# Project 6

Logan Bolton

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*Acknowledgement:* This code was created through the repurposing of code found in the lecture notes and through collaboration with Gemini 2.5 Pro.

```r
library('igraph')
```

```
##
## Attaching package: 'igraph'

## The following objects are masked from 'package:stats':
##
##     decompose, spectrum

## The following object is masked from 'package:base':
##
##     union
```

```r
library(poweRlaw)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:igraph':
##
##     as_data_frame, groups, union

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
library(igraph)
library(ggplot2) # For plotting
```

## 1) Analysis of Random Graphs G(n, p)

Fix an integer n >= 10,000. For various values of the edge probability p such that pn is a constant, use computational experiments (plots and calculations) to verify the following theoretical properties of G(n, p):

### a) Mean degree c

- Verify that the mean degree c = p(n - 1).
- Plot c as a function of p.

```r
n <- 10000 # Number of vertices (n >= 10,000)

num_p_values <- 30 # Number of different p values to test
p_values <- seq(1/n, 10/n, length.out = num_p_values)

observed_mean_degrees <- numeric(length(p_values))
theoretical_mean_degrees <- numeric(length(p_values))

cat("Running simulation for n =", n, "...\n")
```

```
## Running simulation for n = 10000 ...
```

```r
for (i in 1:length(p_values)) {
  p <- p_values[i]

  # Generate a G(n, p) random graph
  # Use directed=FALSE and loops=FALSE for the standard G(n,p) model
  g <- sample_gnp(n = n, p = p, directed = FALSE, loops = FALSE)

  # Calculate the observed mean degree
  # Mean degree = Sum of degrees / n = 2 * number_of_edges / n
  if (gorder(g) > 0) { # Check if the graph has vertices
      degrees <- degree(g)
      observed_mean_degrees[i] <- mean(degrees)
  } else {
      observed_mean_degrees[i] <- 0 # Mean degree is 0 for an empty graph
  }

  theoretical_mean_degrees[i] <- p * (n - 1)
}
cat("Simulation finished.\n\n")
```

```
## Simulation finished.
```

```r
# --- Verification ---
cat("--- Verification Summary ---\n")
```

```
## --- Verification Summary ---
```

```r
differences <- observed_mean_degrees - theoretical_mean_degrees
relative_differences <- differences / theoretical_mean_degrees
# Handle cases where theoretical mean degree might be 0 (though not for p>0)
relative_differences[is.nan(relative_differences)] <- 0
relative_differences[is.infinite(relative_differences)] <- NA # Should not happen here

cat("Range of p values:", range(p_values), "\n")
```

```
## Range of p values: 1e-04 0.001
```

```r
cat("Range of theoretical mean degrees (c):", range(theoretical_mean_degrees), "\n")
```

```
## Range of theoretical mean degrees (c): 0.9999 9.999
```

```r
cat("Range of observed mean degrees:", range(observed_mean_degrees), "\n")
```

```
## Range of observed mean degrees: 0.9888 9.9418
```

```r
cat("Mean absolute difference:", mean(abs(differences)), "\n")
```

```
## Mean absolute difference: 0.02900931
```

```r
cat("Max absolute difference:", max(abs(differences)), "\n")
```

```
## Max absolute difference: 0.06531724
```

```r
cat("Mean absolute relative difference (%):", mean(abs(relative_differences), na.rm = TRUE) * 100, "%\n
```

```
## Mean absolute relative difference (%): 0.6080801 %
```

```r
cat("Max absolute relative difference (%):", max(abs(relative_differences), na.rm = TRUE) * 100, "%\n")
```

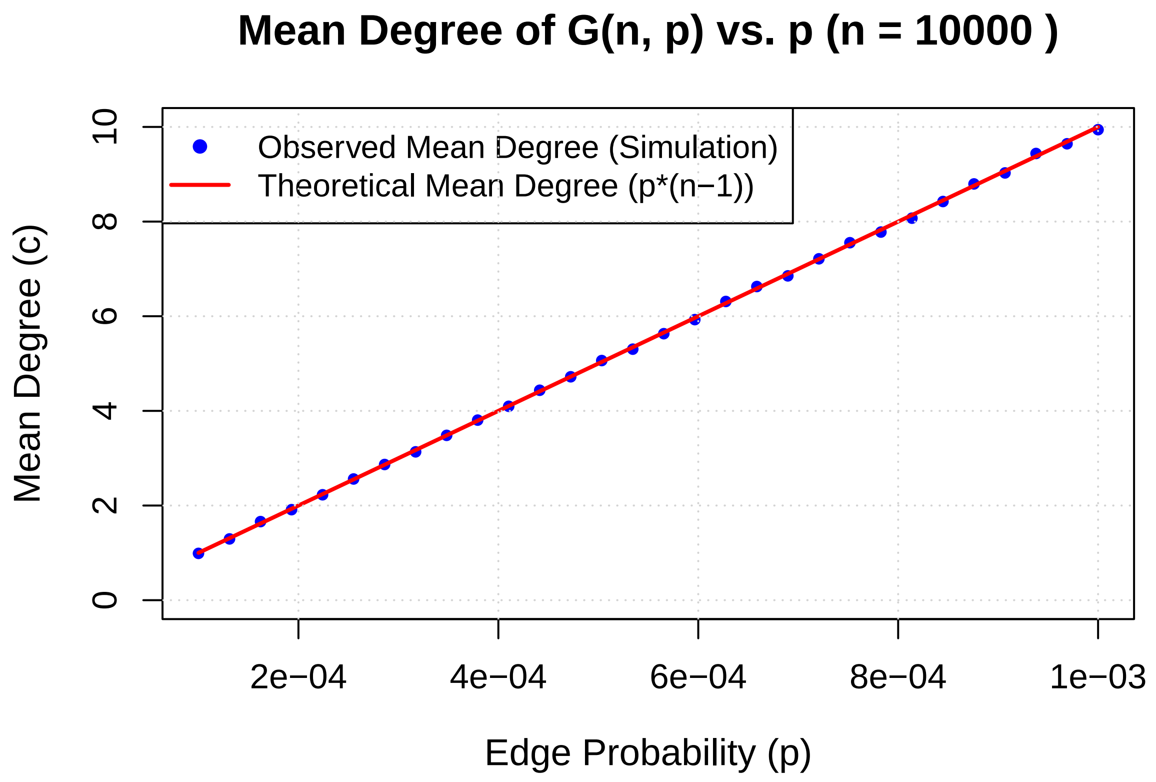
```
## Max absolute relative difference (%): 2.4728 %
```

```r
# Check if observed values are close to theoretical ones (e.g., within 5%)
# Note: Due to randomness, a single run might occasionally exceed a tight tolerance.
tolerance <- 0.05
close_enough <- abs(relative_differences) < tolerance
cat(sprintf("Percentage of simulations where observed c is within %.1f%% of theoretical c: %.2f%%\n",
            tolerance * 100, mean(close_enough, na.rm=TRUE) * 100))
```

```
## Percentage of simulations where observed c is within 5.0% of theoretical c: 100.00%
```

```r
# --- Plotting ---
# Set plot parameters for better readability
par(mar = c(5, 5, 4, 2) + 0.1) # Adjust margins

plot(p_values, observed_mean_degrees,
     type = "p", # Points
     pch = 16,    # Solid circles
     cex = 0.8,   # Smaller points
     col = "blue",
     xlab = "Edge Probability (p)",
     ylab = "Mean Degree (c)",
     main = paste("Mean Degree of G(n, p) vs. p (n =", format(n, scientific = FALSE), ")"),
     ylim = range(c(0, observed_mean_degrees, theoretical_mean_degrees)), # Ensure y-axis starts near 0
     cex.lab = 1.2, # Axis label size
     cex.axis = 1.1, # Axis tick size
     cex.main = 1.3) # Title size

# Add the theoretical line
lines(p_values, theoretical_mean_degrees,
      type = "l", # Line
      col = "red",
      lwd = 2) # Line width

# Add a legend
legend("topleft",
       legend = c("Observed Mean Degree (Simulation)", "Theoretical Mean Degree (p*(n-1))"),
       col = c("blue", "red"),
       pch = c(16, NA), # Point symbol for observed, none for line
       lty = c(NA, 1),  # Line type: none for observed, solid for theoretical
       lwd = c(NA, 2),  # Line width: none for observed, 2 for theoretical
       bg = "white")
```

```r
grid()
```



### b) Degree Distribution pk

Show that pk follows a Poisson distribution pk = e^(-c) × c^k/k! by plotting the empirical degree distribution (histogram) and overlay the theoretical Poisson curve.

```r
n <- 10000
target_c <- 5.0

if (n > 1) {
  p <- target_c / (n - 1)
} else {
  p <- 0 # Avoid division by zero if n=1
}

cat(sprintf("Parameters: n = %d, Target Mean Degree c = %.2f, p = %f\n", n, target_c, p))
```

```
## Parameters: n = 10000, Target Mean Degree c = 5.00, p = 0.000500
```

```r
# --- Generate G(n, p) Graph ---
g <- sample_gnp(n = n, p = p, directed = FALSE, loops = FALSE)
cat("Graph generated.\n")
```

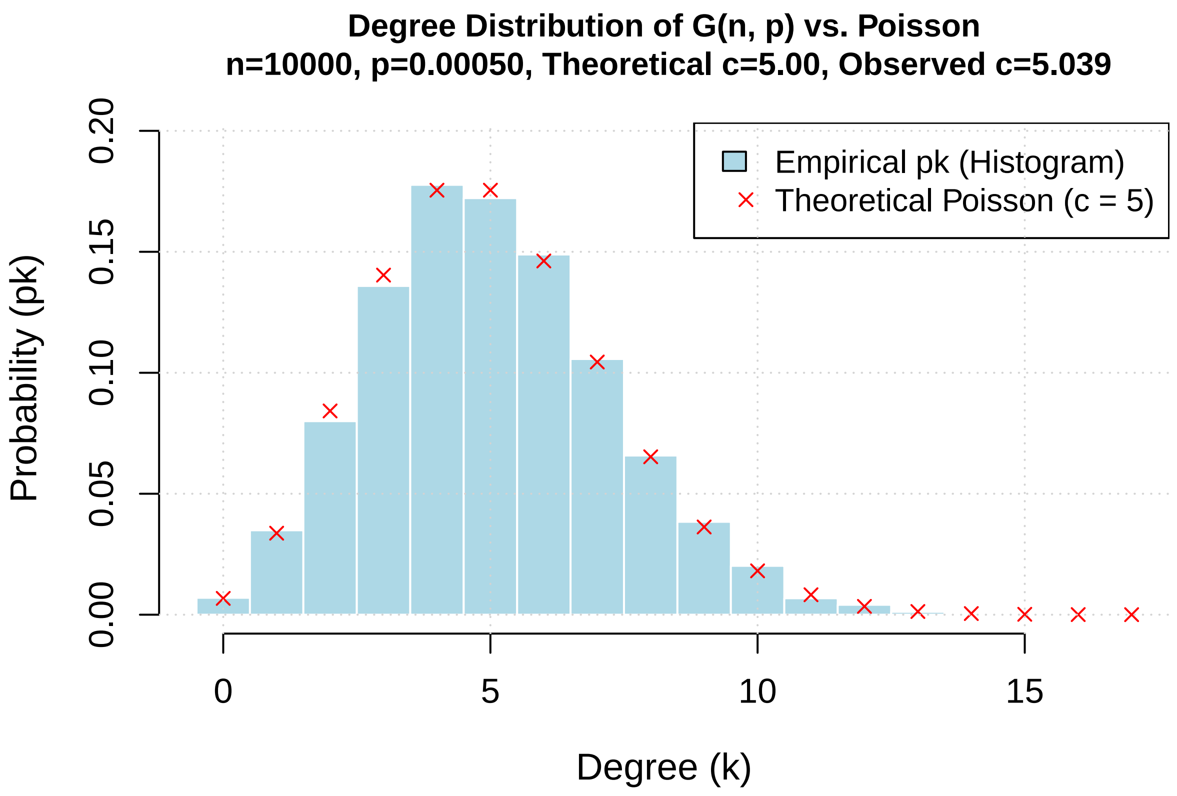
```
## Graph generated.
```

```r
# --- Calculate Empirical Degree Distribution ---
if (gorder(g) > 0) {
    degrees <- degree(g)
    observed_c <- mean(degrees) # Actual mean degree in this instance
    max_degree_observed <- if (length(degrees) > 0) max(degrees) else 0
} else {
    degrees <- numeric(0)
    observed_c <- 0
    max_degree_observed <- 0
    warning("Graph has no vertices.")
}

cat(sprintf("Observed Mean Degree in this sample: %.4f\n", observed_c))
```

```
## Observed Mean Degree in this sample: 5.0386
```

```r
k_range <- 0:(max_degree_observed + 2) # Extend range a bit

# Calculate Poisson probabilities P(X=k) = exp(-c) * c^k / k!
pk_theoretical <- dpois(k_range, lambda = target_c)

if (length(degrees) > 0) {
    # Define breaks to center integers: 0, 1, 2,... become bins [-0.5, 0.5), [0.5, 1.5), [1.5, 2.5) ...
    hist_breaks <- seq(-0.5, max(degrees) + 0.5, by = 1)
    hist_data <- hist(degrees, breaks = hist_breaks, plot = FALSE)
    # Get the maximum density/probability from histogram and theoretical
    ylim_max <- max(c(hist_data$density, pk_theoretical), na.rm = TRUE) * 1.1 # Add 10% margin
    xlim_max <- max(k_range)
} else {
    # Default limits for empty graph case
    hist_data <- list(density = numeric(0), breaks = c(-0.5, 0.5)) # Dummy data
    ylim_max <- max(c(0.1, pk_theoretical), na.rm = TRUE) * 1.1 # Ensure theoretical might still show
    xlim_max <- max(c(10, k_range)) # Sensible default x-limit
}


# Create the base histogram plot
hist(degrees,
     breaks = hist_data$breaks, # Use pre-calculated breaks
     probability = TRUE,        # Y-axis is probability density (equals prob. since width=1)
     col = "lightblue",         # Color for histogram bars
     border = "white",          # Color for bar borders
     xlab = "Degree (k)",
     ylab = "Probability (pk)",
     main = paste("Degree Distribution of G(n, p) vs. Poisson\n",
                  sprintf("n=%d, p=%.5f, Theoretical c=%.2f, Observed c=%.3f",
                          n, p, target_c, observed_c)),
     xlim = c(min(hist_data$breaks), xlim_max), # Use breaks min for xlim start
     ylim = c(0, ylim_max),
     cex.lab = 1.2,
     cex.axis = 1.1,
     cex.main = 1.0) # Smaller main title if long

points(k_range, pk_theoretical,
       pch = 4,     # Crosses symbol
       col = "red",
       cex = 0.9)
```

```r
legend("topright",
       legend = c("Empirical pk (Histogram)", paste0("Theoretical Poisson (c = ", target_c, ")")),
       fill = c("lightblue", NA),  # Color fill for histogram bar in legend
       border = c("black", NA),    # Border for histogram bar in legend
       pch = c(NA, 4),             # Symbol for theoretical points
       col = c(NA, "red"),         # Color for theoretical points
       pt.cex = c(NA, 0.9),        # Size for theoretical points symbol in legend
       bg="white")

grid()
```



