)
```

2 Questions

2.1 Choose a network dataset

Marvel character partnerships, 2018. The dataset can be accessed through this link

2.2 Indicate the number of nodes. It should be larger than 300 but smaller than 10000.

The number of nodes is 350.

```
load("marvel_network.rda")

# for the number of nodes
num_nodes <- vcount(marvel_network)

cat("Number of nodes:", num_nodes)
```

```
Number of nodes: 350
```

2.3 Import that data and create a graph using R.

Reading the data first. The original network will be plotted after a quick data description and cleaning process.

```
marvel_nodes <- read.csv("data/nodes.csv", stringsAsFactors = FALSE,
                         quote = "\"", fill = TRUE)

marvel_links <- read.csv("data/edges.csv", stringsAsFactors = FALSE)
```

2.3.1 Data description

Initially, we have two datasets separately for nodes and links. Later on, they will be merged.

1. The dataset for the nodes includes the following variables:

id: The index number of the character in the network.

character_name: The name of the character, which could be a hero, villain, or neutral character.

group: Indicates the category of the character (e.g., hero, villain, or neutral).

size: Represents the number of partnerships the character has within the network.

x: The X-coordinate that positions the character in the network layout.

y: The Y-coordinate that positions the character in the network layout.

2. The dataset for the links, on the other hand, incorporates the following variables:

source: This column represents the starting character in a partnership (the character initiating or belonging to the partnership).

target: This column indicates the partner in the relationship with the source character.

2.3.2 Data cleaning

Let's read both datasets, treating text as characters (not factors), and ensuring quotes and missing data are handled properly.

```
# to get proper x and y coordinates

marvel_nodes$pos_x <- as.numeric(str_extract(marvel_nodes$X_pos,
                                             "-?\\d+\\.\\d+"))
marvel_nodes$pos_y <- as.numeric(str_extract_all(marvel_nodes$X_pos,
                                                 "-?\\d+\\.\\d+") %>%
                                   sapply(`[`, 2))

# we don't need the X_pos anymore
marvel_nodes$X_pos <- NULL
```

2.3.3 Renaming columns

To improve readability, we will rename certain columns in both datasets. After that, we will remove any alternative names or descriptions that appear in parentheses following a character's name.

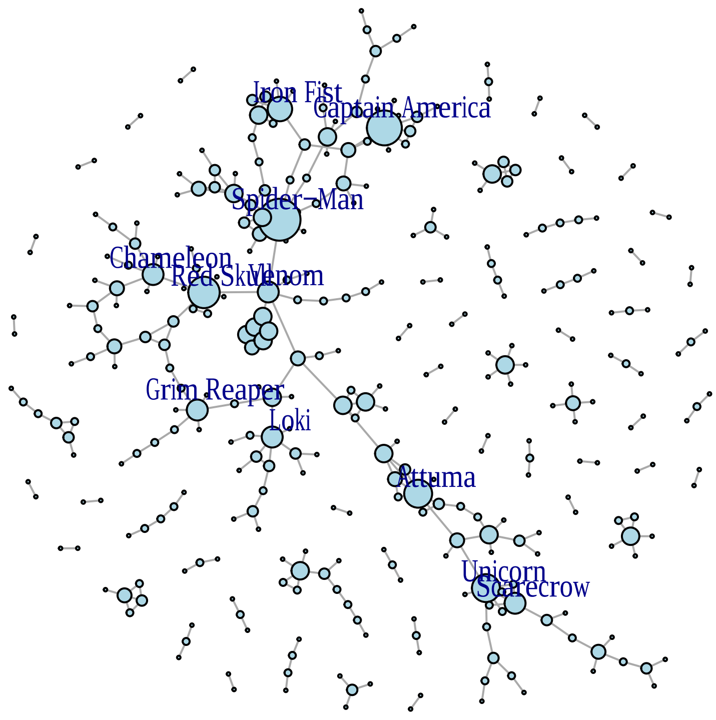
```
marvel_nodes <- marvel_nodes |>
  rename(id = X..index,
         character_name = id,
         x = pos_x,
         y = pos_y) |>
  mutate(id = id + 1) # for best indexing practice

marvel_links <- marvel_links |>
  rename(source = X..source,
         target = target)

marvel_links <- marvel_links |>
  mutate(source = source + 1,
         target = target + 1)
```

```
# let's get rid of anything that is in parentheses in the character_name columns
marvel_nodes$character_name <- gsub(" \\(.*?\\)", "",
                                    marvel_nodes$character_name)
```

2.3.4 Plot

Plotting the network, without distinguishing between heroes, villains, and neutral characters.

```
marvel_network <- graph_from_data_frame(d = marvel_links,
                                        vertices = marvel_nodes,
                                        directed = FALSE)

etiqueta <- ifelse(degree(marvel_network) > 5,
                   V(marvel_network)$character_name, "")

# Plot the network
plot(marvel_network,
     vertex.size = degree(marvel_network),  # Node size by degree
     edge.width = 1,  # No edge value attribute, set to constant
     vertex.color = "lightblue",  # No colour attribute, use a constant color
     vertex.label = etiqueta,
     vertex.label.family = "Marvel",  # Use your font
     vertex.label.dist = 1,
     vertex.label.cex = 1.0)
```




```
save(marvel_network, file = "marvel_network.rda")
```

Let's work on a cleaner plot, ideally we wanted to plot it with those characters that has the biggest sizes (number of partnerships) only, but we were not able to position the node labels clearly.

For the font of use:

```
font_import(pattern = "Marvel")
```

```
Importing fonts may take a few minutes, depending on the number of fonts and the speed of the
Continue? [y/n]
```

```
loadfonts()

