Appendix Team 3 Quantum_Computing

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This R Markdown file will be provided as appendix to the final report of Team 3. Refering this appendix will follow the format of (Appendix I-"outline item of Markdown file"). For example, refering the code of Hypothesis 2 will display as following in the report: (Appendix I-1.2). Please use a browser to interpret the html file.

0. Install & import packages

Install

```
required_packages <- c("tibble", "dplyr", "tidyr", "tidyverse", "igraph", "
    qgraph", "stringr", "ggplot2", "visNetwork", "data.table", "centiserve", "
    reshape2", "remotes", "ggcorrplot")

to_install_packages <- required_packages[!(required_packages %in% installed.
    packages()[,"Package"])]

if(length(to_install_packages)) invisible(install.packages(to_install_packages
    , dependencies = TRUE))

remotes::install_github("clementviolet/omnivor")
```

Import

```
required_packages <- c("tibble", "dplyr", "tidyr", "tidyverse", "igraph", "
    qgraph", "stringr", "ggplot2", "visNetwork", "data.table", "centiserve", "
    reshape2", "ggcorrplot")

invisible(lapply(required_packages, require, character.only = T))
```

1. Data collection & cleaning

Data set is given and contains patents regarding quantum computing.

1.1 Import data

```
df_qc <- read.csv("Quantum␣computing.csv", sep=";")
```

1.2 Clean Data

```
# Drop Rows where Inventors, Applicants or IPC classes or empty or NA
df_qc <- df_qc[!(is.na(df_qc$IPC) | df_qc$IPC==""), ]
df_qc <- df_qc[!(is.na(df_qc$Inventors) | df_qc$Inventors==""), ]
df_qc <- df_qc[!(is.na(df_qc$Applicants) | df_qc$Applicants==""), ]

# df_qc gets transformed where each row represents an inventor
df_qc <- df_qc %>%
  mutate(Inventors=strsplit(Inventors, "\n")) %>%
  unnest(Inventors)

# Clean Inventors & Applicants: Needed to adapt the igraph object cleaning
df_qc$Inventors <- gsub(" ", "_", df_qc$Inventors)
df_qc$Inventors <- gsub("-", ".", df_qc$Inventors)
df_qc$Inventors <- chartr("[]", "..", df_qc$Inventors)
df_qc$Inventors <- chartr("<>", "..", df_qc$Inventors)
df_qc$Applicants <- gsub(" ", "_", df_qc$Applicants)
df_qc$Applicants <- sub("_$", "", df_qc$Applicants)
df_qc$Applicants <- gsub("-", ".", df_qc$Applicants)
df_qc$Applicants <- chartr("[]", "..", df_qc$Applicants)
df_qc$Applicants <- chartr("<>", "..", df_qc$Applicants)

# Replace _ if its last character
df_qc$Inventors <- sub("_$", "", df_qc$Inventors)

# df_qc gets transformed where each row represents an applicant in connection
   with each inventor
df_applicants_qc <- df_qc %>%
  mutate(Applicants=strsplit(Applicants, "\n")) %>%
  unnest(Applicants)
```

2. Create necessary objects

2.1 Create the edge list

```
edge_list <- df_qc %>%
  select(Inventors, Title, Applicants, No) %>%
  inner_join(., select(., Inventors, No), by="No") %>%
  filter(Inventors.x != Inventors.y) %>%
  unique %>%
  arrange(Title, No)

# Include the patents, where there is only one author
for (i in 1:nrow(df_qc)){
  row <- df_qc[i,]
  if(sum(df_qc$No == row$No) == 1){
    edge_list[nrow(edge_list) + 1,] <- list(row$Inventors, row$Title, row$
        Applicants, row$No, row$Inventors)
```

```r
  }
}

#rename to columns
names(edge_list)[names(edge_list) == "Inventors.x"] <- "from"
names(edge_list)[names(edge_list) == "Inventors.y"] <- "to"

# Selecting of applicant type is based on the majority of type occurrences
identify_applicant_type <- function(x){
  industrial <- "_INC_|INC_|LLC_|_LLC_|_CORP_|_CORPORATION_"
  academic <- "UNIV_|_UNIV_|INST_|_INST_"
  if(grepl(industrial, x)){
    return("industrial")
  }else{
    if(grepl(academic, x)){
      return("academic")
    }else{
      return("private")
    }
  }
}

edge_list$group <- NA

for (i in 1:nrow(edge_list)){
  row <- edge_list[i,]
  edge_list[i,"group"] <- identify_applicant_type(row$Applicants)
}
```

2.2 Create the edge matrix

```r
unique_nodes <- unique(c(edge_list$from, edge_list$to))
edges_length <- length(unique_nodes)

edge_matrix <- matrix(, nrow = edges_length, ncol = edges_length, dimnames =
    list(unique_nodes, unique_nodes))

edge_matrix[is.na(edge_matrix)] = 0

for(i in 1:edges_length) {
  prim_inventor <- edge_list[[i,"from"]]
  sec_inventor <- edge_list[[i,"to"]]
  edge_matrix[prim_inventor,sec_inventor] <- edge_matrix[prim_inventor,sec_
      inventor] + 1
}

rm(list=c("prim_inventor","sec_inventor", "i"))
```

2.3 Create the graph object

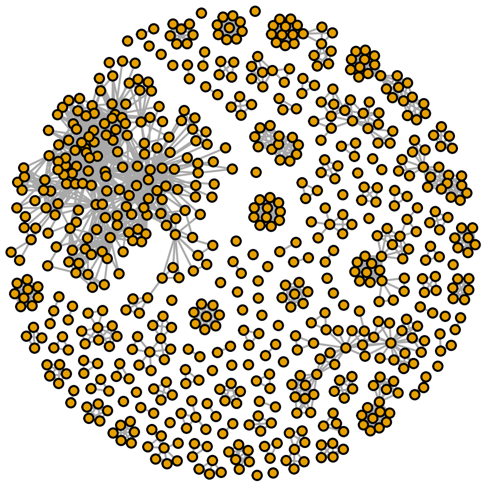
```
df_visNetwork <- data.frame(from=edge_list$from, to=edge_list$to)
network_graph <- graph_from_data_frame(
  df_visNetwork,
  directed = FALSE)  %>%
  simplify(remove.loops = TRUE)
```