**c) Clustering Coefficients**

Verify that both the local and global clustering coefficients of G(n, p) are equal to p.

```r
n <- 20000 # Number of vertices (n >= 10,000)

# Define a range of p values
# For clustering coefficient = p, the p values themselves are the theoretical values
# Use the same range as before for consistency
num_p_values <- 200
p_values <- seq(1/n, 10/n, length.out = num_p_values)
# Alternative: A direct small range like seq(0.0001, 0.001, length.out = 30)

# --- Storage for Results ---
avg_local_cc_observed <- numeric(length(p_values))
global_cc_observed <- numeric(length(p_values))

for (i in 1:length(p_values)) {
  p <- p_values[i]

  # Generate a G(n, p) random graph
  g <- sample_gnp(n = n, p = p, directed = FALSE, loops = FALSE)

  # Calculate Average Local Clustering Coefficient
  # transitivity(..., type="local") gives NaN for nodes with degree < 2
  local_ccs <- transitivity(g, type = "local")
  # Average over nodes where it's defined (degree >= 2)
  avg_local_cc_observed[i] <- mean(local_ccs, na.rm = TRUE)
  # Handle cases where no node has degree >= 2 (results in NaN mean)
  if (is.nan(avg_local_cc_observed[i])) {
      avg_local_cc_observed[i] <- 0 # Assign 0 if undefined
  }


  # Calculate Global Clustering Coefficient (Transitivity)
  # This calculates 3 * triangles / connected_triples
  global_cc_observed[i] <- transitivity(g, type = "global")
   # Handle cases where global transitivity is NaN (no connected triples)
  if (is.nan(global_cc_observed[i])) {
       global_cc_observed[i] <- 0 # Assign 0 if undefined
  }

}

# --- Verification ---
cat("--- Verification Summary ---\n")
```

```
## --- Verification Summary ---
```

```
# Compare Average Local CC to p
diff_local <- avg_local_cc_observed - p_values
rel_diff_local <- diff_local / p_values
rel_diff_local[p_values == 0] <- 0 # Handle p=0 case if included
rel_diff_local[is.infinite(rel_diff_local)] <- NA

cat("Average Local Clustering Coefficient vs. p:\n")
```

```
## Average Local Clustering Coefficient vs. p:
```

```
cat("  Mean absolute difference:", mean(abs(diff_local)), "\n")
```

```
##   Mean absolute difference: 5.460663e-05
```

```
cat("  Max absolute difference:", max(abs(diff_local)), "\n")
```

```
##   Max absolute difference: 0.0001989506
```

```
cat("  Mean abs relative difference (%):", mean(abs(rel_diff_local), na.rm = TRUE) * 100, "%\n")
```

```
##   Mean abs relative difference (%): 31.86554 %
```

```
cat("  Max abs relative difference (%):", max(abs(rel_diff_local), na.rm = TRUE) * 100, "%\n")
```

```
##   Max abs relative difference (%): 207.3486 %
```

```r
# Compare Global CC to p
diff_global <- global_cc_observed - p_values
rel_diff_global <- diff_global / p_values
rel_diff_global[p_values == 0] <- 0 # Handle p=0 case if included
rel_diff_global[is.infinite(rel_diff_global)] <- NA

cat("\nGlobal Clustering Coefficient vs. p:\n")
```

```
##
## Global Clustering Coefficient vs. p:
```

```r
cat("  Mean absolute difference:", mean(abs(diff_global)), "\n")
```

```
##   Mean absolute difference: 4.569919e-05
```

```r
cat("  Max absolute difference:", max(abs(diff_global)), "\n")
```

```
##   Max absolute difference: 0.0002167885
```

```r
cat("  Mean abs relative difference (%):", mean(abs(rel_diff_global), na.rm = TRUE) * 100, "%\n")
```

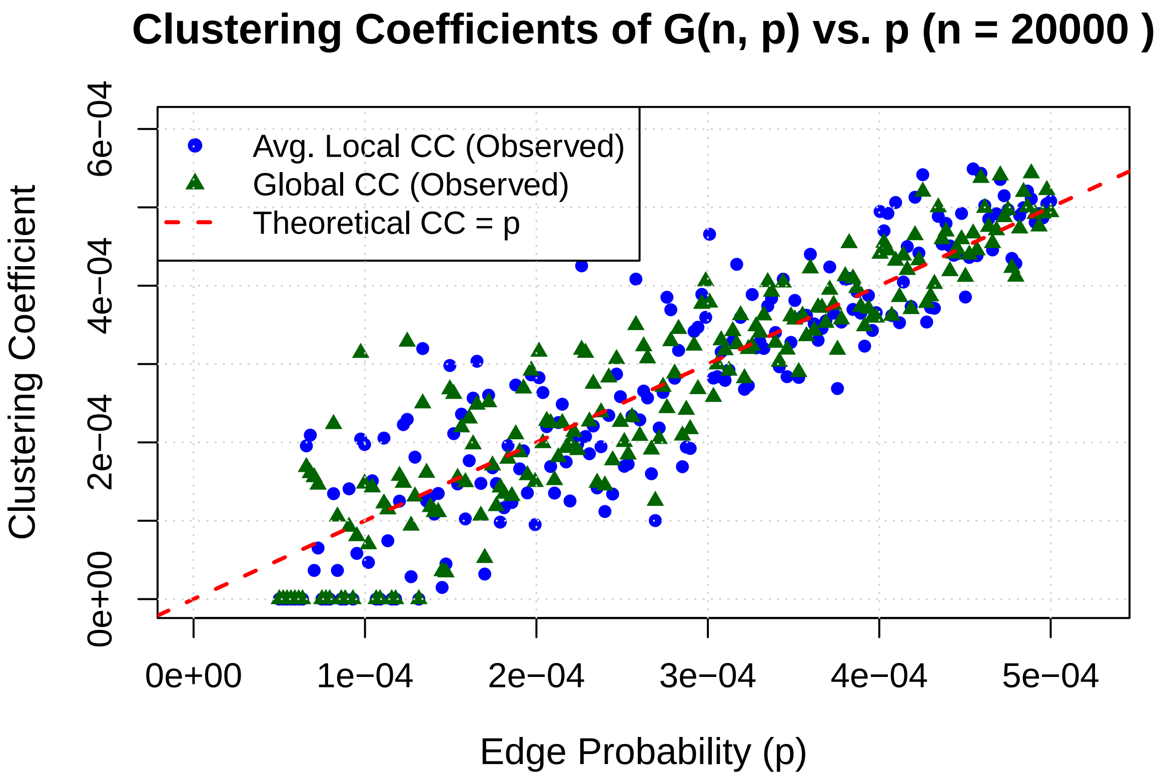
```
##   Mean abs relative difference (%): 28.52009 %
```

```r
cat("  Max abs relative difference (%):", max(abs(rel_diff_global), na.rm = TRUE) * 100, "%\n")
```

```
##   Max abs relative difference (%): 222.3759 %
```

```r
# --- Plotting ---
par(mar = c(5, 5, 4, 2) + 0.1) # Adjust margins

# Determine plot range
y_max <- max(c(0, p_values, avg_local_cc_observed, global_cc_observed), na.rm = TRUE) * 1.1
x_max <- max(p_values) * 1.05

plot(p_values, avg_local_cc_observed,
     pch = 16,    # Solid circles
     cex=0.9,
     col = "blue",
     xlab = "Edge Probability (p)",
     ylab = "Clustering Coefficient",
     main = paste("Clustering Coefficients of G(n, p) vs. p (n =", format(n, scientific = FALSE), ")"),
     xlim = c(0, x_max),
     ylim = c(0, y_max),
     cex.lab = 1.2,
     cex.axis = 1.1,
     cex.main = 1.3)

# Add points for the global clustering coefficient
points(p_values, global_cc_observed,
       pch = 17,    # Triangles
       cex=0.9,
       col = "darkgreen")

# Add the theoretical line CC = p (which is y = x on this plot)
abline(a = 0, b = 1, col = "red", lwd = 2, lty = 2) # y = 0 + 1*x

# Add a legend
```

```
legend("topleft",
       legend = c("Avg. Local CC (Observed)", "Global CC (Observed)", "Theoretical CC = p"),
       col = c("blue", "darkgreen", "red"),
       pch = c(16, 17, NA), # Point symbols
       lty = c(NA, NA, 2),  # Line types (dashed for theoretical)
       lwd = c(NA, NA, 2),  # Line widths
       bg = "white")

# Add grid lines
grid()
```



**d) Giant Component Threshold**

Confirm that the threshold probability for the emergence of a giant component is 1/(n-1).

```
n <- 10000 # Number of vertices (n >= 10,000)
num_simulations_per_p <- 10 # Number of graphs to average over for each p value
num_alpha_points <- 40      # Number of points (alpha values) to plot

# Calculate the theoretical threshold probability
if (n > 1) {
  p_c <- 1 / (n - 1)
} else {
  p_c <- 1 # Or handle n=1 case appropriately
}

# Define a range of multipliers 'alpha' for p, centered around the threshold alpha=1
# We want p = alpha * p_c
alpha_values <- seq(0.1, 3.0, length.out = num_alpha_points)
```

```r
p_values <- alpha_values * p_c

# --- Storage for Results ---
# Store the average relative size of the largest component for each alpha/p
avg_relative_largest_comp_size <- numeric(length(alpha_values))

# --- Computational Experiment ---
cat(sprintf("Running simulations for n=%d. Theoretical threshold p_c ~= %.6f (alpha=1)\n", n, p_c))
```