# setting font globally
par(family = "Marvel")
```

For the colours, we created a unique palette using the colours for the main Marvel superheroes:

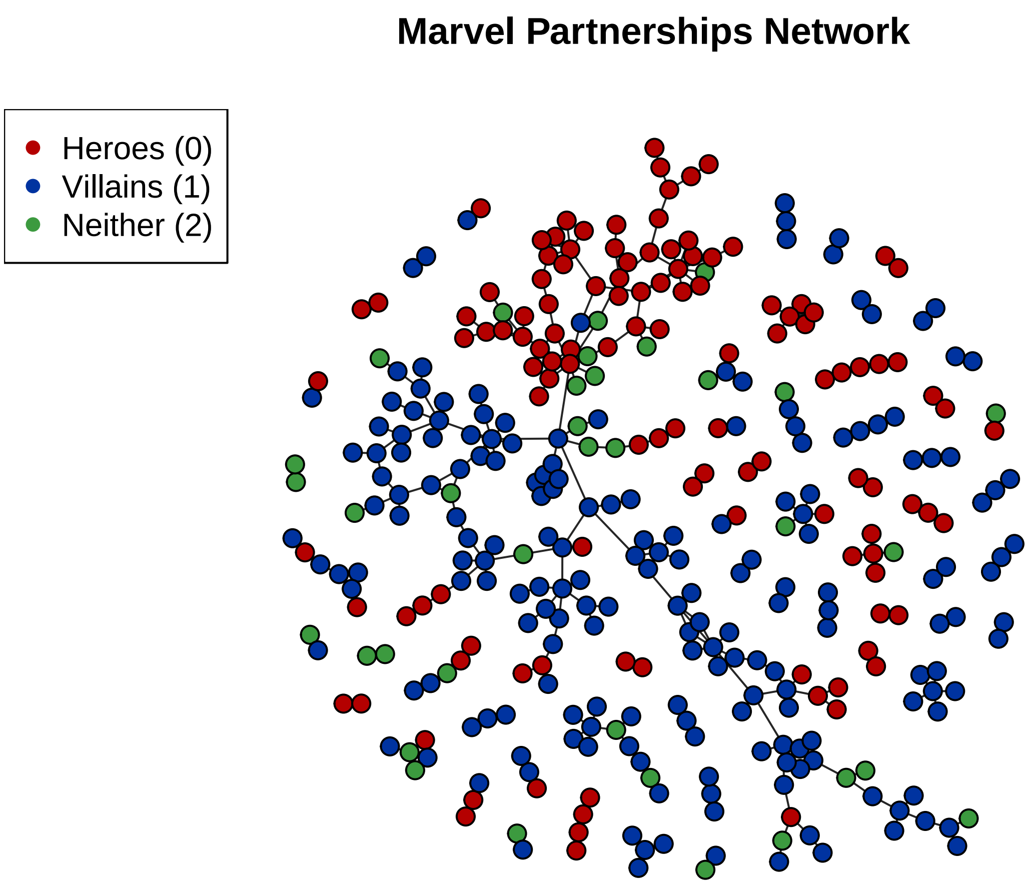
Figure 1: Marvel Color Palette

1. Iron Man Red – #B40000
2. Captain America Blue – #0033A0
3. Hulk Green – #3C9A3F
4. Thor Gold – #D6A400
5. Loki Purple – #6E0B75

```
# defining a color for each group - heroes '0', villains '1', and neither '2'

group_colors <- c("0" = "#B40000", "1" = "#0033A0", "2" = "#3C9A3F")
```

```
V(marvel_network)$group <- marvel_nodes$group

plot(marvel_network,
     vertex.label = NA,
     vertex.size = 5,
     edge.color = "gray15",
     vertex.color = group_colors[as.character(V(marvel_network)$group)],
     layout = cbind(V(marvel_network)$x, V(marvel_network)$y))

title("Marvel Partnerships Network", cex.main = 1.2)

# for the legend
```

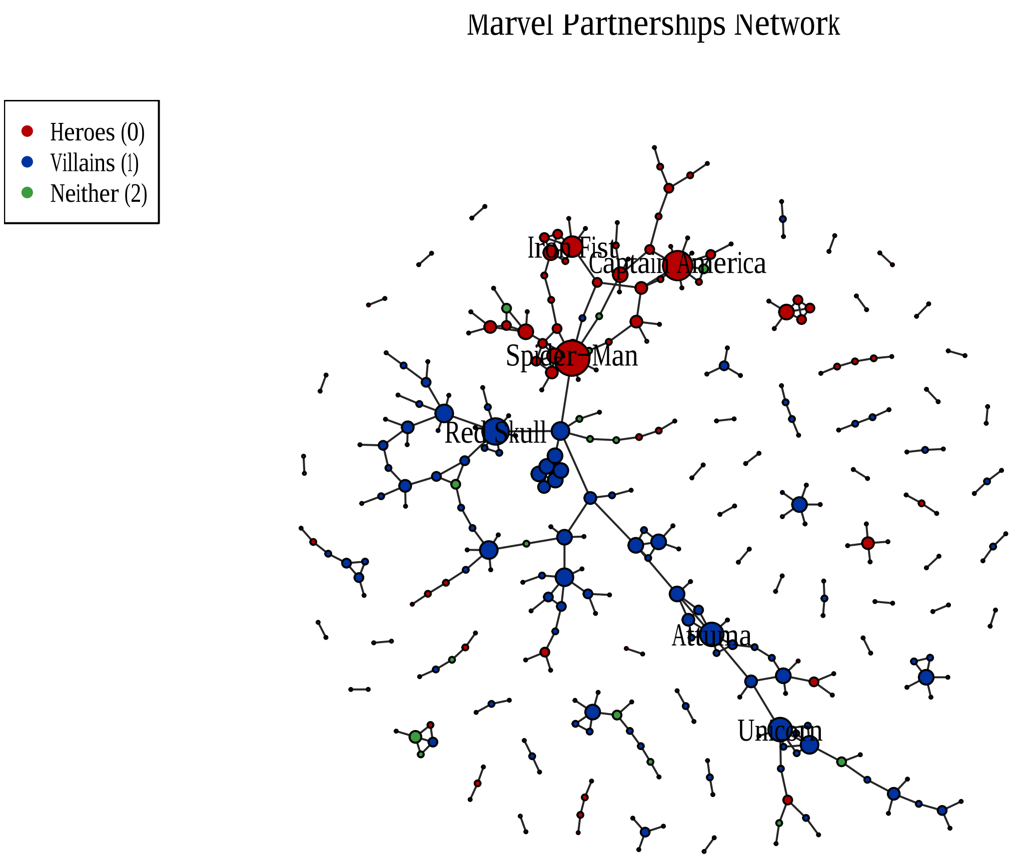
```r
legend("topleft",
       legend = c("Heroes (0)", "Villains (1)", "Neither (2)"),
       col = c("#B40000", "#0033A0", "#3C9A3F"),
       pch = 16,
       bty = "y")
```



Let's see the characters that are represented by bigger nodes, in other words, the ones with most partnerships.

```r
# plot with labels for the biggest nodes

# the degree of each node
degrees <- degree(marvel_network)

# determining a threshold for "biggest" nodes
threshold <- quantile(degrees, 0.98)
```

```r
# identifying nodes with degree above our threshold
big_nodes <- V(marvel_network)[degrees > threshold]$character_name

# plotting the network with labels for the biggest nodes
plot(marvel_network,
     vertex.label = ifelse(degrees > threshold,
                           V(marvel_network)$character_name, NA),
     vertex.size = degrees / max(degrees) * 10,
     edge.color = "gray15",
     vertex.color = group_colors[as.character(V(marvel_network)$group)],
     layout = cbind(V(marvel_network)$x, V(marvel_network)$y),
     vertex.label.family = "Marvel",
     vertex.label.cez = 0.5,
     vertex.label.color = "black")

par(family = "Marvel")
title("Marvel Partnerships Network", cex.main = 1.2)