---

3. Network visualization

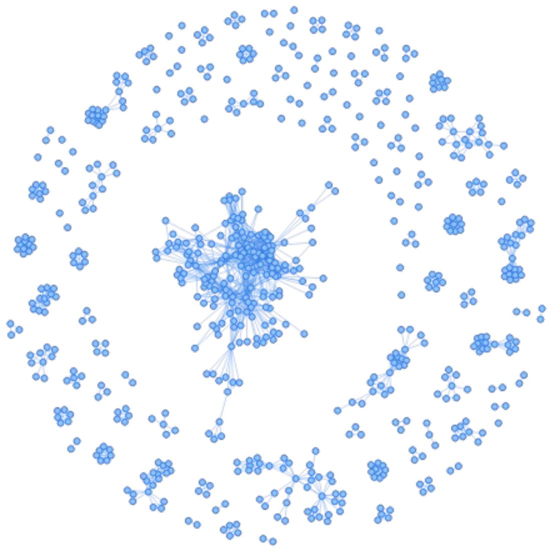
3.1 Preview of network graph with fruchtermanreingold Layout

```
# Use qgraph to plot large graphs
edge_list_from_igraph <- get.edgelist(network_graph,names=FALSE)

qgraph_layout_modified <- qgraph.layout.fruchtermanreingold(edge_list_from_
    igraph,vcount=vcount(network_graph), area=8*(vcount(network_graph)^2),
    repulse.rad=(vcount(network_graph)^3.1))

plot(network_graph,layout=qgraph_layout_modified,vertex.size=4,vertex.label=NA
    )
mtext("Network graph based on fruchtermanreingold layout", side=1)
```


Network graph based on fruchtermanreingold layout

3.2 Preview of network graph with visNetwork

```
vis_data <- toVisNetworkData(network_graph)
vis_network <- visNetwork(nodes = vis_data$nodes, edges = vis_data$edges)

vis_network %>%
  visEdges(arrows = list(to = list(enabled= FALSE)), length=30) %>%
  visIgraphLayout(layout = "layout_nicely")
```



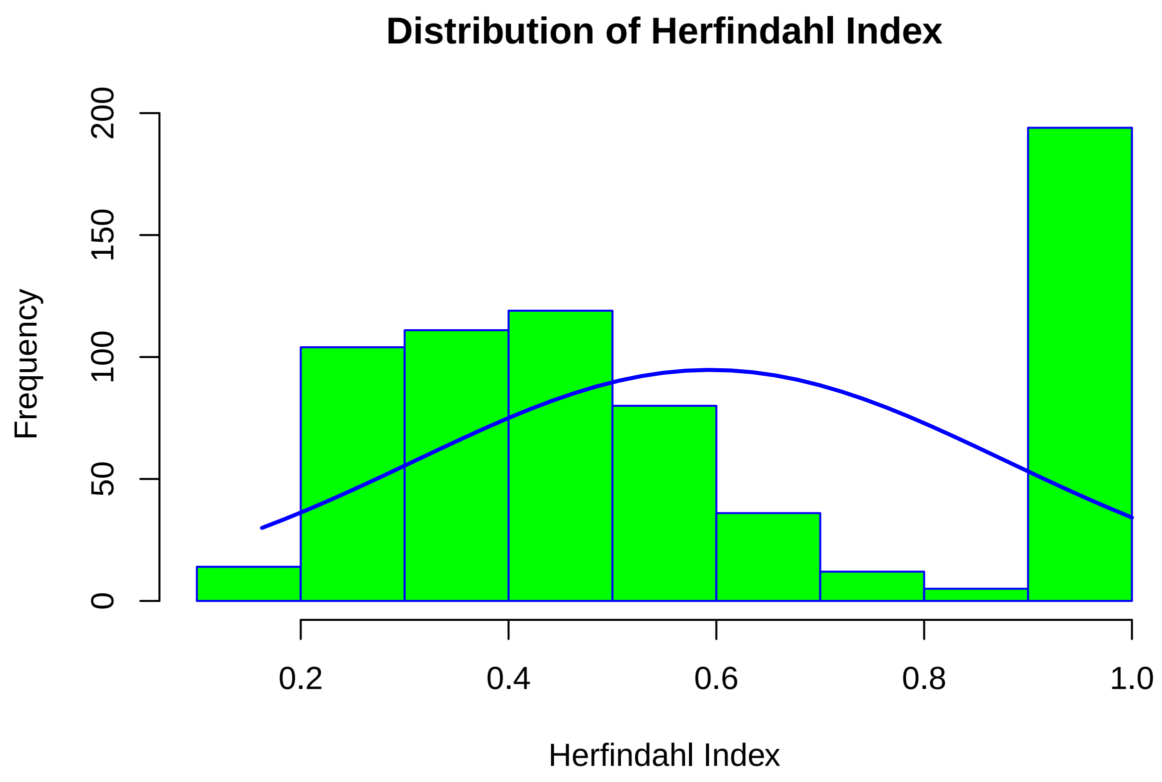
4. Answering Hypothesis

- **H1: We expect more generalists to adopt the broker role in a network than specialists.**