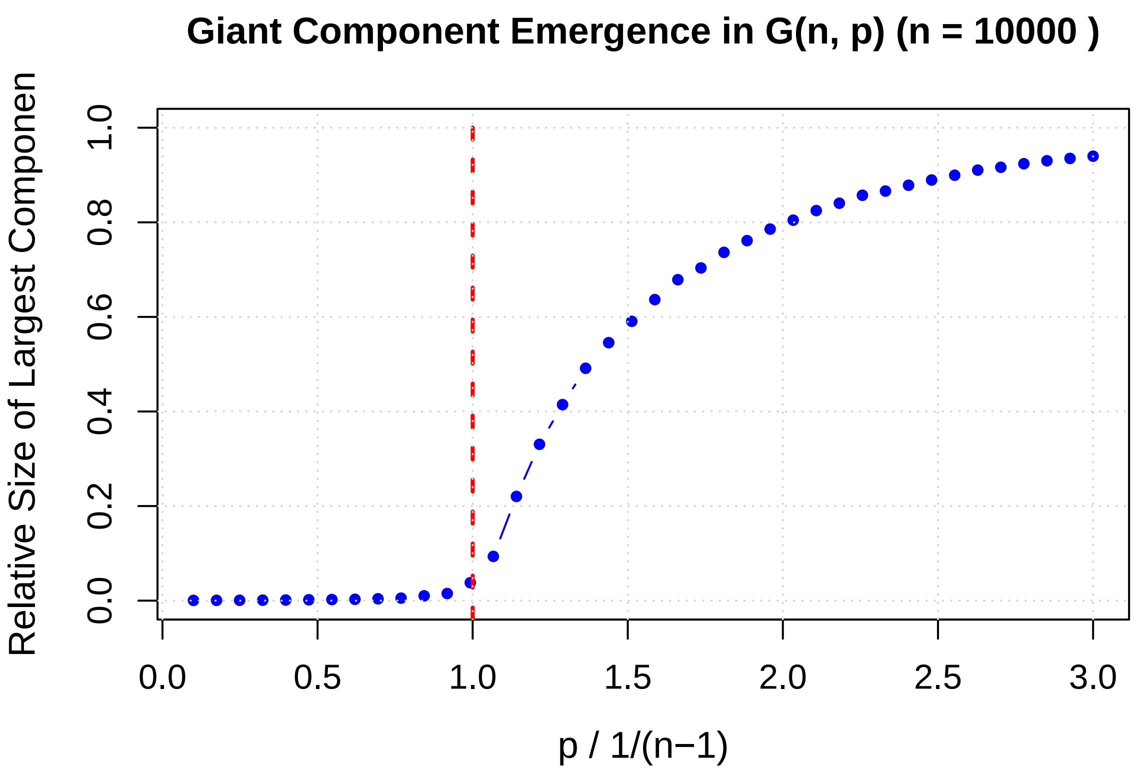
```
## Running simulations for n=10000. Theoretical threshold p_c ~= 0.000100 (alpha=1)
```

```r
for (i in 1:length(alpha_values)) {
  p <- p_values[i]
  alpha <- alpha_values[i]
  current_run_relative_sizes <- numeric(num_simulations_per_p)

  # Run multiple simulations for the current p value
  for (j in 1:num_simulations_per_p) {
    # Generate a G(n, p) random graph
    g <- sample_gnp(n = n, p = p, directed = FALSE, loops = FALSE)

    largest_comp_size <- 0 # Default size
    if (gorder(g) > 0) { # Check if graph is not empty
        comps <- components(g)
        # Check if components were found and csize is not NULL/empty
        if (!is.null(comps$csize) && length(comps$csize) > 0) {
            largest_comp_size <- max(comps$csize)
        } else {
             # If graph has nodes but components() doesn't return sizes
             # (unlikely for igraph), assume isolated nodes.
             # Or if the graph is truly empty (handled by gorder(g)>0 check).
             # If n>0 but no edges, largest component is size 1.
             if (gorder(g) > 0 && gsize(g) == 0) {
                 largest_comp_size <- 1
             } else {
                 largest_comp_size <- 0 # Should not happen normally
             }
        }
    }

    # Calculate relative size for this run
    current_run_relative_sizes[j] <- largest_comp_size / n

  } # End inner loop (simulations for one p)

  # Calculate the average relative size for this p value
  avg_relative_largest_comp_size[i] <- mean(current_run_relative_sizes, na.rm = TRUE)

} # End outer loop (over alpha/p values)
cat("Simulation finished.\n\n")
```

```
## Simulation finished.
```

```r
# --- Plotting ---
par(mar = c(5, 5, 4, 2) + 0.1) # Adjust margins
```

```r
plot(alpha_values, avg_relative_largest_comp_size,
     type = "b", # Plot both points and lines
     pch = 16,
     cex = 0.8,
     col = "blue",
     xlab = expression("p / 1/(n-1)"), # Label using alpha = p/pc
     ylab = "Relative Size of Largest Componen",
     main = paste("Giant Component Emergence in G(n, p) (n =", format(n, scientific = FALSE), ")"),
     ylim = c(0, 1.0), # Relative size is between 0 and 1
     cex.lab = 1.2,
     cex.axis = 1.1,
     cex.main = 1.2)

# Add a vertical line at the theoretical threshold (alpha = 1)
abline(v = 1, col = "red", lwd = 2, lty = 2) # lty=2 for dashed line

grid()
```



**e) Fraction S of Vertices in the Giant Component**

Show that the fraction S of vertices in the giant component satisfies: 1 - S = e^(-cS) by comparing the empirical value of S with the theoretical prediction (using numerical methods if needed).

```r
solve_S_equation <- function(c_val) {
  if (c_val <= 1) {
    return(0) # No giant component expected for c <= 1
  }

  # Define the function whose root we want to find: f(S) = 1 - S - exp(-c*S)
  f <- function(S, c_param) {
    1 - S - exp(-c_param * S)
  }

  # Find the root in the interval (epsilon, 1].
  # We use a small epsilon > 0 because S=0 is always a root,
  # and uniroot needs endpoints with different signs.
  # For c>1, f(epsilon) > 0 and f(1) < 0.
  epsilon <- 1e-9
  result <- tryCatch({
    uniroot(f, interval = c(epsilon, 1), c_param = c_val)
  }, error = function(e) {
    warning(paste("Could not find root for c =", c_val, ":", e$message))
    return(list(root = NA)) # Return NA if uniroot fails
  })

  return(result$root)
}

# --- Parameters ---
n <- 10000 # Number of vertices (n >= 10,000)
num_simulations_per_c <- 10 # Average over multiple runs for smoother results
num_c_points <- 30         # Number of different c values to test

# Choose a range of mean degrees 'c' > 1 (where a giant component exists)
# We'll vary c directly, then calculate p
min_c <- 1.1 # Start slightly above the threshold
max_c <- 10.0
c_values <- seq(min_c, max_c, length.out = num_c_points)
p_values <- c_values / (n - 1) # Calculate corresponding p values

# --- Storage for Results ---
observed_S_avg <- numeric(length(c_values))
theoretical_S <- numeric(length(c_values))

# --- Computational Experiment ---
cat(sprintf("Running simulations for n=%d...\n", n))
```

```
## Running simulations for n=10000...
```

```
for (i in 1:length(c_values)) {
  c_current <- c_values[i]
  p <- p_values[i]
  current_run_S_values <- numeric(num_simulations_per_c)

  # Calculate theoretical S *once* for this c
  theoretical_S[i] <- solve_S_equation(c_current)

  # Run multiple simulations for the current p value
  for (j in 1:num_simulations_per_c) {
    # Generate a G(n, p) random graph
    g <- sample_gnp(n = n, p = p, directed = FALSE, loops = FALSE)

    largest_comp_size <- 0 # Default size
```

```r
    if (gorder(g) > 0) {
        comps <- components(g)
        if (!is.null(comps$csize) && length(comps$csize) > 0) {
            largest_comp_size <- max(comps$csize)
        } else if (gorder(g) > 0 && gsize(g) == 0) {
             largest_comp_size <- 1
        }
    }

    # Calculate observed relative size S for this run
    current_run_S_values[j] <- largest_comp_size / n

  } # End inner loop (simulations for one c)

  # Calculate the average observed S for this c value
  observed_S_avg[i] <- mean(current_run_S_values, na.rm = TRUE)

} # End outer loop (over c values)


# --- Verification ---
cat("--- Verification Summary ---\n")
```

```
## --- Verification Summary ---
```

```r
# Calculate differences (ignore potential NAs from failed root finding)
valid_indices <- !is.na(theoretical_S)
diff_S <- observed_S_avg[valid_indices] - theoretical_S[valid_indices]
rel_diff_S <- diff_S / theoretical_S[valid_indices]
# Handle division by zero if theoretical_S is exactly 0 (shouldn't happen for c>1)
rel_diff_S[theoretical_S[valid_indices] == 0] <- 0
rel_diff_S[is.infinite(rel_diff_S)] <- NA

cat("Comparison of Observed S vs Theoretical S from 1-S=exp(-cS):\n")
```

```
## Comparison of Observed S vs Theoretical S from 1-S=exp(-cS):
```

```r
cat("  Mean absolute difference:", mean(abs(diff_S), na.rm=TRUE), "\n")
```

```
##   Mean absolute difference: 0.0006222491
```

```r
cat("  Max absolute difference:", max(abs(diff_S), na.rm=TRUE), "\n")
```

```
##   Max absolute difference: 0.00624475
```

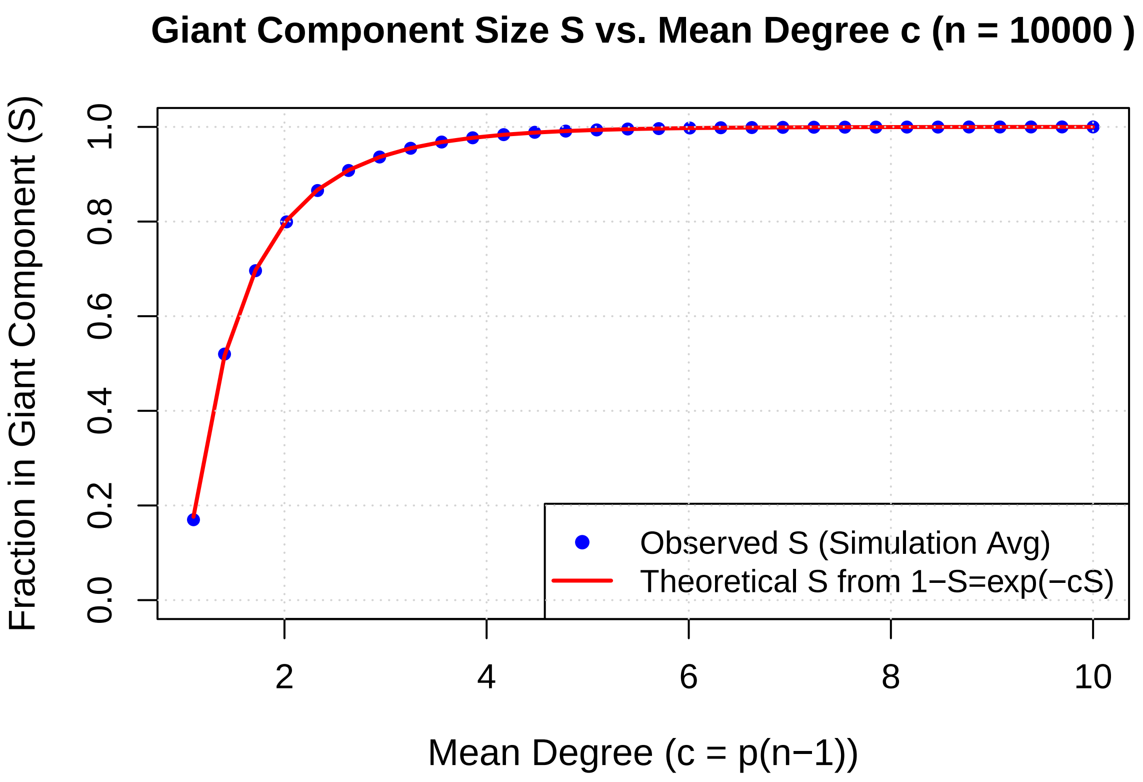
```r
cat("  Mean abs relative difference (%):", mean(abs(rel_diff_S), na.rm = TRUE) * 100, "%\n")
```

```
##   Mean abs relative difference (%): 0.1758673 %
```

```r
cat("  Max abs relative difference (%):", max(abs(rel_diff_S), na.rm = TRUE) * 100, "%\n")
```

```
##   Max abs relative difference (%): 3.545439 %
```

```r
# --- Plotting ---
par(mar = c(5, 5, 4, 2) + 0.1) # Adjust margins

plot(c_values, observed_S_avg,
     type = "p", # Points for observed
     pch = 16,    # Solid circles
     cex = 0.9,
     col = "blue",
     xlab = "Mean Degree (c = p(n-1))",
     ylab = "Fraction in Giant Component (S)",
     main = paste("Giant Component Size S vs. Mean Degree c (n =", format(n, scientific = FALSE), ")"),
     ylim = c(0, 1.0),
     xlim = range(c_values),
     cex.lab = 1.2,
     cex.axis = 1.1,
     cex.main = 1.2)

# Add the theoretical curve
lines(c_values[valid_indices], theoretical_S[valid_indices],
      type = "l", # Line for theoretical
      col = "red",
      lwd = 2)

# Add a legend
legend("bottomright", # Position legend appropriately
       legend = c("Observed S (Simulation Avg)", "Theoretical S from 1-S=exp(-cS)"),
       col = c("blue", "red"),
       pch = c(16, NA), # Point symbol for observed, none for line
       lty = c(NA, 1),  # Line type: none for observed, solid for theoretical
       lwd = c(NA, 2),  # Line width
       bg = "white")

# Add grid lines
grid()
```