# Add legend
legend("topleft",
       legend = c("Heroes (0)", "Villains (1)", "Neither (2)"),
       col = c("#B40000", "#0033A0", "#3C9A3F"),
       pch = 16,
       bty = "y",
       cex = 0.8,
       text.font = 2)
```



2.4 What is the number of nodes and links?

The number of nodes for the Marvel network is 350, meaning that the network consists of 350 different Marvel characters (Heroes, Villains, and Neither).

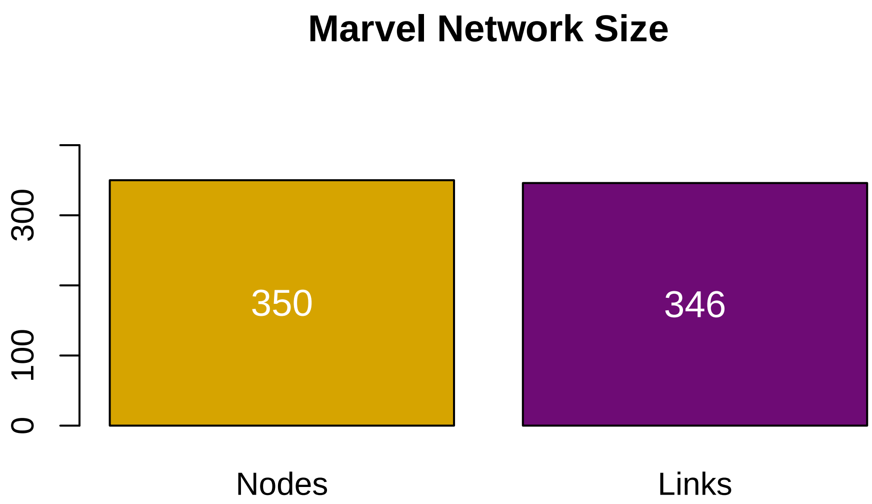
The number of links (the number of partnerships amongst all characters) is 346. This means that there are 346 different partnerships formed by the characters.

```
# extracting number of nodes (characters) and links (partnerships)

num_nodes <- vcount(marvel_network)
num_links <- ecount(marvel_network)

# results
cat("Marvel Network Nodes:", num_nodes,
    "\nMarvel Network Links:", num_links, "\n")
```

```
Marvel Network Nodes: 350
```

```
Marvel Network Links: 346
```

```r
# a simple plot

bp_nodes_links <- barplot(c(num_nodes, num_links),
              names.arg = c("Nodes", "Links"),
              main = "Marvel Network Size",
              col = c("#D6A400", "#6E0B75"),
              ylim = c(0, max(num_nodes, num_links) * 1.3))
text(bp_nodes_links, c(num_nodes, num_links) / 2,
     labels = c(num_nodes, num_links), col = "white", cex = 1.2)
```



2.5 What is the average degree in the network? And the standard deviation of the degree?

We start with calculating the number of connections (links) for each node in the network. The degree function helps us count the number of incoming and outgoing links. This choice is due to the fact that the network is not a directed one (which means that connections go both ways, aka it takes two to tango).

Results show us that, on average, each Marvel character has about 2 (1.977143) partnerships.

As for the standard deviation, the number of partnerships per character typically differs from the average by 1.5 (1.54012). This implies that some characters have more or fewer partnerships by 1.5, which tells us that the number does not vary wildly.

```r
# calculating degrees, average links and standard deviations

degrees <- degree(marvel_network, mode = "all")
avg_degree <- mean(degrees)
std_dev_degree <- sd(degrees)

# results
cat("Average degree:", avg_degree, "\nStandard deviation:",
    std_dev_degree, "\n")
```

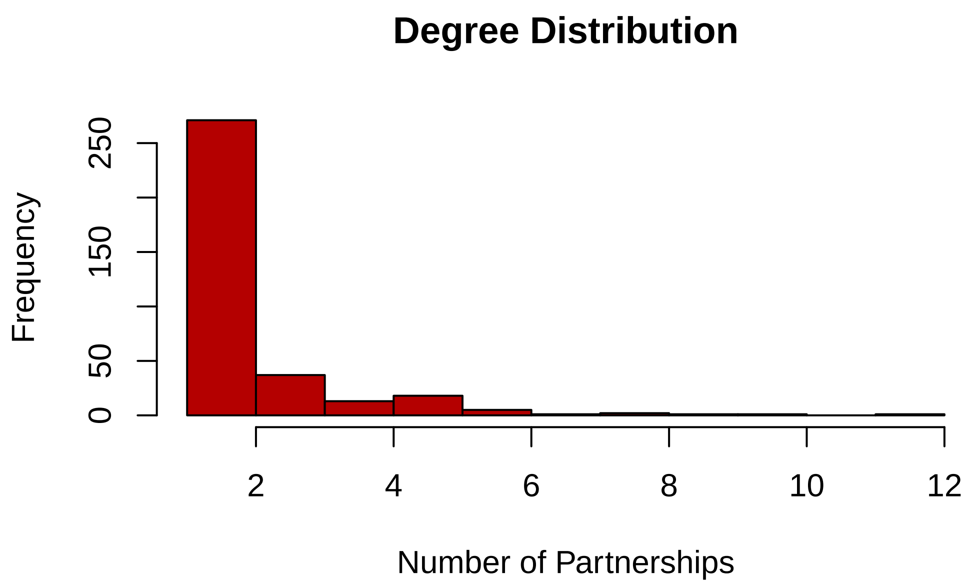
```
Average degree: 1.977143
Standard deviation: 1.54012
```

2.6 Plot the degree distribution in linear-linear scale and in log-log-scale. Does it have a typical connectivity? What is the degree of the most connected node?

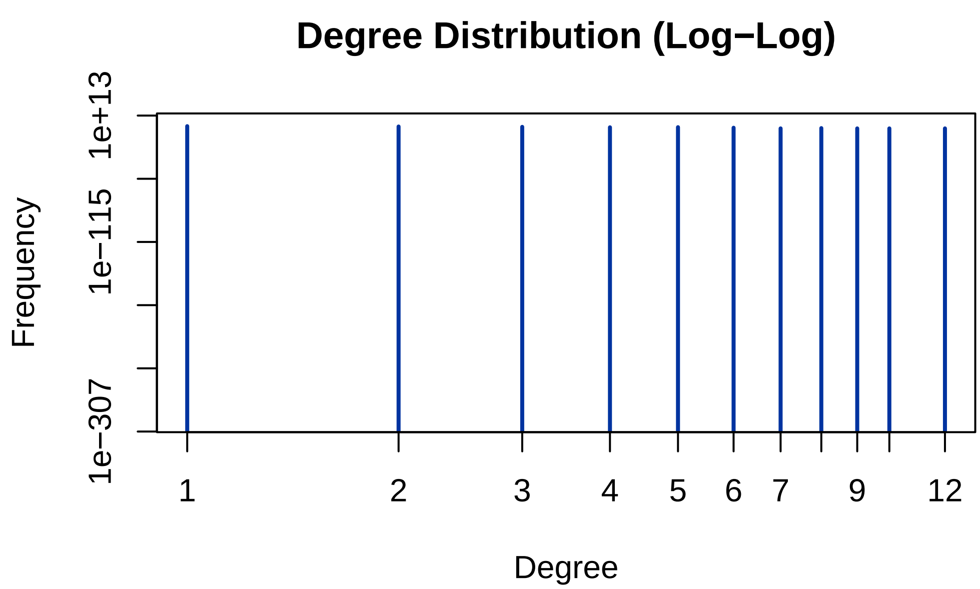
Linear-linear scale shows how many nodes have each degree on regular scales. There is a sharp peak around the lower numbers of partnerships (1,2,3, and 4) with a long tail all the way towards 12, showing us the maximum number of partnerships possessed by a single character. The right-skewed distribution implies an uneven distributiin of partnerships. An interesting finding from this plot is that the number of characters with 4 partnerships is greater than that of characters with 3 partnerships.

The log-log plot of the degree distribution shows a scattered pattern, rather than a straight line, indicating that the network does not follow a power-law distribution typical of scale-free networks. Instead, the degrees (1 to 12) suggest a more random or even connectivity pattern among the characters. This also means that there are no dominant hubs.