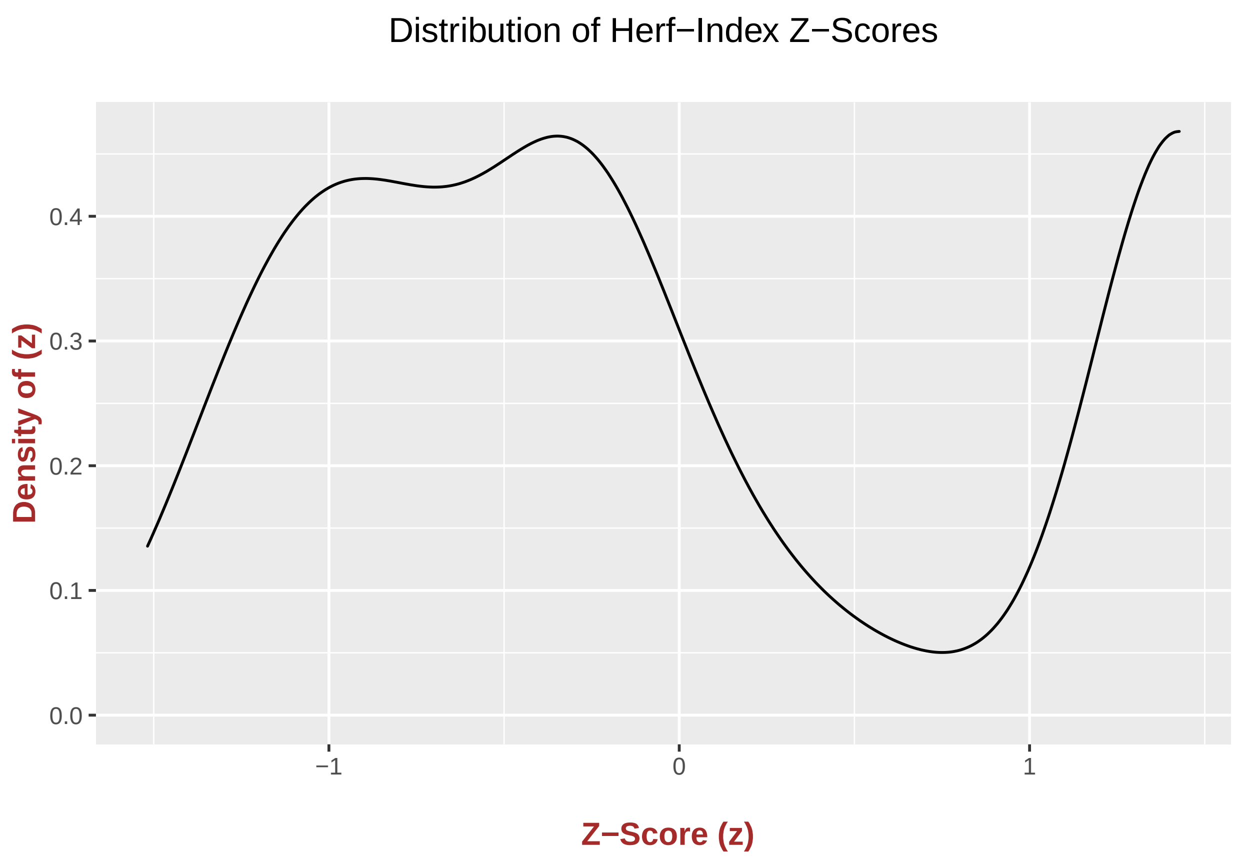
```
# Create data objects that are required for calculations
df_ipc_qc <- df_qc %>%
  mutate(IPC=strsplit(IPC, "\n")) %>%
  unnest(IPC)

df_ipc_qc$IPC <- substring(df_ipc_qc$IPC, 1, 4)

unique_inventors <- unique(df_ipc_qc$Inventors)

df_h1 <- data.frame(Inventor=unique_inventors, Betw_Centr = 0, Degree_Centr=0,
     Degree_Centr_ZScore = 0, Herf_Index = 0, Herf_Index_ZScore = 0, IsBroker=
    "NotBroker", Diversity_Type="None", Applicant_Type="", IsPeripheralPlayer=
    "NotPeripheralPlayer")
```

```
# Measure betweenness centrality for each inventor to determine the brokerage
library(omnivor)

##
## Attache Paket: 'omnivor'

## Die folgenden Objekte sind maskiert von 'package:igraph':
##
##     degree_distribution, diameter

betw_centr <- betweeness_centrality(network_graph, normalized=T) # normalized
    = T or F --> clarify
df_betw_centr <- data.frame(as.list(betw_centr))
t_df_betw_centr <- transpose(df_betw_centr)
t_df_betw_centr$Inventor <- colnames(df_betw_centr)

for(inventor in unique_inventors){
  sub_df_qc <- df_qc[df_qc$Inventors == inventor, ]
  if(nrow(sub_df_qc) > 1){
    centr <- t_df_betw_centr[t_df_betw_centr$Inventor == inventor, "V1"]
    df_h1[df_h1$Inventor == inventor, "Betw_Centr"] <- centr
  }
}

# Mark who is a broker
for(i in 1:nrow(df_h1)){
  row <- df_h1[i,]
  if((row$Betw_Centr > 0)){
    df_h1[df_h1$Inventor == row$Inventor, "IsBroker"] <- "Broker"
  }
}

# Calculate the Herf Index for each inventor
for(inventor in unique_inventors){
  df_ipc_qc_sub <- df_ipc_qc[df_ipc_qc$Inventors == inventor, ]
  ipc_table <- table(df_ipc_qc_sub$IPC)
  total_ipcs <- sum(ipc_table)
  table_as_df <- as.data.frame(ipc_table)
  herf_index <- 0
  for (i in 1:nrow(table_as_df)){
    row <- table_as_df[i,]
    val <- row$Freq
    herf_index <- herf_index + (val / total_ipcs)^2
  }
  df_h1[df_h1$Inventor == inventor, "Herf_Index"] <- herf_index
}

## Plot Herf Index distribution
# Histogram overlaid with kernel density curve
x <- df_h1$Herf_Index
h <- hist(x, main="Distribution␣of␣Herfindahl␣Index", xlab="Herfindahl␣Index",
     border="blue", col="green", freq=T, ylab = "Frequency")
```

```
xfit <- seq(min(x), max(x), length=40)
yfit <- dnorm(xfit, mean=mean(x), sd=sd(x))
yfit <- yfit * diff(h$mids[1:2])*length(x)
lines(xfit, yfit, col="blue", lwd=2)
```



```
# Pre calculations before identifying generalists or specialists
# Calculate Z scores
# z score tells you how far a value is from the average of the data in terms
    of standard deviations.
df_h1 <- df_h1 %>% mutate(Herf_Index_ZScore = (Herf_Index - mean(Herf_Index))/
    sd(Herf_Index))

# Plot Distribution of Herf-Index Z-Scores
ggplot(df_h1, aes(x = Herf_Index_ZScore)) +
  geom_density() +
  labs(x = "\n␣Z-Score␣(z)", y = "Density␣of␣(z)", title = "Distribution␣of␣
      Herf-Index␣Z-Scores\n") +
  theme(plot.title = element_text(hjust = 0.5),
        axis.title.x = element_text(face="bold", colour="brown", size = 12),
        axis.title.y = element_text(face="bold", colour="brown", size = 12))
```