## f) Small Components

- Verify that small components are trees.
- Show that the average size of small components is: R = 2/(2 - c + cS)

```r
solve_S_equation <- function(c_val) {
  if (c_val <= 1) { return(0) }
  f <- function(S, c_param) { 1 - S - exp(-c_param * S) }
  epsilon <- 1e-9
  result <- tryCatch({
    uniroot(f, interval = c(epsilon, 1), c_param = c_val, tol = 1e-9)
  }, error = function(e) {
    # warning(paste("Could not find root for c =", c_val, ":", e$message))
    return(list(root = NA))
  })
  # Check if root finding actually succeeded
  if(is.na(result$root) || !is.numeric(result$root)){
      # Fallback or alternative method could be added here if needed
      # For now, just return NA to indicate failure
      return(NA)
  }
  # Ensure root is within valid bounds (e.g., due to tolerance issues)
  root_val <- result$root
  if (root_val < 0 || root_val > 1) {
      # warning(paste("Root out of bounds (0,1] for c =", c_val))
      return(NA) # Consider it invalid
  }
  return(root_val)
}


# --- Parameters ---
n <- 10000
num_simulations_per_c <- 10 # Average results for stability
num_c_points <- 30

# Range of mean degrees 'c' > 1
min_c <- 1.1
max_c <- 6.0 # Reduce max_c slightly, as S approaches 1, denominator in R -> 2-c+c = 2
c_values <- seq(min_c, max_c, length.out = num_c_points)
p_values <- c_values / (n - 1)

# --- Storage for Results ---
observed_avg_R <- numeric(length(c_values))          # Avg size of small components
observed_frac_trees <- numeric(length(c_values))     # Fraction of small comps that are trees
theoretical_R <- numeric(length(c_values))

# --- Computational Experiment ---
cat(sprintf("Running simulations for n=%d...\n", n))
```

```
## Running simulations for n=10000...
```

```r
for (i in 1:length(c_values)) {
  c_current <- c_values[i]
  p <- p_values[i]
```

```r
# Store results for the simulations for this c
current_run_R_values <- numeric(num_simulations_per_c)
current_run_tree_fractions <- numeric(num_simulations_per_c)
valid_runs_for_R <- 0
valid_runs_for_trees <- 0

# --- Calculate Theoretical R ---
theoretical_S_val <- solve_S_equation(c_current)
if (!is.na(theoretical_S_val) && (2 - c_current + c_current * theoretical_S_val) != 0) {
    theoretical_R[i] <- 2 / (2 - c_current + c_current * theoretical_S_val)
} else {
    theoretical_R[i] <- NA # Undefined if S calculation failed or denominator is zero
}

# --- Inner Loop: Multiple simulations per c ---
for (j in 1:num_simulations_per_c) {
  g <- sample_gnp(n = n, p = p, directed = FALSE, loops = FALSE)

  if (gorder(g) == 0) next # Skip empty graph

  comps <- components(g)
  comp_sizes <- comps$csize
  num_components <- length(comp_sizes)

  if (num_components == 0) next # Skip if no components found

  # Identify Giant Component (GC) and small components
  idx_gc <- which.max(comp_sizes)
  size_gc <- comp_sizes[idx_gc]

  small_comp_indices <- setdiff(1:num_components, idx_gc)
  num_small_components <- length(small_comp_indices)

  # --- Analysis of Small Components ---
  if (num_small_components > 0) {
    small_comp_sizes <- comp_sizes[small_comp_indices]

    # 1. Calculate Average Size R for this run
    observed_R_this_run <- mean(small_comp_sizes)
    current_run_R_values[j] <- observed_R_this_run
    valid_runs_for_R <- valid_runs_for_R + 1

    # 2. Check how many small components are trees
    num_trees_among_small <- 0
    for (k_idx in small_comp_indices) {
      # Get vertices in this small component
      verts_in_comp_k <- which(comps$membership == k_idx)
      size_k <- length(verts_in_comp_k) # Should equal comp_sizes[k_idx]

      if (size_k == 1) {
        # Single node component is trivially a tree (0 edges = 1 - 1)
        num_trees_among_small <- num_trees_among_small + 1
      } else {
          # Create induced subgraph for this component
          sub_g <- induced_subgraph(g, vids = verts_in_comp_k, impl = "auto")
          num_edges_in_comp = gsize(sub_g)
          # Check tree condition: |E| = |V| - 1
          if (num_edges_in_comp == size_k - 1) {
            num_trees_among_small <- num_trees_among_small + 1
          }
        }
      } # End loop over small components

      # Calculate fraction of small components that are trees for this run
      frac_trees_this_run <- num_trees_among_small / num_small_components
      current_run_tree_fractions[j] <- frac_trees_this_run
      valid_runs_for_trees <- valid_runs_for_trees + 1

    } else {
      # No small components (graph might be connected or empty)
      # Assign NA or decide how to handle this. Let's use NA for averaging.
      current_run_R_values[j] <- NA
      current_run_tree_fractions[j] <- NA # Or 1.0 if vacuously true? Let's use NA.
    }

  } # End inner loop (simulations for one c)

  # --- Aggregate results for this c ---
  observed_avg_R[i] <- mean(current_run_R_values, na.rm = TRUE)
  observed_frac_trees[i] <- mean(current_run_tree_fractions, na.rm = TRUE)
   # If all runs resulted in NA (e.g., always connected), the mean will be NaN. Handle this.
   if(is.nan(observed_avg_R[i])) observed_avg_R[i] <- NA
   if(is.nan(observed_frac_trees[i])) observed_frac_trees[i] <- NA


} # End outer loop (over c values)
cat("Simulation finished.\n\n")
```

```
## Simulation finished.
```

```
cat("--- Verification Summary ---\n")
```

```
## --- Verification Summary ---
```

```
cat("Fraction of Small Components that are Trees:\n")
```

```
## Fraction of Small Components that are Trees:
```

```
# Check if any results were obtained
valid_tree_indices <- !is.na(observed_frac_trees)
if(any(valid_tree_indices)) {
    cat(sprintf("  Observed Mean Fraction: %.5f\n", mean(observed_frac_trees, na.rm=TRUE)))
    cat(sprintf("  Observed Min Fraction: %.5f\n", min(observed_frac_trees, na.rm=TRUE)))
    cat(sprintf("  %% of c values where avg fraction was > 0.999: %.1f%%\n",
                100 * mean(observed_frac_trees[valid_tree_indices] > 0.999)))
} else {
    cat("  No valid tree fraction data obtained.\n")
}
```

```
##   Observed Mean Fraction: 0.99999
##   Observed Min Fraction: 0.99984
##   % of c values where avg fraction was > 0.999: 100.0%
```

```r
cat("\nAverage Size (R) of Small Components:\n")
```

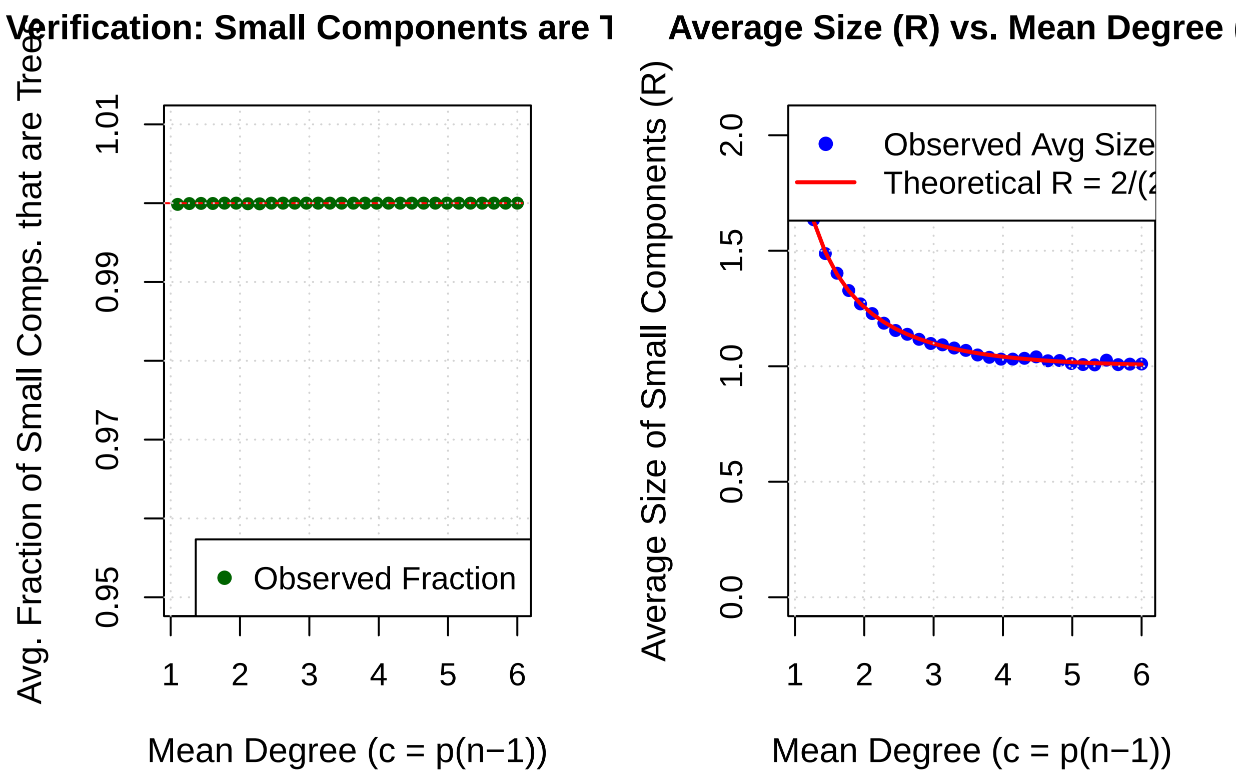
```
##
## Average Size (R) of Small Components:
```

```r
# Compare Observed R vs Theoretical R (only where theoretical R is defined)
valid_R_indices <- !is.na(observed_avg_R) & !is.na(theoretical_R)
if (any(valid_R_indices)) {
    diff_R <- observed_avg_R[valid_R_indices] - theoretical_R[valid_R_indices]
    rel_diff_R <- diff_R / theoretical_R[valid_R_indices]
    rel_diff_R[is.infinite(rel_diff_R)] <- NA # Avoid Inf if theoretical R is near 0

    cat("  Comparison vs Theoretical R = 2 / (2 - c + cS):\n")
    cat(sprintf("    Mean absolute difference: %.4f\n", mean(abs(diff_R), na.rm=TRUE)))
    cat(sprintf("    Max absolute difference: %.4f\n", max(abs(diff_R), na.rm=TRUE)))
    cat(sprintf("    Mean abs relative difference (%%): %.2f%%\n", 100 * mean(abs(rel_diff_R), na.rm=TRU
    cat(sprintf("    Max abs relative difference (%%): %.2f%%\n", 100 * max(abs(rel_diff_R), na.rm=TRUE
} else {
     cat("  No valid data for comparing observed and theoretical R.\n")
}
```

```
##   Comparison vs Theoretical R = 2 / (2 - c + cS):
##     Mean absolute difference: 0.0060
##     Max absolute difference: 0.0325
##     Mean abs relative difference (%): 0.51%
##     Max abs relative difference (%): 1.78%
```

```r
# --- Plotting ---

# Plot 1: Fraction of Small Components that are Trees
par(mfrow = c(1, 2), mar = c(5, 4.5, 4, 2) + 0.1) # Arrange plots side-by-side

plot(c_values[valid_tree_indices], observed_frac_trees[valid_tree_indices],
     type = "b", pch = 16, col = "darkgreen", cex = 0.9,
     xlab = "Mean Degree (c = p(n-1))",
     ylab = "Avg. Fraction of Small Comps. that are Trees",
     main = "Verification: Small Components are Trees",
     ylim = c(min(0.95, min(observed_frac_trees, na.rm=T)), 1.01), # Zoom in near 1.0
     cex.lab = 1.1, cex.axis = 1.0, cex.main = 1.1)
abline(h = 1, col = "red", lty = 2) # Line at y=1.0
grid()
legend("bottomright", legend="Observed Fraction", col="darkgreen", pch=16, bg="white")


# Plot 2: Average Size of Small Components (R)
plot(c_values[valid_R_indices], observed_avg_R[valid_R_indices],
     type = "p", pch = 16, col = "blue", cex = 0.9,
     xlab = "Mean Degree (c = p(n-1))",
     ylab = "Average Size of Small Components (R)",
     main = "Average Size (R) vs. Mean Degree (c)",
     ylim = c(0, max(observed_avg_R[valid_R_indices], theoretical_R[valid_R_indices], na.rm = TRUE) * 1
     cex.lab = 1.1, cex.axis = 1.0, cex.main = 1.1)
```

```r
# Add theoretical curve R = 2 / (2 - c + cS)
lines(c_values[valid_R_indices], theoretical_R[valid_R_indices],
      col = "red", lwd = 2)

grid()
legend("topleft",
       legend = c("Observed Avg Size (R)", "Theoretical R = 2/(2-c+cS)"),
       col = c("blue", "red"),
       pch = c(16, NA), lty = c(NA, 1), lwd = c(NA, 2), bg = "white")
```