```r
# we previously calculated the degrees for all nodes:

# print(degrees)

# distribution of partnership numbers (linear-linear)

degrees <- degree(marvel_network, mode = "all")
hist(degrees, main = "Degree Distribution",
     xlab = "Number of Partnerships", col = "#B40000")
```




```
# log-log

plot(table(degrees), log = "xy", main = "Degree Distribution (Log-Log)",
     xlab = "Degree", ylab = "Frequency", pch = 16, col = "#0033A0")
```




```
max_degree <- max(degrees)
```

2.7 What is the clustering coefficient (transitivity) in the network?

Transitivity measures how often nodes' neighbors are also connected. The transitivity value of 0.2194149 indicates that the network is more spread out than being tightly knit.

```
clustering_coeff <- transitivity(marvel_network, type = "global")

#results
cat("Clustering coefficient:", clustering_coeff, "\n")
```

```
Clustering coefficient: 0.2194149
```

2.8 What is the assortativity (degree) in the network?

Assortativity measures if nodes with similar degrees connect (positive value) or if high-degree nodes connect to low-degree ones (negative value).

As explained earlier, we use 'directed = FALSE' because our network is bidirectional, meaning that a link (partnership) requires two parties.

The result (assortativity degree of -0.011047) shows that in the Marvel network, characters with high numbers of partnerships slightly tend to connect with those with fewer partnerships, but the effect is very weak (because it is very close to 0), almost random.

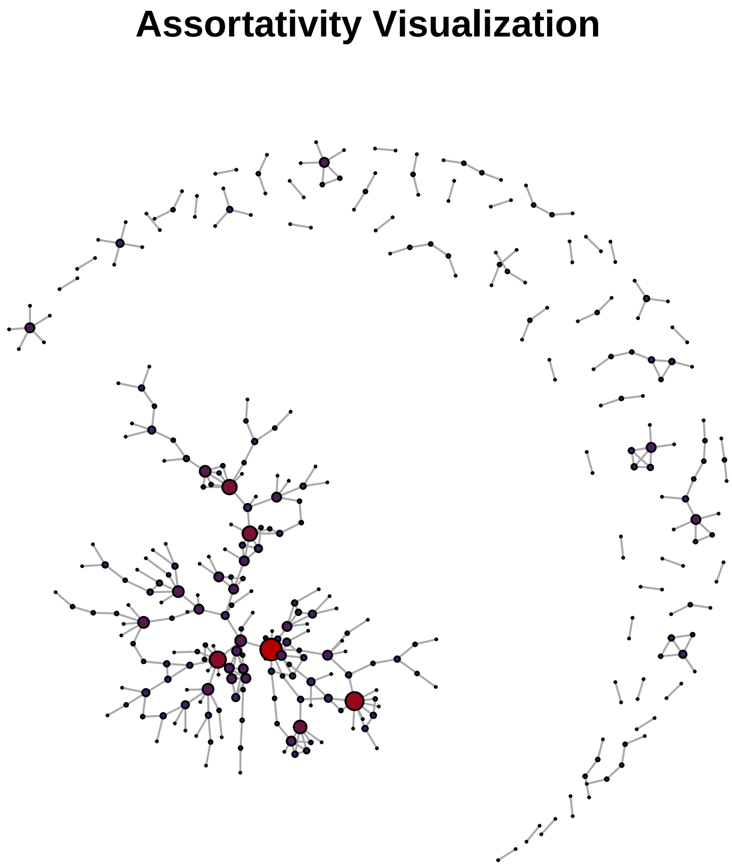
```
assortativity_degree <- assortativity_degree(marvel_network, directed = FALSE)

# result
cat("Assortativity (degree):", assortativity_degree, "\n")
```

```
Assortativity (degree): -0.011047
```

Visually:

```
V(marvel_network)$degree <- degree(marvel_network, mode = "all")

# Plot with igraph using a different layout
plot(marvel_network,
     layout = layout_with_kk(marvel_network),  # kamada-kawaii layout
     vertex.size = V(marvel_network)$degree / 2,
     vertex.color = colorRampPalette(c("#0033A0",
                                       "#B40000"))(max(V(marvel_network)$degree) + 1)[V(marve
```

```
    vertex.label = NA,
    edge.alpha = 0.5,
    main = "Assortativity Visualization")
```



2.9 Using the Louvain method, does the network have a community structure?

Initially we wanted to check if there's a community structure with and without edge weights. However, our network is not one that shows the strength or times of occurrence of edges, rather, it only shows the number of partnerships that existed at some point. That is why we decided to assess the community structure with 'weights = NULL'.

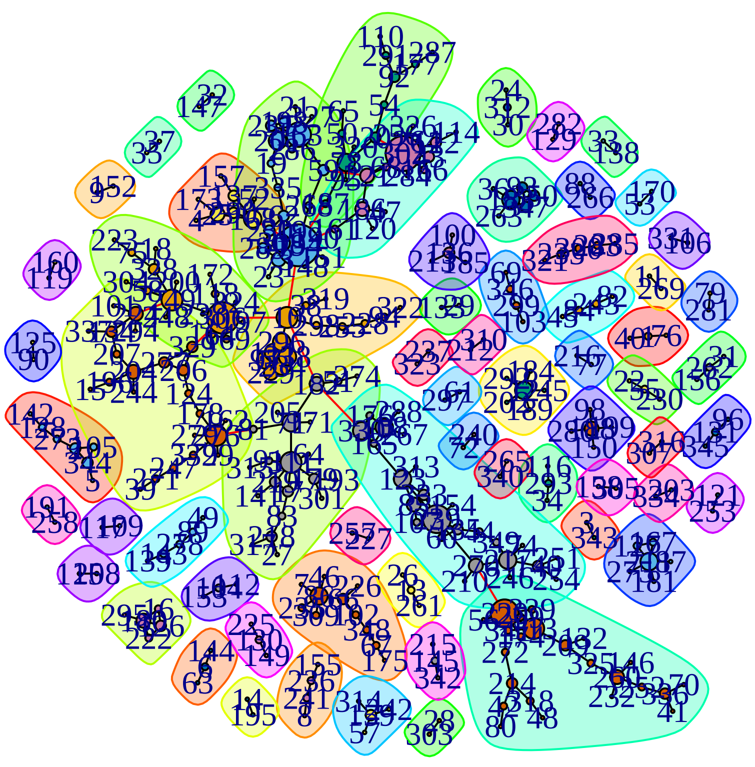
So, yes, the network exhibits a clear community structure, as shown in the plot where nodes are grouped into distinct clusters with distinct colors and labeled IDs, indicating that characters form close groups with more internal connections than external ones, a hallmark of community structure.