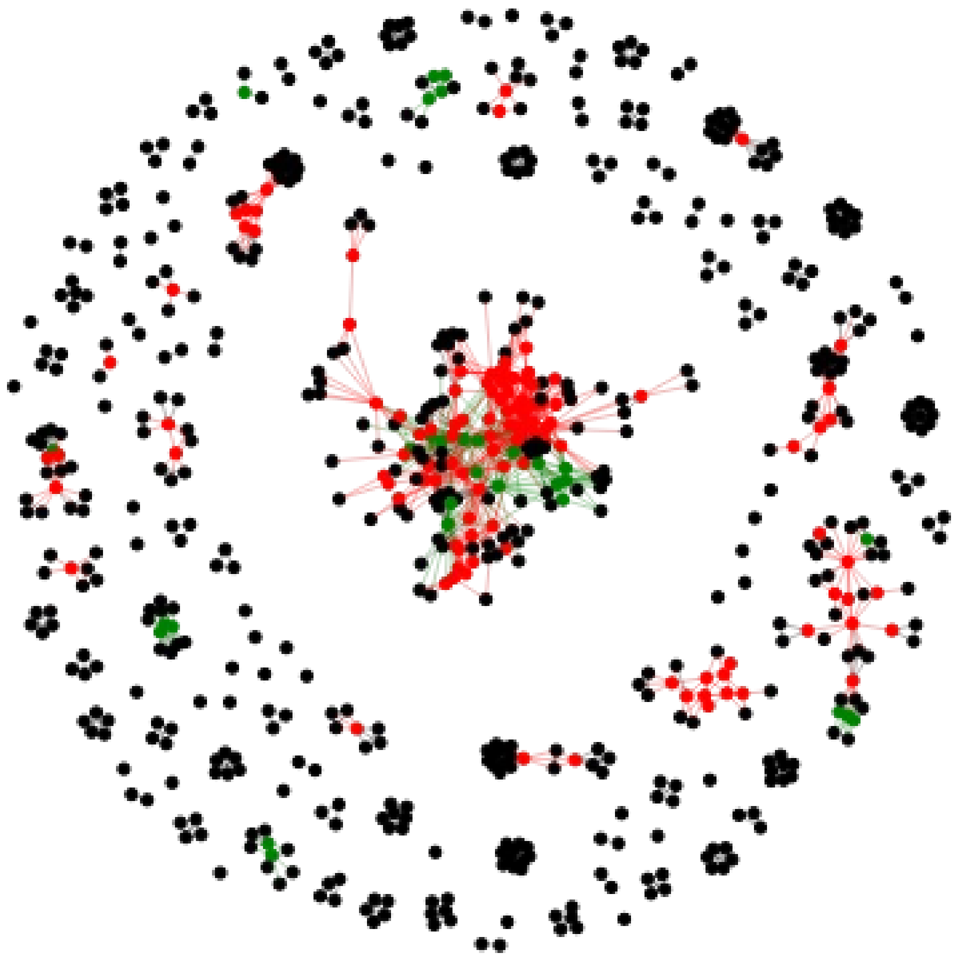


```
# Evaluate who is a Specialist
# H >= (Top 10% Herfindhal index z-score distribution)
# Calculate top 10%
# P(Z > c) = 0.1 ==> P(Z < c) = 0.9
# use linear interpolation to approximate nearest values
# For further information, see: https://socratic.org/questions/what-is-the-z-
    score-corresponding-to-the-top-10-percent-of-any-data-set
nearest_value_z_top10_roof <- 1.29 # Z score for 0.9015, Standard normal table
nearest_value_z_top10_floor <- 1.28 # Z score 0.8997, Standard normal table
nearest_value_p_top10_roof <- 0.9015
nearest_value_p_top10_floor <- 0.8997

top10_way_0.9 <- ((0.9 - nearest_value_p_top10_roof) / (nearest_value_p_top10_
    floor - nearest_value_p_top10_roof))

z_score_top_10 <- nearest_value_z_top10_roof + ((nearest_value_z_top10_floor -
      nearest_value_z_top10_roof) * (top10_way_0.9))

raw_score_top_10 <- mean(df_h1$Herf_Index) + ((z_score_top_10) * sd(df_h1$Herf
    _Index))

cat("Author␣with␣a␣Herf␣Index␣over", raw_score_top_10, "are␣evaluated␣as␣part␣
    of␣the␣top␣10%.")

## Author with a Herf Index over 0.9585829 are evaluated as part of the top
    10%.
```

```r
for(i in 1:nrow(df_h1)){
  row <- df_h1[i,]
  sub_df_qc <- df_qc[df_qc$Inventors == row$Inventor, ]
  # Include amount of published pantents evaluation of inventor, to avoid
      inventor that have only published one patent, where no clear IPC classes
        diversity is observable
  # TODO: CRITICAL OPINION, CHECK
  if((row$Herf_Index >= raw_score_top_10) & (nrow(sub_df_qc) > 1)){
    df_h1[df_h1$Inventor == row$Inventor, "Diversity_Type"] <- "Specialist"
  }
}

# Evaluate who is a Generalist
# Lowest 10% Herfindhal index distribution
# For more information, see: https://www.dummies.com/article/academics-the-
    arts/math/statistics/how-to-find-a-percentile-for-a-normal-distribution
    -169600/
# Use linear interpolation
nearest_value_z_lowest10_roof <- -1.28 # Z score for 0.1003, Standard normal
    table
nearest_value_z_lowest10_floor <- -1.29 # Z score for 0.0985, Standard normal
    table
nearest_value_p_lowest10_roof <- 0.1003
nearest_value_p_lowest10_floor <- 0.0985

lowest10_way_0.9 <- ((0.1 - nearest_value_p_lowest10_roof) / (nearest_value_p_
    lowest10_floor - nearest_value_p_lowest10_roof))

z_score_lowest_10 <- nearest_value_z_lowest10_roof + ((nearest_value_z_
    lowest10_floor - nearest_value_z_lowest10_roof) * (lowest10_way_0.9))

raw_score_lowest_10 <- mean(df_h1$Herf_Index) + ((z_score_lowest_10) * sd(df_
    h1$Herf_Index))

cat("Author␣with␣a␣Herf␣Index␣under", raw_score_lowest_10, "are␣evaluated␣as␣
    part␣of␣the␣lowest␣10%.")

## Author with a Herf Index under 0.2298311 are evaluated as part of the
    lowest 10%.

for(i in 1:nrow(df_h1)){
  row <- df_h1[i,]
  sub_df_qc <- df_qc[df_qc$Inventors == row$Inventor, ]
  # Include amount of published patents evaluation of inventor, to avoid
      inventor that have only published one patent, where no clear IPC classes
        diversity is observable
  # TODO: CRITICAL OPINION, CHECK
  if((row$Herf_Index <= raw_score_lowest_10) & (nrow(sub_df_qc) > 1)){
    df_h1[df_h1$Inventor == row$Inventor, "Diversity_Type"] <- "Generalist"
  }
}

# Connect brokerage and generalist/specialist distribution in final numbers
broker_diversity <- df_h1[df_h1$IsBroker == "Broker" & df_h1$Diversity_Type !=
     "None",]
```

```
cat("In␣total", nrow(broker_diversity) ,"brokers␣with␣given␣diversity␣types␣
    were␣identified.")

## In total 30 brokers with given diversity types were identified.

print(table(broker_diversity$Diversity_Type))

##
## Generalist Specialist
##         20         10

cat("From␣these␣brokers,␣we␣identified␣20␣Generalists,␣which␣equals␣to␣a␣
    distribution␣of", (20/nrow(broker_diversity)) * 100, "%␣\n")

## From these brokers, we identified 20 Generalists, which equals to a
    distribution of 66.66667 %

cat("From␣these␣brokers,␣we␣identified␣10␣Specialists,␣which␣equals␣to␣a␣
    distribution␣of", (10/nrow(broker_diversity)) * 100, "%")

## From these brokers, we identified 10 Specialists, which equals to a
    distribution of 33.33333 %

print("There␣are␣more␣generalists␣than␣specialists␣based␣on␣the␣broker␣
    distribution.")

## [1] "There are more generalists than specialists based on the broker
    distribution."

# Visualize key players
nodes_groups <- vector()

for (current_node in vis_data$nodes$id){
  if (current_node %in% df_h1$Inventor[df_h1$IsBroker == "Broker"]){
    if(current_node %in% broker_diversity$Inventor){
      nodes_groups <- c(nodes_groups, "Green")
    }else{
      nodes_groups <- c(nodes_groups, "Red")
    }
  }else{
    nodes_groups <- c(nodes_groups, "Black")
  }
}

#vis_data$nodes$group <- nodes_groups
vis_data$nodes$color <- nodes_groups

vis_network_2 <- visNetwork(nodes = vis_data$nodes, edges = vis_data$edges,
    width = "100%")

# Red Nodes = Broker in general
# Green Nodes = Broker with Diversity Type
# Black Nodes = Others
```