**g) Fraction of Vertices in Small Components**

Verify that the fraction of vertices in small components follows (e^(-sc)*(sc)^(s-1))/s!

```r
solve_S_equation <- function(c_val) {
  if (c_val <= 1) {
    return(0)
  }
  f <- function(S, c_param) { 1 - S - exp(-c_param * S) }
  epsilon <- 1e-9
  result <- tryCatch({
    uniroot(f, interval = c(epsilon, 1), c_param = c_val, tol = 1e-9)
  }, error = function(e) {
    warning(paste("Could not find root for S, c =", c_val, ":", e$message))
    return(list(root = NA))
  })
  if(is.na(result$root) || !is.numeric(result$root)){ return(NA) }
  root_val <- result$root
  if (root_val < 0 || root_val > 1) { return(NA) }
  return(root_val)
}

# --- Parameters ---
n <- 10000
c_fixed <- 1.5 # Mean degree > 1
p <- c_fixed / (n - 1)
num_simulations <- 100 # Increase for smoother empirical curve

cat(sprintf("Parameters: n=%d, c=%.2f, p=%.6f\n", n, c_fixed, p))
```

```
## Parameters: n=10000, c=1.50, p=0.000150
```

```r
cat(sprintf("Running %d simulations...\n", num_simulations))
```

```
## Running 100 simulations...
```

```r
# --- Storage for all small component sizes ---
all_small_comp_sizes <- list()
total_small_components_collected <- 0

# --- Simulation Loop ---
for (sim in 1:num_simulations) {
  g <- sample_gnp(n = n, p = p, directed = FALSE, loops = FALSE)

  if (gorder(g) == 0) next

  comps <- components(g)
  comp_sizes <- comps$csize
  num_components <- length(comp_sizes)

  if (num_components <= 1) next # Need at least one small component

  # Identify Giant Component (GC)
  idx_gc <- which.max(comp_sizes)

  # Get sizes of small components
  small_comp_indices <- setdiff(1:num_components, idx_gc)
  if (length(small_comp_indices) > 0) {
      current_small_sizes <- comp_sizes[small_comp_indices]
      all_small_comp_sizes[[length(all_small_comp_sizes) + 1]] <- current_small_sizes
      total_small_components_collected <- total_small_components_collected + length(current_small_sizes
  }

  if (sim %% 20 == 0 || sim == num_simulations) cat(sprintf("  Simulation %d completed.\n", sim))

} # End simulation loop
```

```
##   Simulation 20 completed.
##   Simulation 40 completed.
##   Simulation 60 completed.
##   Simulation 80 completed.
##   Simulation 100 completed.
```

```r
cat(sprintf("Finished simulations. Collected %d small components.\n", total_small_components_collected)
```

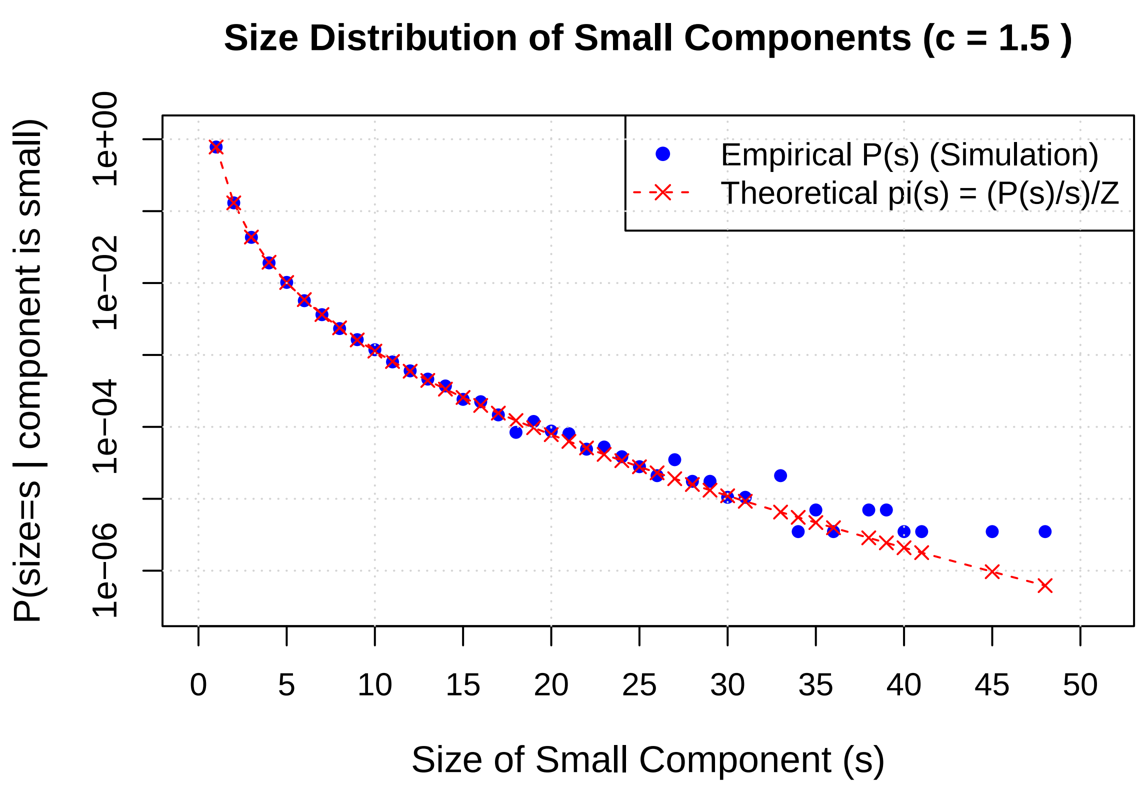
```
## Finished simulations. Collected 285978 small components.
```

```r
# --- Process Collected Data ---
if (total_small_components_collected > 0) {
  # Combine all sizes into one vector
  all_sizes_vector <- unlist(all_small_comp_sizes)

  # Calculate empirical frequency distribution
  # P_emp(s) = (Number of small components of size s) / (Total number of small components)
  size_counts <- table(all_sizes_vector)
  s_values_observed <- as.numeric(names(size_counts))
  pk_empirical <- as.numeric(size_counts) / total_small_components_collected

  # Limit max s for plotting if needed (distribution decays quickly)
  max_s_plot <- min(max(s_values_observed), 50) # Adjust as needed
  # Ensure we only work with s values >= 1 for theoretical part
  s_values_plot_indices <- which(s_values_observed >= 1 & s_values_observed <= max_s_plot)
  s_values_plot <- s_values_observed[s_values_plot_indices]
  pk_empirical_plot <- pk_empirical[s_values_plot_indices]


  # --- Calculate Theoretical Distribution P(s) (Unnormalized mu(s)) ---
  # P(s) = Prob(random vertex is in finite component of size s)
  # Using P(s) = [ (c*s)^(s-1) / s! ] * exp(-c*s)
  pk_theoretical_unnormalized_mu <- numeric(length(s_values_plot))

  for (idx in 1:length(s_values_plot)) {
      s <- s_values_plot[idx]
      # s=1 case
      if (s == 1) {
          log_pk <- -c_fixed
      } else { # s > 1 case
          # Use logs for numerical stability: log(P) = (s-1)*log(c*s) - lgamma(s+1) - c*s
          cs_term = c_fixed * s
          # Check for potential numerical issues or invalid inputs
          if (cs_term <= 0 || !is.finite(cs_term)) {
              log_pk <- -Inf
          } else {
              term1 <- (s - 1) * log(cs_term)
              term2 <- lgamma(s + 1) # log(s!)
              term3 <- c_fixed * s
              # Ensure terms are finite before subtraction
              if (is.finite(term1) && is.finite(term2) && is.finite(term3)) {
                   log_pk <- term1 - term2 - term3
              } else {
                  log_pk <- -Inf # Assign -Inf if any term calculation failed
              }
          }
      }
      # Check for NaN/Inf before exponentiating
      if (is.finite(log_pk)) {
            pk_theoretical_unnormalized_mu[idx] <- exp(log_pk)
```

```
    } else {
          pk_theoretical_unnormalized_mu[idx] <- 0 # Assign 0 if calculation failed
    }
}

# --- Calculate Terms for pi(s) Distribution ---
# pi(s) is proportional to P(s) / s
# This represents the expected number of components of size s (up to a factor n)
terms_pi_s <- pk_theoretical_unnormalized_mu / s_values_plot
# Handle potential division by zero for s=0 (should not be in s_values_plot now)
# Handle potential NaN if pk_theoretical_unnormalized_mu was 0
terms_pi_s[!is.finite(terms_pi_s)] <- 0

# --- Calculate Normalization Constant Z for pi(s) ---
# Z = Sum_{k=1}^\infty (P(k) / k) approximated over the plotted range
# This represents the expected total number of small components (up to a factor n)
normalization_constant_Z <- sum(terms_pi_s, na.rm = TRUE)
cat(sprintf("Normalization Constant Z = Sum(P(k)/k) approx = %.5f\n", normalization_constant_Z))

# --- FINAL Correctly Normalized Theoretical Distribution pi(s) ---
# pi(s) = P(size=s | component is small) = (P(s) / s) / Z
 if (normalization_constant_Z > 1e-12) { # Avoid division by zero
      pk_theoretical_normalized_pi <- terms_pi_s / normalization_constant_Z
 } else {
     pk_theoretical_normalized_pi <- terms_pi_s * 0 # Set to zero if Z is effectively zero
     warning("Normalization constant Z = Sum(P(k)/k) is close to zero.")
 }

# --- Plotting ---
par(mar = c(5, 5, 4, 2) + 0.1) # Adjust margins

# Determine plot range carefully for log scale
# Filter out zero probabilities before taking min for log scale
y_min_emp <- min(pk_empirical_plot[pk_empirical_plot > 0], na.rm = TRUE)
y_min_the <- min(pk_theoretical_normalized_pi[pk_theoretical_normalized_pi > 0], na.rm = TRUE)
y_min_plot <- min(y_min_emp, y_min_the, na.rm = TRUE) * 0.5 # Add buffer below min
if (!is.finite(y_min_plot) || y_min_plot <= 0) y_min_plot <- 1e-8 # Fallback if all are zero or NA

y_max_plot <- max(c(pk_empirical_plot, pk_theoretical_normalized_pi), na.rm = TRUE) * 1.5 # Buffer ab

plot(s_values_plot, pk_empirical_plot,
     type = "p", # Points
     pch = 16,   # Solid circles
     col = "blue",
     cex = 0.9,
     log = "y",  # Log scale for y-axis
     xlab = "Size of Small Component (s)",
     ylab = "P(size=s | component is small)", # Correct label interpretation
     main = paste("Size Distribution of Small Components (c =", c_fixed, ")"),
     ylim = c(y_min_plot, y_max_plot),
     xlim = c(0, max_s_plot + 1),
     cex.lab = 1.2, cex.axis = 1.1, cex.main = 1.2,
     xaxt = "n") # Suppress default x-axis to draw custom ticks
```

```r
  axis(1, at = seq(0, max_s_plot, by = 5)) # Custom x-axis ticks

  # Overlay the NEW theoretical probabilities pi(s)
  points(s_values_plot, pk_theoretical_normalized_pi,
         type = "p", # Points
         pch = 4,    # Crosses
         col = "red",
         cex = 0.9)
  lines(s_values_plot, pk_theoretical_normalized_pi, # Add lines for theoretical
         type = "l",
         col = "red",
         lty = 2) # Dashed line


  # Add a legend
  legend("topright",
         legend = c("Empirical P(s) (Simulation)", "Theoretical pi(s) = (P(s)/s)/Z"), # Updated legend
         col = c("blue", "red"),
         pch = c(16, 4), # Point symbols
         lty = c(NA, 2), # Line type for theoretical
         bg = "white")

  # Add grid lines (corrected)
  grid()

} else {
  cat("No small components were collected during the simulations.\n")
  cat("Try increasing num_simulations or using a 'c' value closer to 1.\n")
}
```

```
## Normalization Constant Z = Sum(P(k)/k) approx = 0.28665
```