```
set.seed(616)
comm_without_weights <- cluster_louvain(marvel_network,weights=NULL)

sizes(comm_without_weights)
```

```
Community sizes
 1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26
 3  7  2  8  3 11  4  2 14  2  6  3  2 23  5 21 17 22 13  3  3  2  2  3  2  2
27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52
 3  2  6 23 15 25  4  5  2  4  2  4  2  2  2  6  2  2  3  5  4  3  2  2  2  2
53 54 55 56 57 58 59 60 61 62 63 64 65
 2  2  3  3  2  2  2  2  2  5  2  2  2
```

Plotting the community structure

```
plot(comm_without_weights, marvel_network)
```

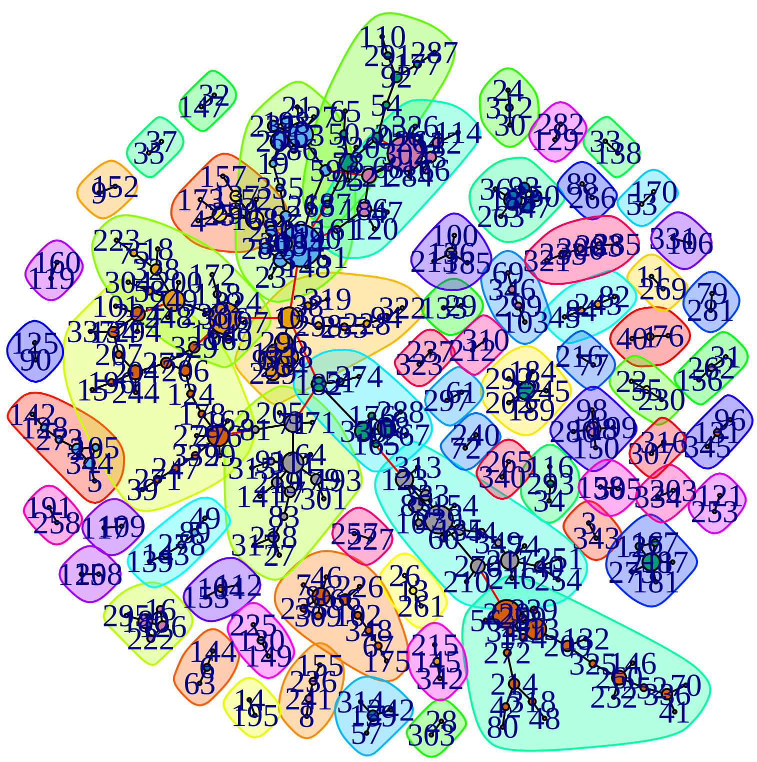


Let's check the community structure with weights just in case. Results are pretty much the same. Does this most probably imply that the network does not suit for a weighted assessment of community structure?

```r
comm_with_weights <- cluster_louvain(marvel_network,
                                     weights = E(marvel_network)$size)
sizes(comm_with_weights)
```

```
Community sizes
 1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26
 3  7  2  8  3 11  4  2 14  2  6  3  2 23  5 18 17 22 13  3  3  2  2  3  2  2
27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52
 3  2  6 23 15 19  4  5  9  2  4  2  4  2  2  2  6  2  2  3  5  4  3  2  2  2
53 54 55 56 57 58 59 60 61 62 63 64 65 66
 2  2  2  3  3  2  2  2  2  2  5  2  2  2
```

```r
# plotting

plot(comm_with_weights, marvel_network)
```



2.10 If so, what is its modularity?

The modularity score of 0.9116242 indicates a very strong community structure in the Marvel network, as values close to 1 suggest that the Louvain method found highly distinct groups where characters are much more connected within their communities than expected in a random network.

This aligns with the visual clustering in our plot, confirming that the network has well-defined, meaningful communities.

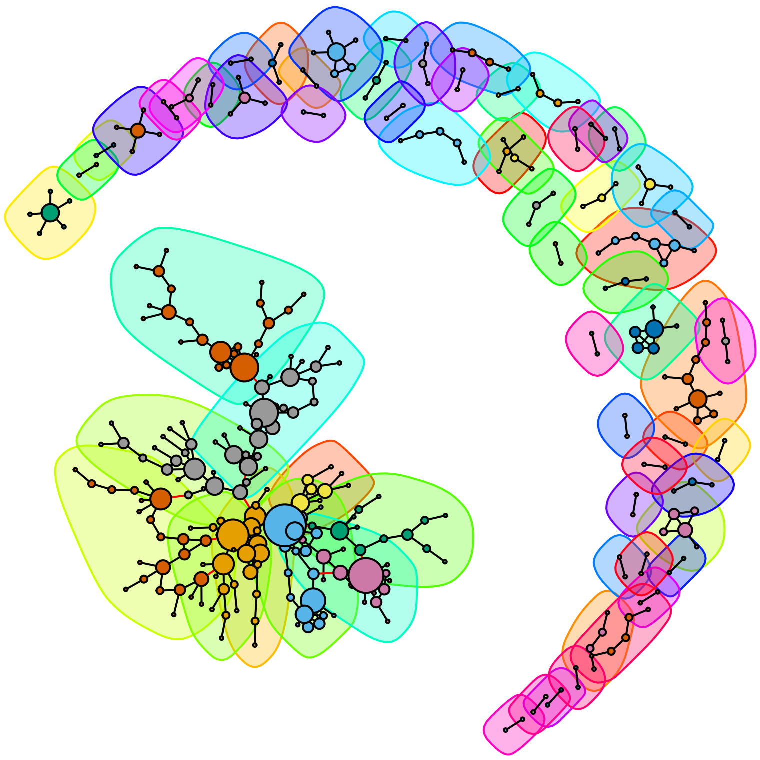
```
set.seed(616)
modularity(comm_without_weights)
```

```
[1] 0.9116242
```

Below plot visualizes the network with communities from comm_without_weights, using the Kamada-Kawai layout ll, coloring nodes by community, and omitting vertex labels for clarity.

The Kamada-Kawai layout tries to put characters closer if they're partners and further apart if they're not, making the plot and structure easier to understand.

```
ll <- layout.kamada.kawai(marvel_network)
plot(comm_without_weights,marvel_network,layout=ll,vertex.label="")
```



2.11 Test that the clustering coefficient in the network cannot be statistically explained by a configuration model in which the nodes have the same degree distribution as the original.

After generating a degree-preserving rewired version of the Marvel network across 100 random times, we find that the clustering coefficient drops from 0.219 (the original Marvel network clustering coefficient) to 0.006382979 (the mean of the simulated clusterings). The p-value of 0 feels fishy in the beginning, however, it only indicates that none of the simulations were as high as or higher than the original one.

This significant decrease suggests that the clustering structure observed in the real network is not explained by the degree distribution alone. Instead, it reflects meaningful group structures, such as narrative teams or recurring character associations in the Marvel universe.

The original Marvel network has much higher clustering than its degree-preserving random counterpart: characters that are connected to the same person tend to be connected to each other — suggesting intentional grouping or narrative structure (such as teams like Avengers or X-Men).

In the rewired version, where the number of connections for each character is preserved but partners are randomized, that natural tendency disappears.