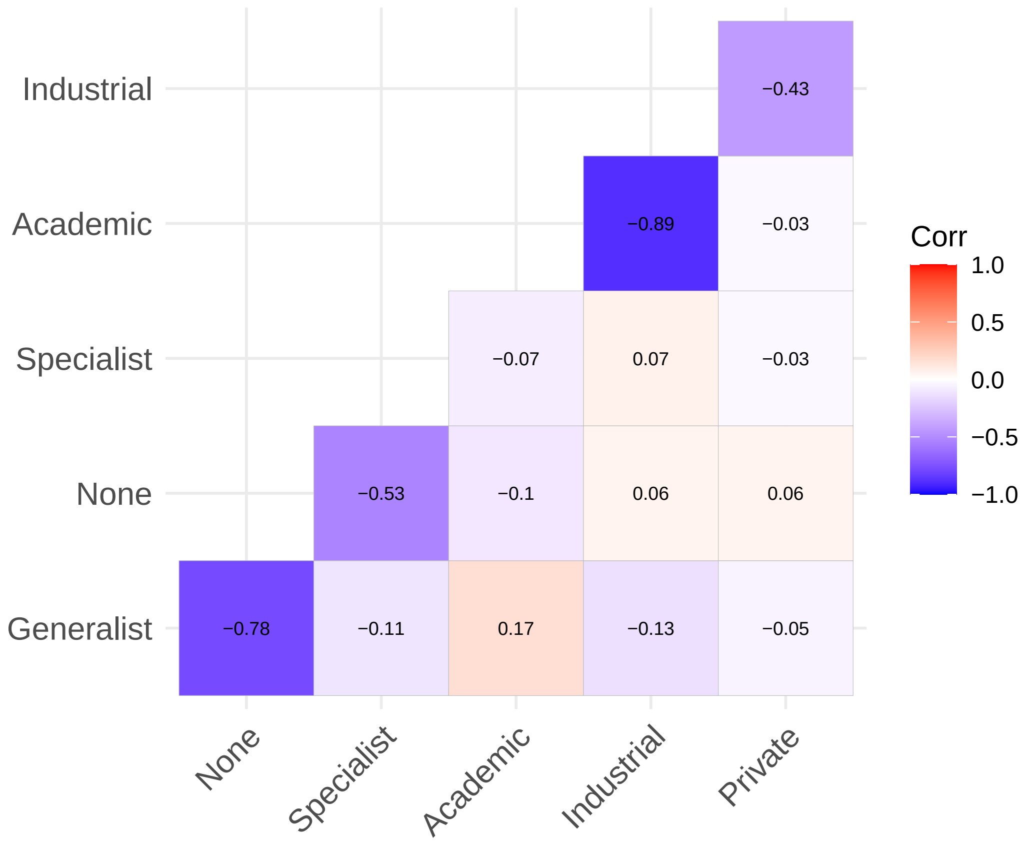
```
vis_network_2 %>%
  visPhysics(solver = "forceAtlas2Based", forceAtlas2Based = list(
     gravitationalConstant = -100, avoidOverlap = 1)) %>%
  visIgraphLayout(layout = "layout_nicely", physics = FALSE, smooth=F)
```