**h) Diameter**

Show that the diameter of G(n, p) follows: diameter = A + ln(n)/ln(c) where A is a constant.

```
target_c <- 5.0

n_values <- c(10000, 15000, 20000, 25000, 30000) # Linear scale

# Number of replicates for each n to average out randomness
num_replicates <- 5 # Increase if results are too noisy and time permits

cat(sprintf("Target Average Degree (c): %.2f\n", target_c))
```

```
## Target Average Degree (c): 5.00
```

```
cat("N values to test:", paste(n_values, collapse=", "), "\n")
```

```
## N values to test: 10000, 15000, 20000, 25000, 30000
```

```
cat("Replicates per n:", num_replicates, "\n")
```

```
## Replicates per n: 5
```

```
# --- Storage for Results ---
results <- data.frame(
  n = integer(),
  log_n = numeric(),
  p = numeric(),
  avg_diameter = numeric(),
  sd_diameter = numeric() # Standard deviation of diameter across replicates
)
```

```r
# --- Computational Experiment ---
cat("Running simulations...\n")
```

```
## Running simulations...
```

```r
start_time <- Sys.time()

for (n in n_values) {
  if (n <= 1) next # Skip n=1

  # Calculate p for this n to keep c constant
  p <- target_c / (n - 1)

  # Ensure p is valid
  if (p < 0 || p > 1) {
    cat(sprintf("Skipping n=%d, invalid p=%.5f\n", n, p))
    next
  }

  cat(sprintf("Processing n = %d (p = %.6f)...\n", n, p))
  diameters_for_n <- numeric(num_replicates)

  for (i in 1:num_replicates) {
    g <- sample_gnp(n = n, p = p, directed = FALSE, loops = FALSE)

    # Check connectivity and find largest component
    comp_info <- components(g, mode = "weak") # "strong" or "weak" is same for undirected

    if (comp_info$no == 0) {
        # Empty graph case (shouldn't happen for n>0)
        diameters_for_n[i] <- NA # Or 0? Or handle as error?
        warning(paste("Empty graph generated for n=", n))
    } else if (comp_info$no == 1) {
      # Graph is connected
      diameters_for_n[i] <- diameter(g, unconnected = FALSE) # Use FALSE since known connected
    } else {
      # Graph is disconnected, find diameter of the largest component
      largest_comp_id <- which.max(comp_info$csize)
      nodes_in_largest <- which(comp_info$membership == largest_comp_id)

      # Create subgraph of the largest component
      sg <- induced_subgraph(g, vids = nodes_in_largest)

      if (gorder(sg) > 1) {
          diameters_for_n[i] <- diameter(sg, unconnected = FALSE)
      } else {
          # Largest component has only 1 node (or 0 somehow)
          diameters_for_n[i] <- 0
      }
    }
    # Optional: progress within replicates
    # cat(sprintf("  Rep %d/%d, diameter=%d\n", i, num_replicates, diameters_for_n[i]))
  }
  # Store average and standard deviation
  valid_diameters <- diameters_for_n[!is.na(diameters_for_n)]
  if (length(valid_diameters) > 0) {
      results <- rbind(results, data.frame(
        n = n,
        log_n = log(n), # Natural logarithm
        p = p,
        avg_diameter = mean(valid_diameters),
        sd_diameter = sd(valid_diameters)
     ))
  } else {
      cat(sprintf("Warning: No valid diameters calculated for n=%d\n", n))
  }

}
```

```
## Processing n = 10000 (p = 0.000500)...
## Processing n = 15000 (p = 0.000333)...
## Processing n = 20000 (p = 0.000250)...
## Processing n = 25000 (p = 0.000200)...
## Processing n = 30000 (p = 0.000167)...
```

```r
end_time <- Sys.time()
cat("Simulations finished. Time taken:", format(end_time - start_time), "\n\n")
```

```
## Simulations finished. Time taken: 5.3083 mins
```

```r
# --- Analysis ---
print("--- Simulation Results ---")
```

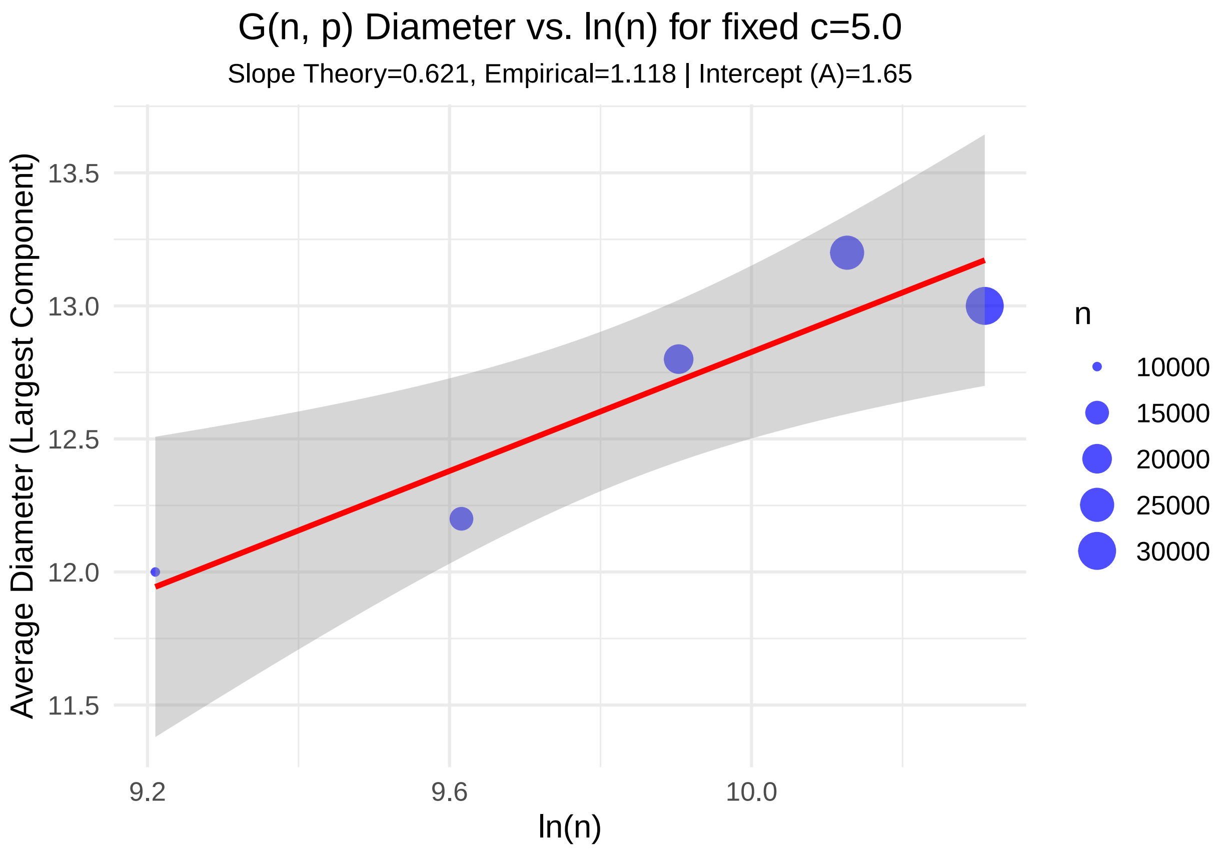
```
## [1] "--- Simulation Results ---"
```

```r
print(results)
```

```
##       n     log_n            p avg_diameter sd_diameter
## 1 10000  9.210340 0.0005000500         12.0   0.7071068
## 2 15000  9.615805 0.0003333556         12.2   0.4472136
## 3 20000  9.903488 0.0002500125         12.8   0.4472136
## 4 25000 10.126631 0.0002000080         13.2   0.4472136
## 5 30000 10.308953 0.0001666722         13.0   0.7071068
```

```r
if (nrow(results) < 2) {
  cat("Not enough data points for regression analysis.\n")
} else {
  # Calculate theoretical slope
  theoretical_slope <- 1 / log(target_c)
  cat(sprintf("\nTheoretical slope (1 / ln(c)) = 1 / ln(%.2f) = %.4f\n",
              target_c, theoretical_slope))

  # Perform linear regression: avg_diameter ~ log(n)
  model <- lm(avg_diameter ~ log_n, data = results)

  cat("\n--- Linear Regression: avg_diameter ~ log(n) ---\n")
  print(summary(model))

  # Extract coefficients
  intercept_A <- coef(model)[1]
  empirical_slope_B <- coef(model)[2]

  cat(sprintf("\nEstimated Intercept (A): %.4f\n", intercept_A))
  cat(sprintf("Estimated Slope (B): %.4f\n", empirical_slope_B))

  # Compare empirical slope with theoretical slope
  cat(sprintf("\nComparison:\n"))
  cat(sprintf("  Theoretical Slope = %.4f\n", theoretical_slope))
  cat(sprintf("  Empirical Slope   = %.4f\n", empirical_slope_B))
  cat(sprintf("  Relative Difference = %.2f %%\n",
              100 * abs(empirical_slope_B - theoretical_slope) / theoretical_slope))

  # --- Plotting ---
  plot_title <- sprintf("G(n, p) Diameter vs. ln(n) for fixed c=%.1f", target_c)
  plot_subtitle <- sprintf("Slope Theory=%.3f, Empirical=%.3f | Intercept (A)=%.2f",
                          theoretical_slope, empirical_slope_B, intercept_A)

  gg <- ggplot(results, aes(x = log_n, y = avg_diameter)) +
    geom_point(aes(size = n), color = "blue", alpha = 0.7) + # Size points by n
    geom_smooth(method = "lm", se = TRUE, color = "red", formula = y ~ x) + # Add regression line + CI
    # Optional: Add error bars if sd_diameter is meaningful
    # geom_errorbar(aes(ymin = avg_diameter - sd_diameter, ymax = avg_diameter + sd_diameter),
    #               width = 0.05, alpha = 0.5) +
    labs(
      title = plot_title,
      subtitle = plot_subtitle,
      x = "ln(n)",
      y = "Average Diameter (Largest Component)",
      size = "n" # Legend title for size
    ) +
    theme_minimal(base_size = 12) +
    theme(plot.title = element_text(hjust = 0.5),
          plot.subtitle = element_text(hjust = 0.5, size=10))

  print(gg)
}
```

```
##
## Theoretical slope (1 / ln(c)) = 1 / ln(5.00) = 0.6213
##
## --- Linear Regression: avg_diameter ~ log(n) ---
##
## Call:
## lm(formula = avg_diameter ~ log_n, data = results)
##
## Residuals:
##        1        2        3        4        5
##  0.05595 -0.19721  0.08127  0.23188 -0.17189
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.6503     2.3789   0.694   0.5377
## log_n         1.1176     0.2417   4.623   0.0191 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2097 on 3 degrees of freedom
## Multiple R-squared:  0.8769, Adjusted R-squared:  0.8359
## F-statistic: 21.37 on 1 and 3 DF,  p-value: 0.01905
##
##
## Estimated Intercept (A): 1.6503
## Estimated Slope (B): 1.1176
##
## Comparison:
##   Theoretical Slope = 0.6213
##   Empirical Slope   = 1.1176
##   Relative Difference = 79.87 %
```



## 2) Empirical Analysis of Real-World Network

Analyze the ca-GrQc dataset from https://snap.stanford.edu/data/ca-GrQc.html in the Stanford Large Network Dataset Collection.

```r
txt_file <- "/Users/log/Github/Spring2025Classes/social_networks/project6/ca-GrQc.txt"

edges <- read.table(txt_file, skip = 4, header = FALSE)
colnames(edges) <- c("FromNodeId", "ToNodeId")
g <- graph_from_data_frame(edges, directed = FALSE)
g <- simplify(g, remove.multiple = TRUE, remove.loops = TRUE)
```

```r
print(paste("Number of nodes:", vcount(g)))
```

```
## [1] "Number of nodes: 5242"
```

```r
print(paste("Number of edges:", ecount(g)))
```

```
## [1] "Number of edges: 14484"
```