```
set.seed(616)

sim_clustering <- replicate(100, {
  g_rewired <- rewire(marvel_network,
                      with = keeping_degseq(niter = ecount(marvel_network) * 10))
  transitivity(g_rewired, type = "global")
})

observed_clustering <- transitivity(marvel_network, type = "global")

# computing p-value, meaning the proportion of simulated clustering   observed)
p_val <- mean(sim_clustering >= observed_clustering)

cat("Observed clustering:", observed_clustering, "\n")
```

```
Observed clustering: 0.2194149
```

```
cat("Mean simulated clustering:", mean(sim_clustering), "\n")
```

```
Mean simulated clustering: 0.006382979
```

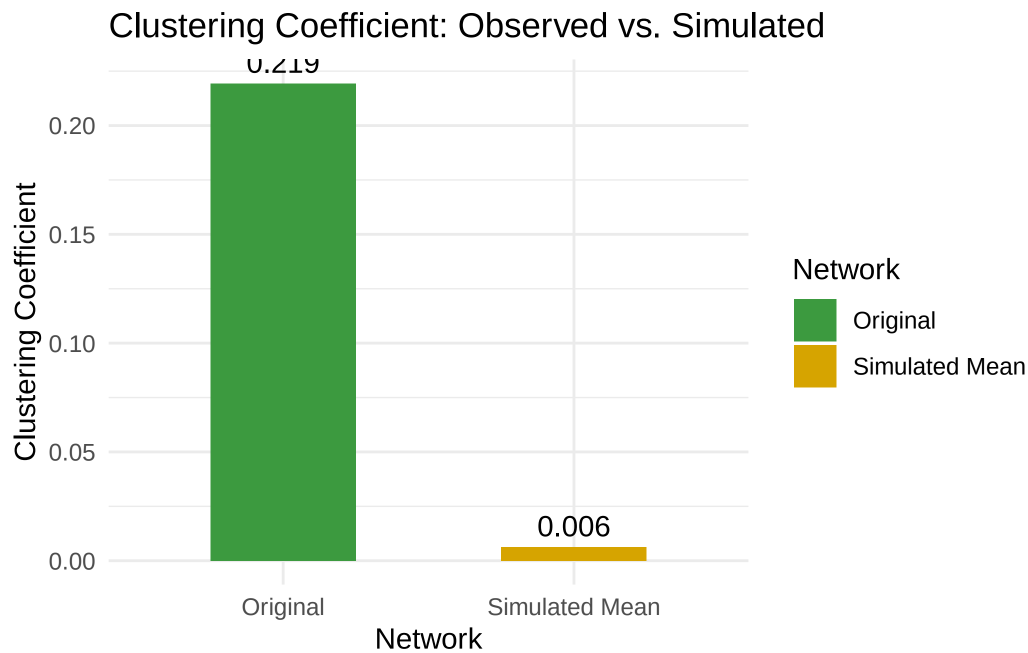
```
cat("p-value:", p_val, "\n")
```

```
p-value: 0
```

2.11.1 Comparing the two networks

```
data <- data.frame(
  Network = c("Original", "Simulated Mean"),
  Clustering = c(observed_clustering, mean(sim_clustering))
)

ggplot(data, aes(x = Network, y = Clustering, fill = Network)) +
  geom_col(width = 0.5) +
  geom_text(aes(label = round(Clustering, 3)), vjust = -0.5) +
  scale_fill_manual(values = c("Original" = "#3C9A3F",
                               "Simulated Mean" = "#D6A400")) +
  labs(title = "Clustering Coefficient: Observed vs. Simulated",
```

```
      y = "Clustering Coefficient") +
  theme_minimal()
```



2.12 Visualize the neighborhood of the node with the largest centrality (closeness).

igraph package has several ways to calculate centrality of nodes and edges. Let's try them and see how the results differ.

2.12.1 PageRank: calculates Google's PageRank for vertices

Below chunk calculates the PageRank scores for nodes in marvel_network, which measures node importance based on connections — nodes with more links from other important nodes get higher scores.

The results show Spider-Man, Captain America, Red Skull, Selene, Unicorn, and Grim Reaper as the top 6, indicating they are the most influential characters in the network, likely due to their connections to other highly connected characters, such as Spider-Man and Captain America linking to many key Avengers or Red Skull to major villains.

```r
# pageRank centrality computation
page_rank_marvel <- page_rank(marvel_network)

# top characters

top_pr <- page_rank_marvel$vector %>%
  sort(decreasing = TRUE) %>% head()

data.frame(
  character_name = V(marvel_network)$character_name[as.numeric(names(top_pr))],
  page_rank = top_pr
)
```

```
     character_name   page_rank
194       Spider-Man 0.010885939
302 Captain America 0.010575984
306        Red Skull 0.009778847
12            Selene 0.008108108
220          Unicorn 0.007716852
276      Grim Reaper 0.007562538
```

2.12.2 Closeness: distance (steps) to any other vertex

Closeness calculates the closeness centrality for each node in the network, measuring how close a node is to all others. Higher values mean closer, fewer steps to reach others.

The results, with closeness of 1 for Silver Sable, U.S. Agent, Hercules, Sabretooth, Mojo, and Trevor Fitzroy, indicate these characters have the highest closeness, meaning they are in small, isolated components, where they are directly connected to all others in their component, inflating their scores. We consider that these characters have perfect centrality scores because the closeness method assesses their local communities, rather than the network as a whole.

```r
# closeness  computation
closeness_marvel <- closeness(marvel_network)

# to get the top characters

top_closeness <- 1/closeness_marvel %>% sort(decreasing = TRUE) %>% head()
data.frame(
  character_name = V(marvel_network)$character_name[as.numeric(names(top_closeness))],
  inverse_closeness = top_closeness
)
```

```
   character_name inverse_closeness
3    Silver Sable                 1
9      U.S. Agent                 1
11       Hercules                 1
14     Sabretooth                 1
28           Mojo                 1
29 Trevor Fitzroy                 1
```

Betweenness method looks into the number of shortest paths going through an edge.

The results show Venom, Doctor Doom, Spider-Man, Puppet Master, Krang, and Attuma as the top six characters, meaning they are key bridges in the network, frequently connecting other characters.