- **H2: We expect that more generalists who adopt the broker role in a network to be of academic origin.**

```
# We are continuing using the dataframe from H1.
# Determine origin of each inventor / view & use dataframe "edge_list"
# Selecting of applicant type is based on the majority of type occurrences,
    see function "identify_applicant_type" in 2.1
df_h2 <- data.frame(from=edge_list$from, to=edge_list$to, group=edge_list$
    group)

for(i in 1:nrow(df_h1)){
  row <- df_h1[i,]
  df_sub <- df_h2[df_h2$from == row$Inventor, ]
  df_h1[df_h1$Inventor == row$Inventor, "Applicant_Type"] <- names(which.max(
      table(df_sub$group)))
}

table_applicant_type <- table(df_h1$Applicant_Type)
cat("Overall␣Distribution␣of␣applicant␣types␣through␣all␣Inventors")

## Overall Distribution of applicant types through all Inventors

print(table_applicant_type)

##
##   academic industrial    private
##         55        514        106

df_applicant_type <- as.data.frame(table_applicant_type)
df_applicant_type$Distribution <- df_applicant_type$Freq / sum(df_applicant_
    type$Freq)

# Calculate distribution of diversities types of the identified generalist who
     are brokers
generalist_with_applicant_type <- df_h1[df_h1$IsBroker == "Broker" & df_h1$
    Diversity_Type == "Generalist",]

# Output results in numbers
print(table(generalist_with_applicant_type$Applicant_Type))

##
##   academic industrial
##          3         17

amount_generalists <- nrow(generalist_with_applicant_type)

cat("From", amount_generalists,"generalists,␣we␣identified␣3␣of␣academic␣
    origin,␣which␣equals␣to␣a␣distribution␣of", (3/amount_generalists) * 100,
    "%␣\n")

## From 20 generalists, we identified 3 of academic origin, which equals to a
    distribution of 15 %
```

```
cat("From", amount_generalists,"generalists, we identified 17 of industrial 
    origin, which equals to a distribution of", (17/amount_generalists) * 100,
     "% \n")

## From 20 generalists, we identified 17 of industrial origin, which equals to
     a distribution of 85 %

# Draw Conclusion from subset on larger distribution by utilizing correlation
    factor
pairwise_comp <- df_h1[c(7,8,9)]

pairwise_comp$IsBroker <- factor(pairwise_comp$IsBroker)
pairwise_comp$Diversity_Type <- factor(pairwise_comp$Diversity_Type)
pairwise_comp$Applicant_Type <- factor(pairwise_comp$Applicant_Type)

pairwise_comp <- pairwise_comp[pairwise_comp$IsBroker == "Broker",]

mm <- model.matrix(~ IsBroker + Diversity_Type + Applicant_Type, data=pairwise
    _comp, contrasts.arg = lapply(pairwise_comp[, sapply(pairwise_comp, is.
    factor), drop = FALSE], contrasts, contrasts = FALSE))

mm_cor <- cor(mm, use="pairwise.complete.obs", method = c("pearson", "kendall"
    , "spearman"))

## Warning in cor(mm, use = "pairwise.complete.obs", method = c("pearson", :
## Standardabweichung ist Null

colnames(mm_cor) <- c("(Intercept)", "Broker", "NotBroker", "Generalist", "
    None", "Specialist", "Academic", "Industrial", "Private")
rownames(mm_cor) <- c("(Intercept)", "Broker", "NotBroker", "Generalist", "
    None", "Specialist", "Academic", "Industrial", "Private")

mm_cor %>% ggcorrplot(show.diag = F, type = "lower", lab=TRUE, lab_size=2.5)
```



```
cat("Correlation␣of␣Generalist␣and␣Academic␣is␣0.17,␣given␣that␣the␣inspected␣
    inventors␣are␣brokers.")
```

```
## Correlation of Generalist and Academic is 0.17, given that the inspected
    inventors are brokers.
```

```
cat("Correlation␣of␣Generalist␣and␣Industrial␣is␣−0.13,␣given␣that␣the␣
    inspected␣inventors␣are␣brokers.")
```