## Optimize this

### a) Construct a graph G based on the data set

Analyze some basic network properties of G including order, size, density, connectivity (if G is not connected, find the number of components of G and the fraction of vertices in the largest component), and clustering coefficient.

```r
num_nodes <- vcount(g)
print(paste("Order (Number of Nodes):", num_nodes))
```

```
## [1] "Order (Number of Nodes): 5242"
```

```r
# 2. Size (Number of Edges)
num_edges <- ecount(g)
print(paste("Size (Number of Edges):", num_edges))
```

```
## [1] "Size (Number of Edges): 14484"
```

```r
# 3. Density
# Density = E / E_max, where E is the number of edges, E_max is the max possible edges.
# For an undirected graph without loops, E_max = N * (N - 1) / 2
graph_density <- edge_density(g)
print(paste("Density:", sprintf("%.6f", graph_density))) # Format for readability
```

```
## [1] "Density: 0.001054"
```

```r
# 4. Connectivity
is_graph_connected <- is_connected(g)
print(paste("Is the graph connected?", is_graph_connected))
```

```
## [1] "Is the graph connected? FALSE"
```

```r
if (!is_graph_connected) {
  components_info <- components(g)
  num_components <- components_info$no
  print(paste("Number of connected components:", num_components))

  # Size of the largest component
  lcc_size <- max(components_info$csize)
  print(paste("Size of the largest connected component (LCC):", lcc_size))

  # Fraction of vertices in the largest component
  fraction_in_lcc <- lcc_size / num_nodes
  print(paste("Fraction of vertices in LCC:", sprintf("%.4f", fraction_in_lcc)))
} else {
  print("The graph is connected, consisting of a single component.")
  # If connected, LCC size is total nodes, fraction is 1.
  lcc_size <- num_nodes
  fraction_in_lcc <- 1.0
  print(paste("Size of the largest connected component (LCC):", lcc_size))
  print(paste("Fraction of vertices in LCC:", sprintf("%.4f", fraction_in_lcc)))
}
```

```
## [1] "Number of connected components: 355"
## [1] "Size of the largest connected component (LCC): 4158"
## [1] "Fraction of vertices in LCC: 0.7932"
```

```
# 5. Clustering Coefficient (Transitivity)
# igraph provides two main types:
# - Global clustering coefficient (transitivity): ratio of triangles to connected triples
# - Average clustering coefficient: average of the local clustering coefficient for each node

global_cc <- transitivity(g, type = "global")
average_cc <- transitivity(g, type = "average")

print(paste("Global Clustering Coefficient (Transitivity):", sprintf("%.4f", global_cc)))
```

```
## [1] "Global Clustering Coefficient (Transitivity): 0.6298"
```

```
print(paste("Average Clustering Coefficient:", sprintf("%.4f", average_cc)))
```

```
## [1] "Average Clustering Coefficient: 0.6865"
```

```
# Store results for potential later use
basic_properties <- list(
  order = num_nodes,
  size = num_edges,
  density = graph_density,
  is_connected = is_graph_connected,
  num_components = if (!is_graph_connected) components_info$no else 1,
  lcc_size = lcc_size,
  fraction_in_lcc = fraction_in_lcc,
  global_clustering_coeff = global_cc,
  average_clustering_coeff = average_cc
)
```

### b) Generate a configuration model G*

Generate a configuration model G* that has the same degree sequence as that of G's.

```
g_undir <- as.undirected(g, mode = "collapse")
```

```
## Warning: `as.undirected()` was deprecated in igraph 2.1.0.
## i Please use `as_undirected()` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
deg_seq_original <- degree(g_undir)
print(paste("Successfully extracted degree sequence from the original graph. Number of degrees:", lengt
```

```
## [1] "Successfully extracted degree sequence from the original graph. Number of degrees: 5242"
```

```
# Check if the sum of degrees is even (necessary condition for graph construction)
if (sum(deg_seq_original) %% 2 != 0) {
  stop("Sum of degrees is odd. Cannot construct a graph with this degree sequence. This is unexpected f
} else {
```

```r
    print("Sum of degrees is even, proceeding to generate G*.")
}
```

```
## [1] "Sum of degrees is even, proceeding to generate G*."
```

```r
# 2. Generate the configuration model graph G* using sample_degseq
# We use the degree sequence from the original graph 'g_undir'.
# The method 'fast.heur.simple' is recommended by igraph warnings over 'simple.no.multiple'.
# It attempts to create a simple graph (no loops, no multiple edges) matching the degree sequence.
# Note: The *pure* configuration model allows loops and multi-edges (methods 'simple' or 'vl'),
# but often the goal is to compare against a simple graph, hence this method choice.
print("Generating Configuration Model graph G*...")
```

```
## [1] "Generating Configuration Model graph G*..."
```

```r
G_star <- sample_degseq(deg_seq_original, method = "fast.heur.simple")
print("Configuration Model graph G* generated successfully.")
```

```
## [1] "Configuration Model graph G* generated successfully."
```

```r
# 3. Optional Verification: Check if G* has the correct degree sequence
deg_seq_G_star <- degree(G_star)
if (length(deg_seq_original) == length(deg_seq_G_star) && all(sort(deg_seq_original) == sort(deg_seq_G_s
  print("Verification successful: G* has the same degree sequence as G.")
} else {
  warning("Verification potentially failed: The degree sequence of G* does not perfectly match G. This m
  # You could add more detailed comparison here if needed
  # print(summary(deg_seq_original))
  # print(summary(deg_seq_G_star))
}
```

```
## [1] "Verification successful: G* has the same degree sequence as G."
```

```r
deg_seq_G_star <- degree(G_star)
print("Extracted degree sequence from the Configuration Model graph G*.")
```

```
## [1] "Extracted degree sequence from the Configuration Model graph G*."
```

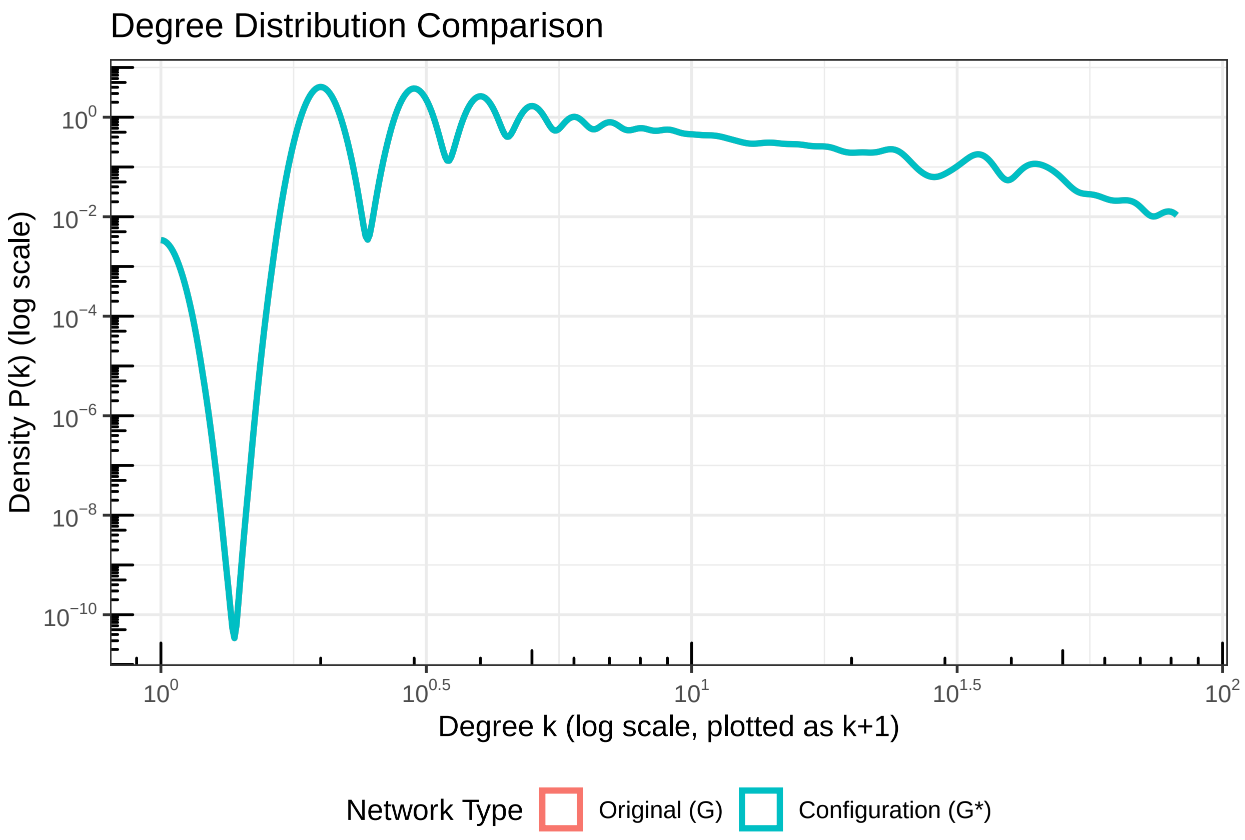
```r
# Create a data frame suitable for ggplot
# Combine degree sequences and add a factor to identify the network
deg_df <- data.frame(
  Degree = c(deg_seq_original, deg_seq_G_star),
  Network = factor(
              rep(c("Original (G)", "Configuration (G*)"),
                  times = c(length(deg_seq_original), length(deg_seq_G_star))),
              levels = c("Original (G)", "Configuration (G*)") # Control plotting order
            )
)

print("Created combined data frame for plotting.")
```

```
## [1] "Created combined data frame for plotting."
```

```r
head(deg_df) # Show the first few rows
```

```
##   Degree      Network
## 1      8 Original (G)
## 2     13 Original (G)
## 3      29 Original (G)
## 4      20 Original (G)
## 5       4 Original (G)
## 6      25 Original (G)
```

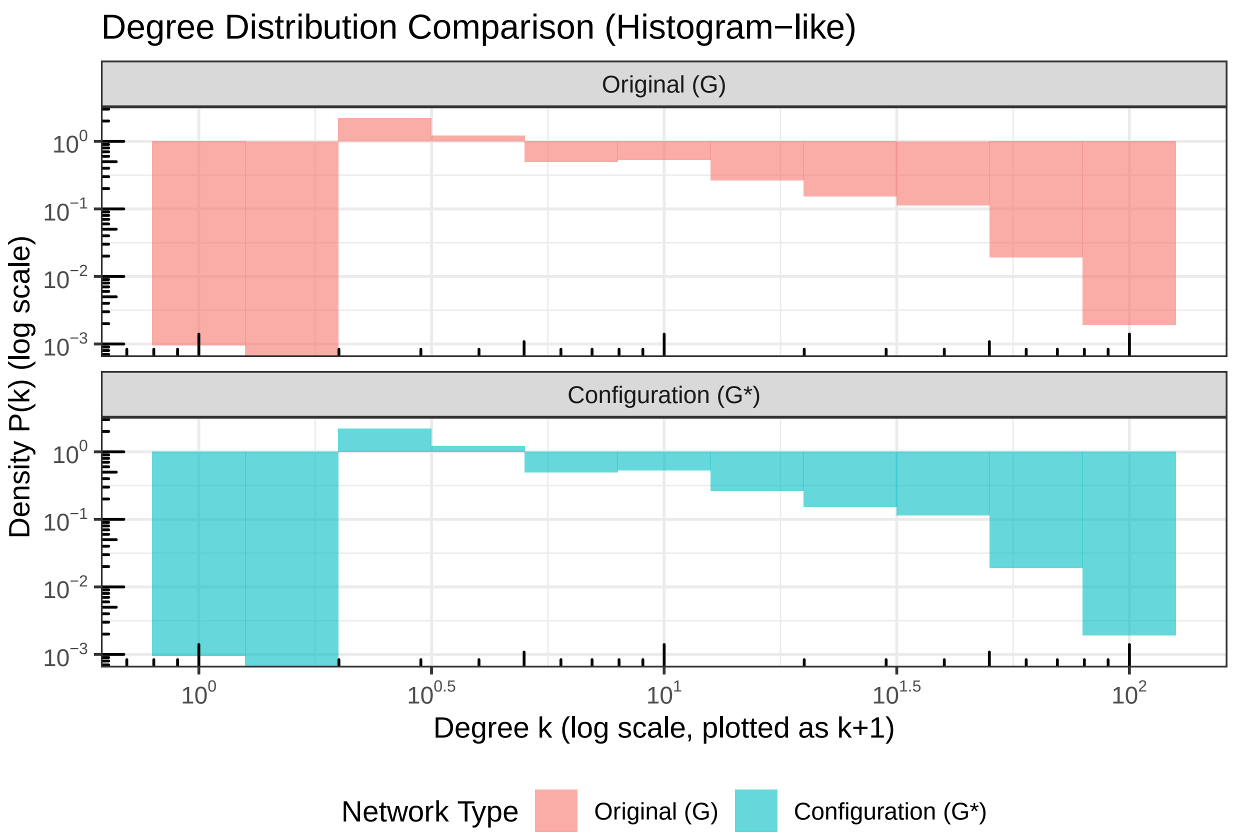
```r
# --- Plotting the Degree Distributions ---

# Using density plots on a log-log scale is common for network degrees

plot_deg_dist <- ggplot(deg_df, aes(x = Degree + 1, color = Network)) + # Add 1 to Degree to avoid log(
  geom_density(alpha = 0.7, linewidth = 1.1, adjust=0.5) + # Use geom_density for smoothed distribution
  scale_x_log10(breaks = scales::trans_breaks("log10", function(x) 10^x), # Log scale for x-axis
                labels = scales::trans_format("log10", scales::math_format(10^.x))) +
  scale_y_log10(breaks = scales::trans_breaks("log10", function(x) 10^x), # Log scale for y-axis
                labels = scales::trans_format("log10", scales::math_format(10^.x))) +
  labs(
    title = "Degree Distribution Comparison",
    x = "Degree k (log scale, plotted as k+1)",
    y = "Density P(k) (log scale)",
    color = "Network Type" # Legend title
  ) +
  theme_bw() + # A clean theme
  theme(legend.position = "bottom") +
  annotation_logticks() # Add log tick marks

# Print the plot
print(plot_deg_dist)
```



```r
# --- Alternative: Histogram-like plot using stat_bin ---
# This gives a feel closer to the binned plots in the original example, but automated by ggplot
# Note: You might need to adjust binwidth or bins for a good look

plot_deg_hist <- ggplot(deg_df, aes(x = Degree + 1, fill = Network)) + # Add 1 to Degree to avoid log(0
  # Use stat_bin to create histogram bars, position="identity" overlays them
  # Use ..density.. on y-axis to get probability density
  stat_bin(aes(y = ..density..), binwidth = 0.2, position = "identity", alpha = 0.6) +
  scale_x_log10(breaks = scales::trans_breaks("log10", function(x) 10^x),
                labels = scales::trans_format("log10", scales::math_format(10^.x))) +
  scale_y_log10(breaks = scales::trans_breaks("log10", function(x) 10^x),
                labels = scales::trans_format("log10", scales::math_format(10^.x)),
                limits = c(NA, NA)) + # Adjust y-limits if needed, NA keeps defaults
  labs(
    title = "Degree Distribution Comparison (Histogram-like)",
    x = "Degree k (log scale, plotted as k+1)",
    y = "Density P(k) (log scale)",
    fill = "Network Type"
  ) +
  theme_bw() +
  theme(legend.position = "bottom") +
  annotation_logticks() +
  facet_wrap(~Network, ncol=1) # Separate panels for clarity

print(plot_deg_hist)
```

```
## Warning: The dot-dot notation (`..density..`) was deprecated in ggplot2 3.4.0.
## i Please use `after_stat(density)` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
## Warning in scale_y_log10(breaks = scales::trans_breaks("log10", function(x)
## 10^x), : log-10 transformation introduced infinite values.
```