```r
# betweenness centrality computation
betweenness_marvel <- betweenness(marvel_network)

# top characters
top_betweenness <- betweenness_marvel %>% sort(decreasing = TRUE) %>% head()
data.frame(
  character_name = V(marvel_network)$character_name[as.numeric(names(top_betweenness))],
  betweenness = top_betweenness
)
```

```
    character_name betweenness
10           Venom    10704.50
182    Doctor Doom     9108.00
194     Spider-Man     7904.25
330  Puppet Master     6461.50
123          Krang     5739.00
239         Attuma     5361.50
```

2.12.2.1 Harmonic Centrality

As suggested, we decided to calculate the harmonic centrality for our characters in the network. We did so using the harmonic_centrality function from the igraph package. Harmonic centrality is a measure that gives higher scores to nodes that are closer to other nodes in the network. It is particularly useful in networks where shortest path calculations are important.

Below are the top 6 characters by harmonic centrality scores.

```r
library(tidygraph)
# harmonic centrality
cent_harmonic <- harmonic_centrality(marvel_network)

centrality_df <- data.frame(
  character_name = V(marvel_network)$character_name,
  harmonic_centrality = harmonic_centrality(marvel_network)
)

top_harmonic <- centrality_df[order(-centrality_df$harmonic_centrality), ][1:6, ]
print(top_harmonic)
```

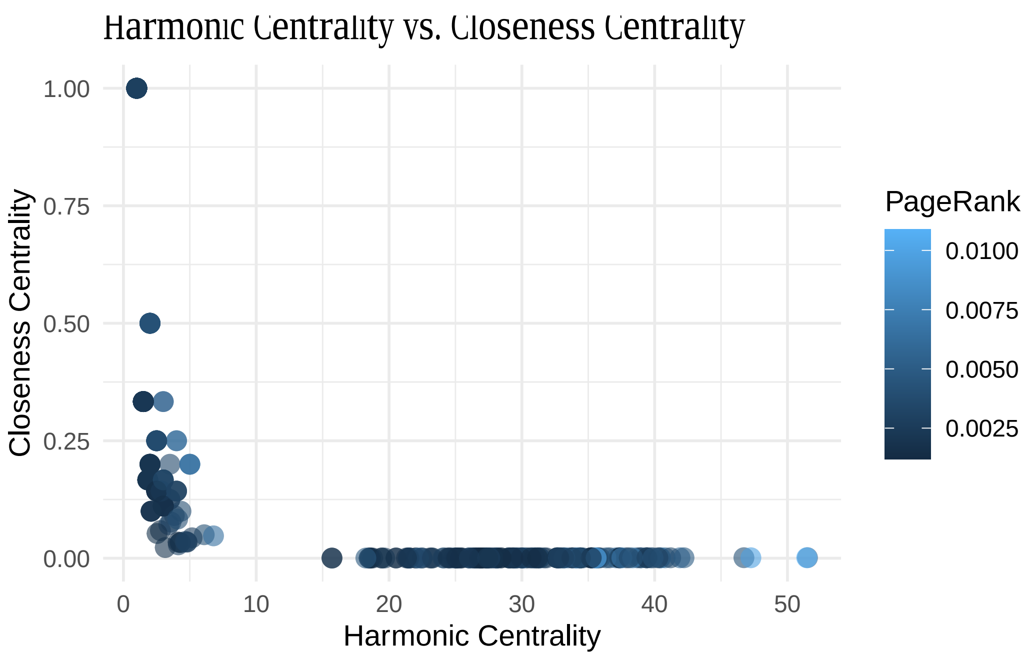
```
    character_name harmonic_centrality
10           Venom            51.50792
194      Spider-Man           51.45044
306       Red Skull           47.24529
182     Doctor Doom           46.72146
330  Puppet Master            42.20920
71      Enchantress           41.90316
```

We can use a scatter plot or a bar plot to visualize the harmonic centrality of nodes. We used a scatter plot with ggplot2 to compare harmonic centrality with other centrality measures.

This plot compares harmonic centrality with closeness centrality, with nodes colored by their PageRank. This allows us to see how these centrality measures relate to each other. Nodes with high harmonic centrality and closeness centrality are likely important connectors in the network.

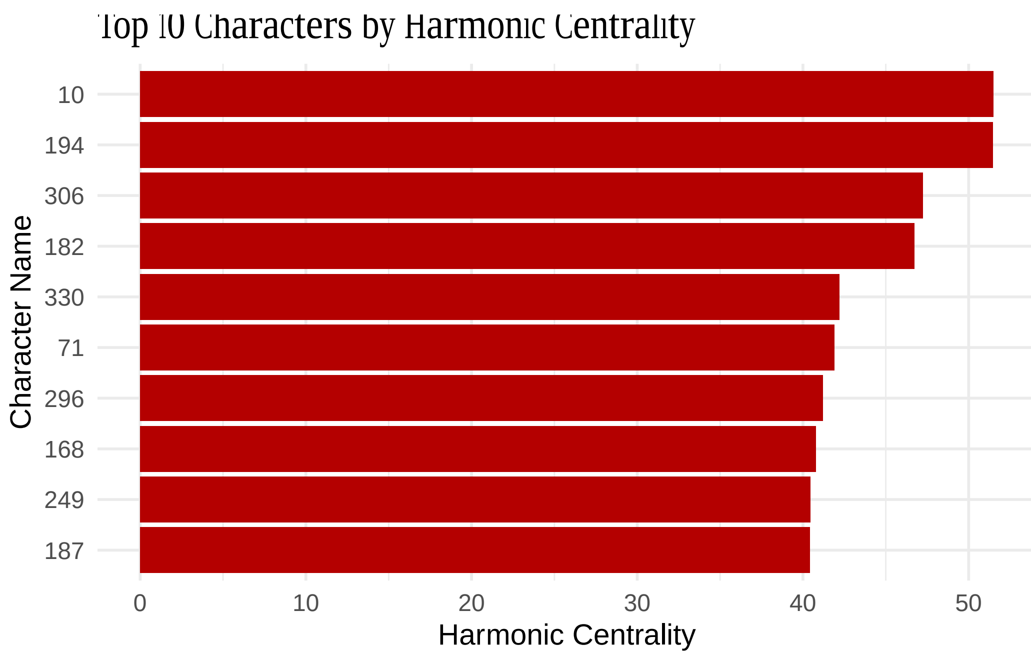
```r
centrality_df <- data.frame(
  character_name = V(marvel_network)$name,
  harmonic_centrality = harmonic_centrality(marvel_network),
  closeness = closeness(marvel_network),
  page_rank = page_rank(marvel_network)$vector
)


# harmonic centrality vs. other centrality measures
ggplot(centrality_df, aes(x = harmonic_centrality,
                          y = closeness, color = page_rank)) +
  geom_point(alpha = 0.6, size = 3) +
  labs(title = "Harmonic Centrality vs. Closeness Centrality",
       x = "Harmonic Centrality",
```

```r
         y = "Closeness Centrality",
         color = "PageRank") +
  theme_minimal() +
  theme(plot.title = element_text(family = "Marvel", size = 16))
```



Alternatively, we can visualize the top nodes by harmonic centrality through a bar plot. This plot shows the top 10 characters by harmonic centrality, allowing us to easily identify the most central nodes.