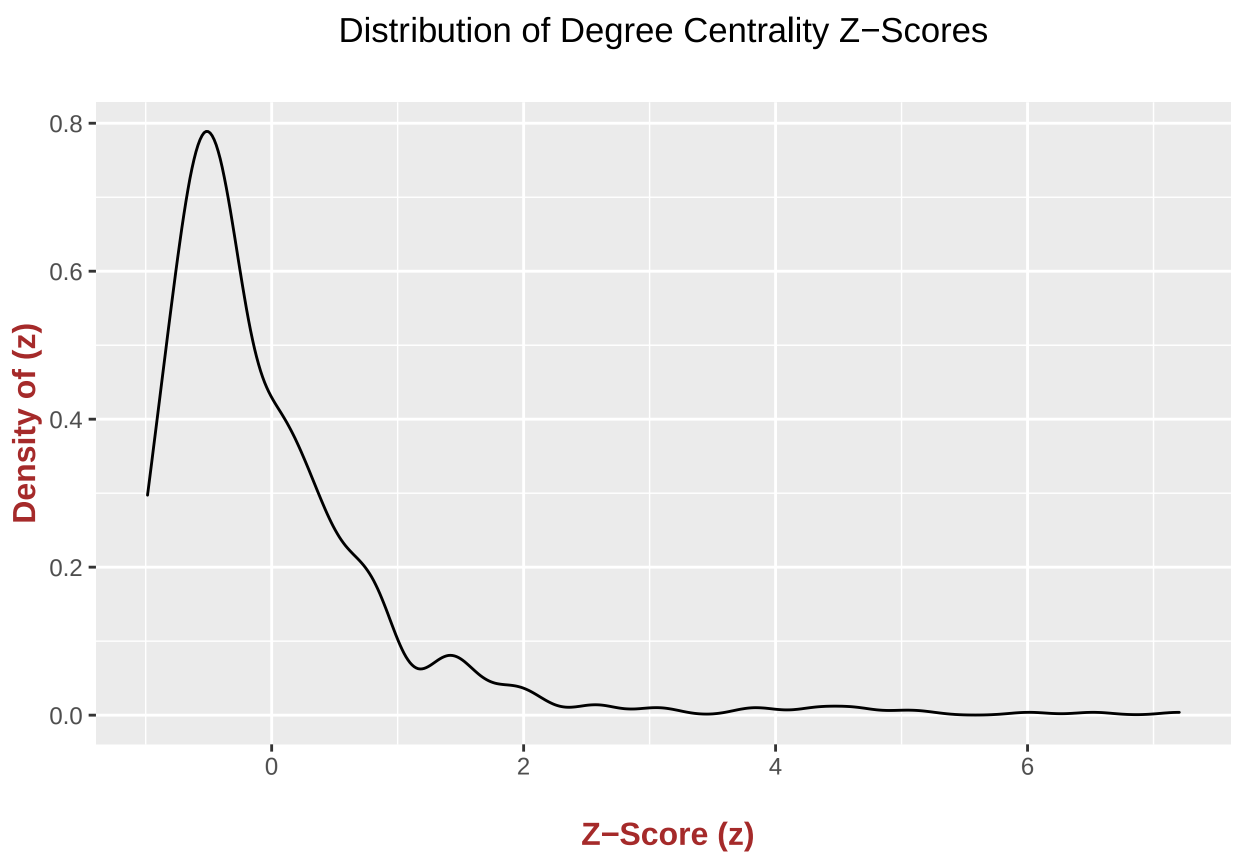
```
## Correlation of Generalist and Industrial is −0.13, given that the inspected
     inventors are brokers.
```

```
cat("Despite␣the␣measurement␣of", amount_generalists,"generalists,␣where␣3␣
    inventors␣are␣of␣academic␣origin,␣the␣overall␣correlation␣factor␣of␣
    generalist␣in␣combination␣with␣academic␣is␣higher.")
```

```
## Despite the measurement of 20 generalists, where 3 inventors are of
    academic origin, the overall correlation factor of generalist in
    combination with academic is higher.
```

- **H3: We expect peripheral players to be specialists.**

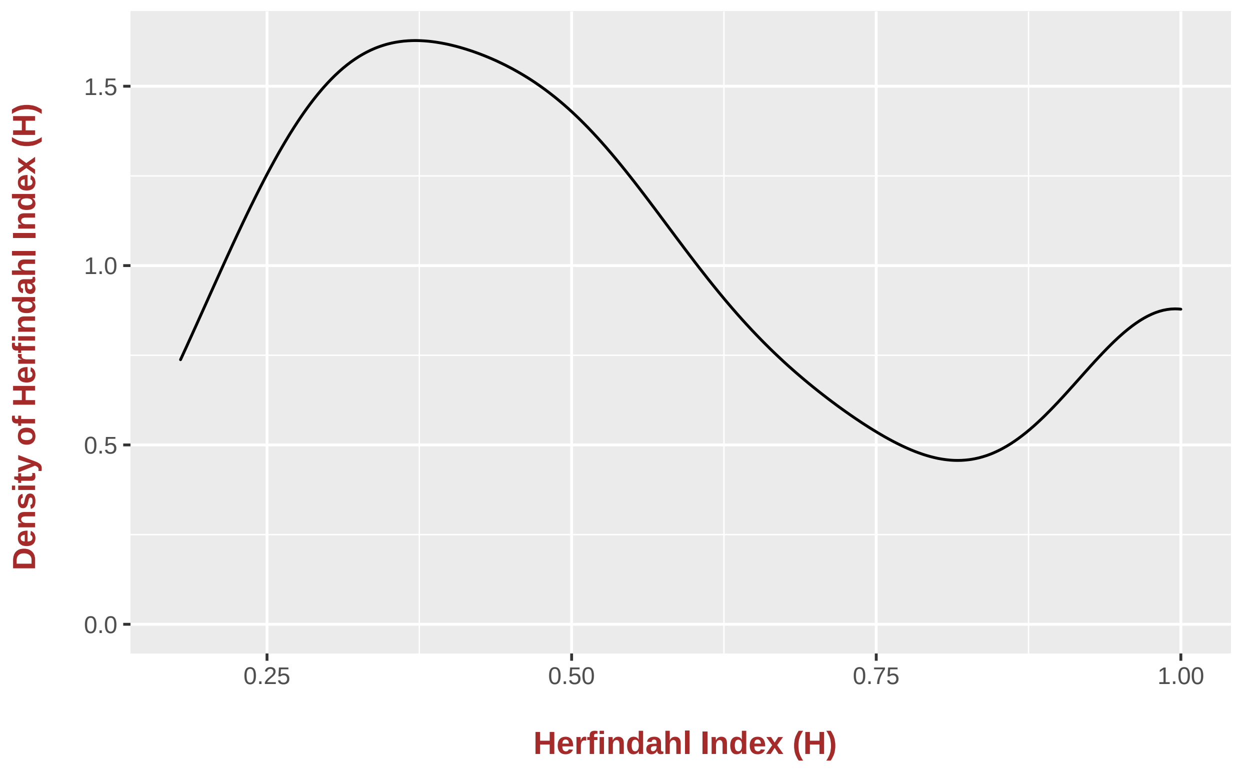
```
# Calculate out-degree centrality for each inventor
degree_centrality <- degree(network_graph, mode = "out", normalized = T)
df_degree_centr <- data.frame(as.list(degree_centrality))
t_df_degree_centr <- transpose(df_degree_centr)
t_df_degree_centr$Inventor <- colnames(df_degree_centr)

# Add out-degree centrality to df_h1
for(i in 1:nrow(t_df_degree_centr)){
  row <- t_df_degree_centr[i,]
  df_h1[df_h1$Inventor == row$Inventor, "Degree_Centr"] <- row$V1
}

# Calculate Z scores for Degree_Centr
# Adapt approach from H1 towards calculating lowest 10%
df_h1 <- df_h1 %>% mutate(Degree_Centr_ZScore = (Degree_Centr - mean(Degree_
    Centr))/sd(Degree_Centr))

mean_degree_centr <- (mean(df_h1$Degree_Centr))
cat("Mean␣of␣degree␣centrality␣distribution:",mean_degree_centr,"\n")

## Mean of degree centrality distribution: 0.008567975

sd_degree_centr <- sd(df_h1$Degree_Centr)
cat("Standard␣Deviation␣of␣degree␣centrality␣distribution:",sd_degree_centr,"\
    n")

## Standard Deviation of degree centrality distribution: 0.008695654

raw_score_lowest_10_degree_centr <- abs(mean(df_h1$Degree_Centr) + (z_score_
    lowest_10 * sd(df_h1$Degree_Centr))) # Take absolute value, as standard
    deviation is larger than mean --> TODO: CHECK IF ABS() IS ALLOWED

cat("Author␣with␣a␣Degree␣Centrality␣of␣under", raw_score_lowest_10_degree_
    centr, "are␣evaluated␣as␣part␣of␣the␣lowest␣10%␣and␣therefore␣are␣
    peripheral␣players.")

## Author with a Degree Centrality of under 0.002576956 are evaluated as part
    of the lowest 10% and therefore are peripheral players.

# Plot Distribution of Degree Centrality Z-Scores
ggplot(df_h1, aes(x = Degree_Centr_ZScore)) +
  geom_density() +
  labs(x = "\n␣Z-Score␣(z)", y = "Density␣of␣(z)", title = "Distribution␣of␣
      Degree␣Centrality␣Z-Scores\n") +
  theme(plot.title = element_text(hjust = 0.5),
        axis.title.x = element_text(face="bold", colour="brown", size = 12),
        axis.title.y = element_text(face="bold", colour="brown", size = 12))
```



```
# Get the distribution of generalist/specialist based on the peripheral
    players
for(i in 1:nrow(df_h1)){
  row <- df_h1[i,]
  sub_df_qc <- df_qc[df_qc$Inventors == row$Inventor, ]
  if(row$Degree_Centr <= raw_score_lowest_10_degree_centr){
    df_h1[df_h1$Inventor == row$Inventor, "IsPeripheralPlayer"] <- "
        PeripheralPlayer"
  }
}

peripheral_diversity <- df_h1[df_h1$IsPeripheralPlaye == "PeripheralPlayer" &
    df_h1$Diversity_Type != "None",]

table(peripheral_diversity$Diversity_Type)

##
## Generalist Specialist
##          1          1

print("Only␣one␣of␣each␣Diversity␣Types␣identified.")

## [1] "Only one of each Diversity Types identified."

print("Based␣on␣that␣measurement␣no␣answer␣towards␣the␣hypothesis␣3␣can␣be␣
    made.")
```

```
## [1] "Based on that measurement no answer towards the hypothesis 3 can be
    made."

# Get the distribution of Herf Index based on the peripheral players
df_peripheral <- df_h1[df_h1$IsPeripheralPlaye == "PeripheralPlayer",]

ggplot(df_peripheral, aes(x = Herf_Index)) +
  geom_density() +
  labs(x = "\n Herfindahl Index (H)",
       y = "Density of Herfindahl Index (H) \n",
       title = "Distribution of Herf Index based on peripheral players\n") +
  theme(plot.title = element_text(hjust = 0.5),
        axis.title.x = element_text(face="bold", colour="brown", size = 12),
        axis.title.y = element_text(face="bold", colour="brown", size = 12))
```

Distribution of Herf Index based on peripheral players



```
print("Interpretation of Herfindahl Index Distribution based on existing 
    peripheral players:")

## [1] "Interpretation of Herfindahl Index Distribution based on existing
    peripheral players:"

print("There is a trends towards a lower herf index value observable.")

## [1] "There is a trends towards a lower herf index value observable."

print("This allows us to derive an orientation of peripheral players towards 
    the generalists segment. This is contrary to our stated hypothesis.")
```

```
## [1] "This allows us to derive an orientation of peripheral players towards
   the generalists segment. This is contrary to our stated hypothesis."

# Visualize results
vis_data_h3 <- toVisNetworkData(network_graph)
vis_network_h3 <- visNetwork(nodes = vis_data_h3$nodes, edges = vis_data_h3$
   edges)

nodes_groups_h3 <- vector()

for (current_node in vis_data_h3$nodes$id){
  if (current_node %in% df_h1$Inventor[df_h1$IsPeripheralPlayer == "
     PeripheralPlayer"]){
    nodes_groups_h3 <- c(nodes_groups_h3, "Blue")
  }else{
    nodes_groups_h3 <- c(nodes_groups_h3, "Black")
  }
}

vis_data_h3$nodes$color <- nodes_groups_h3

vis_network_h3 <- visNetwork(nodes = vis_data_h3$nodes, edges = vis_data_h3$
   edges, width = "100%")

# Blue Nodes = Peripheral Players
# Black Nodes = Not Peripheral Players
vis_network_h3 %>%
  visPhysics(solver = "forceAtlas2Based",
             forceAtlas2Based = list(gravitationalConstant = -100,
                avoidOverlap = 1)) %>%
  visIgraphLayout(layout = "layout_nicely", physics = FALSE, smooth=F)
```