```r
# top nodes by harmonic centrality
top_harmonic_plot <- centrality_df[order(-centrality_df$harmonic_centrality), ][1:10, ]

ggplot(top_harmonic_plot, aes(x = reorder(character_name, harmonic_centrality),
                              y = harmonic_centrality)) +
  geom_bar(stat = "identity", fill = "#B40000") +
  coord_flip() +
  labs(title = "Top 10 Characters by Harmonic Centrality",
       x = "Character Name",
       y = "Harmonic Centrality") +
  theme_minimal() +
  theme(plot.title = element_text(family = "Marvel", size = 16))
```



2.12.3 The neighbourhood of the most central node - VENOM

According to our harmonic centrality measure, Venom is the most central character in the entire Marvel network. Indeed, if we zoom in even on his 1-step neighbourhood, we see that he formed partnerships with different type of characters such as heroes (Spider-Man), villains (Red Skull, Doctor Doom, Carnage), and neutral characters (Magneto, Eddie Brock).

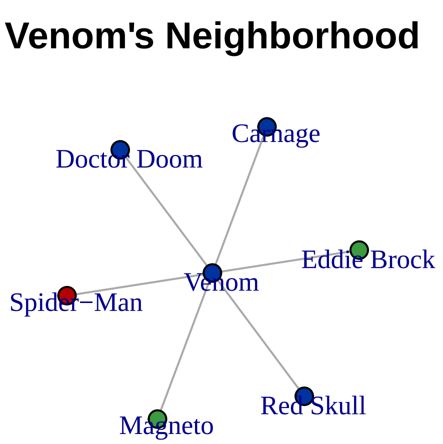
Note that Eddie Brock is the human form of Venom, who is considered to be (or to have become) a neutral/antihero character.

```
# venom's id
venom_id <- marvel_nodes$id[marvel_nodes$character_name == "Venom"]
print(venom_id)
```

```
[1] 10
```

```
# detecting the node
venom_node <- which(V(marvel_network)$name == as.character(venom_id))

# venom's neighbourhood
venom_neighborhood <- ego(marvel_network, order = 1, nodes = venom_node,
                          mode = "all")[[1]]
```

```r
# venom's subgraph
venom_subgraph <- induced_subgraph(marvel_network, venom_neighborhood)

# ensuring nodes are represented with names
V(venom_subgraph)$label <-
  marvel_nodes$character_name[match(V(venom_subgraph)$name, marvel_nodes$id)]

node_groups <- marvel_nodes$group[match(V(venom_subgraph)$name, marvel_nodes$id)]

node_groups <- as.numeric(node_groups)

#  group colors
group_colors <- c("0" = "#B40000", "1" = "#0033A0", "2" = "#3C9A3F")

# group values to colors
vertex_colors <- group_colors[as.character(node_groups)]

# plotting venom's neighbourhood
plot(venom_subgraph,
     layout = layout_with_fr(venom_subgraph),
     vertex.label = V(venom_subgraph)$label,
     vertex.label.cex = 0.8,
     vertex.label.dist = 1.2,
     vertex.label.degree = pi/4,
     vertex.color = vertex_colors,
     vertex.size = 12,
     main = "Venom's Neighborhood",
     margin = -0.05)
```



2.12.3.1 Comparison

To visually support our choices regarding the different centrality measures, we wanted to create a plot to highlight how each measure ranks the characters in the network.

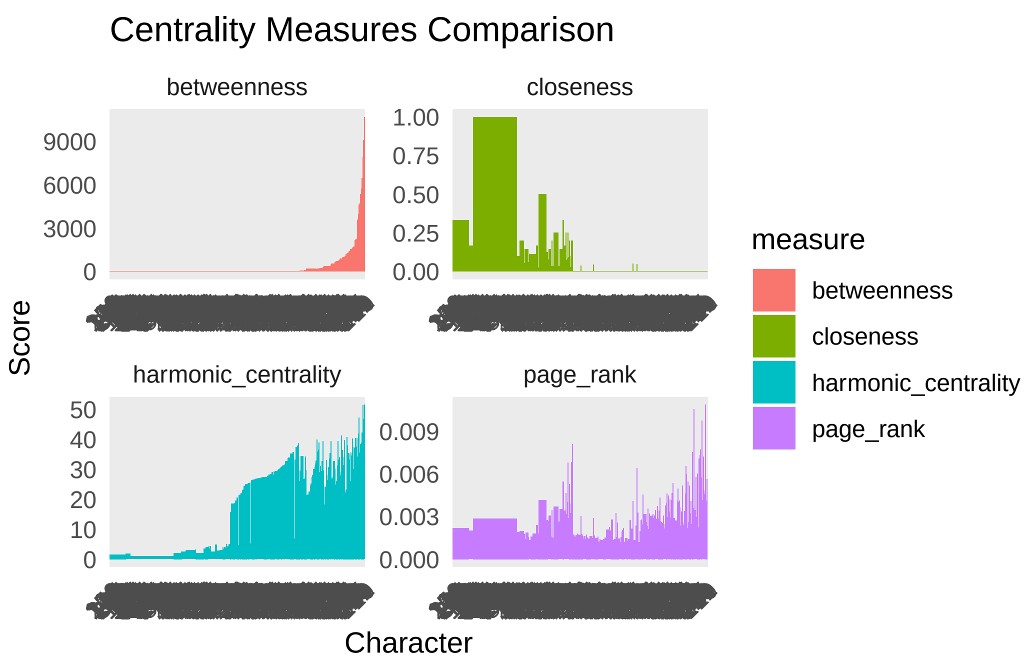
This visualization helped us gain a comprehensive understanding of how different centrality measures rank the characters in our network and how these measures relate to each other.

A bar plot can be used to compare the rankings of characters across different centrality measures. This can help identify which characters are most central according to each measure.

Although some of the labels are not read properly, we can, by looking at the distributions, say that betweenness method yields confusing results by attributing no centrality to most characters whereas closeness method detects most characters as having a centrality score of 1 (which is the perfect score). This is due to the fact that closeness method sometimes assesses characters based on their local communities in the network, rather than the network as a whole, therefore spotting perfect centrality.

Harmonic centrality and PageRank methods seem to provide more robust results, assigning a range of centrality scores across characters. We, upon the suggestion of the Professor, decided earlier to use harmonic centrality to answer the question of most central node and its neighbourhood.

```r
centrality_df$betweenness <- betweenness(marvel_network)

# adjusting the data for plotting
centrality_long <- pivot_longer(centrality_df,
                                cols = c("betweenness", "page_rank",
                                         "closeness",
                                         "harmonic_centrality"),
                                names_to = "measure", values_to = "score")

# plot
ggplot(centrality_long, aes(x = reorder(character_name, score),
                            y = score, fill = measure)) +
  geom_bar(stat = "identity", position = "dodge") +
  facet_wrap(~ measure, scales = "free") +
  labs(title = "Centrality Measures Comparison", x = "Character",
       y = "Score") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```


Centrality Measures Comparison
betweenness
closeness
harmonic_centrality
page_rank
9000
6000
3000
0
1.00
0.75
0.50
0.25
0.00
50
40
30
20
10
0
0.009
0.006
0.003
0.000
Score
Character
measure
betweenness
closeness
harmonic_centrality
page_rank