### c) Analyze model properties Analyze some basic network properties of G*.

```
num_nodes_star <- vcount(G_star)
print(paste("G* Order (Number of Nodes):", num_nodes_star))
```

```
## [1] "G* Order (Number of Nodes): 5242"
```

```
# 2. Size (Number of Edges)
# Should be the same as the original graph because the degree sequence sum is preserved
num_edges_star <- ecount(G_star)
print(paste("G* Size (Number of Edges):", num_edges_star))
```

```
## [1] "G* Size (Number of Edges): 14484"
```

```
# 3. Density
# Density = E / E_max, where E is the number of edges, E_max is the max possible edges.
# For an undirected graph without loops, E_max = N * (N - 1) / 2
# Should be the same as the original graph if N and E are the same.
graph_density_star <- edge_density(G_star)
print(paste("G* Density:", sprintf("%.6f", graph_density_star))) # Format for readability
```

```
## [1] "G* Density: 0.001054"
```

```
# 4. Connectivity
is_connected_star <- is_connected(G_star)
print(paste("Is G* connected?", is_connected_star))
```

```
## [1] "Is G* connected? FALSE"
```

```
if (!is_connected_star) {
  components_info_star <- components(G_star)
```

```r
  num_components_star <- components_info_star$no
  print(paste("G* Number of connected components:", num_components_star))

  # Size of the largest component in G*
  lcc_size_star <- max(components_info_star$csize)
  print(paste("G* Size of the largest connected component (LCC):", lcc_size_star))

  # Fraction of vertices in the largest component in G*
  fraction_in_lcc_star <- lcc_size_star / num_nodes_star
  print(paste("G* Fraction of vertices in LCC:", sprintf("%.4f", fraction_in_lcc_star)))
} else {
  print("G* is connected, consisting of a single component.")
  # If connected, LCC size is total nodes, fraction is 1.
  lcc_size_star <- num_nodes_star
  fraction_in_lcc_star <- 1.0
  print(paste("G* Size of the largest connected component (LCC):", lcc_size_star))
  print(paste("G* Fraction of vertices in LCC:", sprintf("%.4f", fraction_in_lcc_star)))
}
```

```
## [1] "G* Number of connected components: 22"
## [1] "G* Size of the largest connected component (LCC): 5197"
## [1] "G* Fraction of vertices in LCC: 0.9914"
```

```r
# 5. Clustering Coefficient (Transitivity)
# Global clustering coefficient (transitivity)
global_cc_star <- transitivity(G_star, type = "global")

# Average clustering coefficient
# Note: transitivity(type="average") might return NaN if degrees are low or graph is small.
# A more robust way is often to calculate local CC for each node and average non-NaN values.
local_cc_vector_star <- transitivity(G_star, type = "local")
average_cc_star <- mean(local_cc_vector_star, na.rm = TRUE) # Average excluding NaNs

print(paste("G* Global Clustering Coefficient (Transitivity):", sprintf("%.4f", global_cc_star)))
```

```
## [1] "G* Global Clustering Coefficient (Transitivity): 0.0081"
```

```r
print(paste("G* Average Clustering Coefficient:", sprintf("%.4f", average_cc_star)))
```

```
## [1] "G* Average Clustering Coefficient: 0.0081"
```

```r
# Store results for potential later use or comparison
basic_properties_star <- list(
  order = num_nodes_star,
  size = num_edges_star,
  density = graph_density_star,
  is_connected = is_connected_star,
  num_components = if (!is_connected_star) components_info_star$no else 1,
  lcc_size = lcc_size_star,
  fraction_in_lcc = fraction_in_lcc_star,
  global_clustering_coeff = global_cc_star,
  average_clustering_coeff = average_cc_star
)

print("--- Analysis of G* complete ---")
```

```
## [1] "--- Analysis of G* complete ---"
```

```
if (exists("basic_properties")) {
    print("--- Comparison G vs G* ---")
    print(paste("Order: G =", basic_properties$order))
    print(paste("Size: G =", basic_properties$size))
    print(paste("Density: G =", sprintf("%.6f", basic_properties$density)))
    print(paste("Connected: G =", basic_properties$is_connected))
    print(paste("# Components: G =", basic_properties$num_components))
    print(paste("LCC Fraction: G =", sprintf("%.4f", basic_properties$fraction_in_lcc)))
    print(paste("Global CC: G =", sprintf("%.4f", basic_properties$global_clustering_coeff)))
    print(paste("Average CC: G =", sprintf("%.4f", basic_properties$average_clustering_coeff)))
    print("---------------------------")
}
```

```
## [1] "--- Comparison G vs G* ---"
## [1] "Order: G = 5242"
## [1] "Size: G = 14484"
## [1] "Density: G = 0.001054"
## [1] "Connected: G = FALSE"
## [1] "# Components: G = 355"
## [1] "LCC Fraction: G = 0.7932"
## [1] "Global CC: G = 0.6298"
## [1] "Average CC: G = 0.6865"
## [1] "---------------------------"
```

### d) Compare networks

identify similarities and differences between G and G*.

```
if (exists("basic_properties")) {
    print("--- Comparison G vs G* ---")
    print(paste("Order: G =", basic_properties$order, ", G* =", basic_properties_star$order))
    print(paste("Size: G =", basic_properties$size, ", G* =", basic_properties_star$size))
    print(paste("Density: G =", sprintf("%.6f", basic_properties$density), ", G* =", sprintf("%.6f", bas
    print(paste("Connected: G =", basic_properties$is_connected, ", G* =", basic_properties_star$is_conn
    print(paste("# Components: G =", basic_properties$num_components, ", G* =", basic_properties_star$nu
    print(paste("LCC Fraction: G =", sprintf("%.4f", basic_properties$fraction_in_lcc), ", G* =", sprin
    print(paste("Global CC: G =", sprintf("%.4f", basic_properties$global_clustering_coeff), ", G* =", s
    print(paste("Average CC: G =", sprintf("%.4f", basic_properties$average_clustering_coeff), ", G* ="
    print("---------------------------")
}
```

```
## [1] "--- Comparison G vs G* ---"
## [1] "Order: G = 5242 , G* = 5242"
## [1] "Size: G = 14484 , G* = 14484"
## [1] "Density: G = 0.001054 , G* = 0.001054"
## [1] "Connected: G = FALSE , G* = FALSE"
## [1] "# Components: G = 355 , G* = 22"
## [1] "LCC Fraction: G = 0.7932 , G* = 0.9914"
## [1] "Global CC: G = 0.6298 , G* = 0.0081"
## [1] "Average CC: G = 0.6865 , G* = 0.0081"
## [1] "---------------------------"
```

```
print("--- Calculating Assortativity ---")
```

```
## [1] "--- Calculating Assortativity ---"
```

```r
assort_g <- assortativity_degree(g_undir, directed = FALSE)
assort_g_star <- assortativity_degree(G_star, directed = FALSE)

print(paste("Assortativity (G):", sprintf("%.4f", assort_g)))
```

```
## [1] "Assortativity (G): 0.6593"
```

```r
print(paste("Assortativity (G*):", sprintf("%.4f", assort_g_star)))
```

```
## [1] "Assortativity (G*): -0.0068"
```

```r
print("Interpretation: Positive values indicate assortativity (high-degree nodes connect to high-degree
```

```
## [1] "Interpretation: Positive values indicate assortativity (high-degree nodes connect to high-degre
```

```r
print("----------------------------------")
```

```
## [1] "----------------------------------"
```

```r
# --- 2. Average Path Length ---
print("--- Calculating Average Path Length (may take time) ---")
```

```
## [1] "--- Calculating Average Path Length (may take time) ---"
```

```r
avg_path_g <- mean_distance(g_undir, directed = FALSE)
avg_path_g_star <- mean_distance(G_star, directed = FALSE)

print(paste("Average Path Length (G):", sprintf("%.4f", avg_path_g)))
```

```
## [1] "Average Path Length (G): 6.0485"
```

```r
print(paste("Average Path Length (G*):", sprintf("%.4f", avg_path_g_star)))
```

```
## [1] "Average Path Length (G*): 4.3367"
```

```r
# --- 3. Diameter ---
print("--- Calculating Diameter (may take time) ---")
```

```
## [1] "--- Calculating Diameter (may take time) ---"
```

```r
diam_g <- diameter(g_undir, directed = FALSE, unconnected = TRUE)
diam_g_star <- diameter(G_star, directed = FALSE, unconnected = TRUE)

print(paste("Diameter (G):", diam_g))
```

```
## [1] "Diameter (G): 17"
```

```r
print(paste("Diameter (G*):", diam_g_star))
```

```
## [1] "Diameter (G*): 11"
```

```r
print("(Note: For disconnected graphs, diameter is often calculated for the LCC or reported as Inf)")
```

```
## [1] "(Note: For disconnected graphs, diameter is often calculated for the LCC or reported as Inf)"
```

```r
print("----------------------------------")
```

```
## [1] "----------------------------------"
```

```r
# --- 4. Centrality Distributions ---
print("--- Calculating Centrality Distributions (may take time) ---")
```

```
## [1] "--- Calculating Centrality Distributions (may take time) ---"
```

```r
# a) Betweenness Centrality
print("Calculating Betweenness...")
```

```
## [1] "Calculating Betweenness..."
```

```r
btw_g <- betweenness(g_undir, directed = FALSE, normalized = TRUE)
btw_g_star <- betweenness(G_star, directed = FALSE, normalized = TRUE)

# b) Closeness Centrality
print("Calculating Closeness...")
```

```
## [1] "Calculating Closeness..."
```

```r
close_g <- closeness(g_undir, mode = "total", normalized = TRUE)
close_g_star <- closeness(G_star, mode = "total", normalized = TRUE)

# c) Eigenvector Centrality
print("Calculating Eigenvector...")
```

```
## [1] "Calculating Eigenvector..."
```

```r
eig_g_result <- eigen_centrality(g_undir, directed = FALSE, scale = TRUE)
```

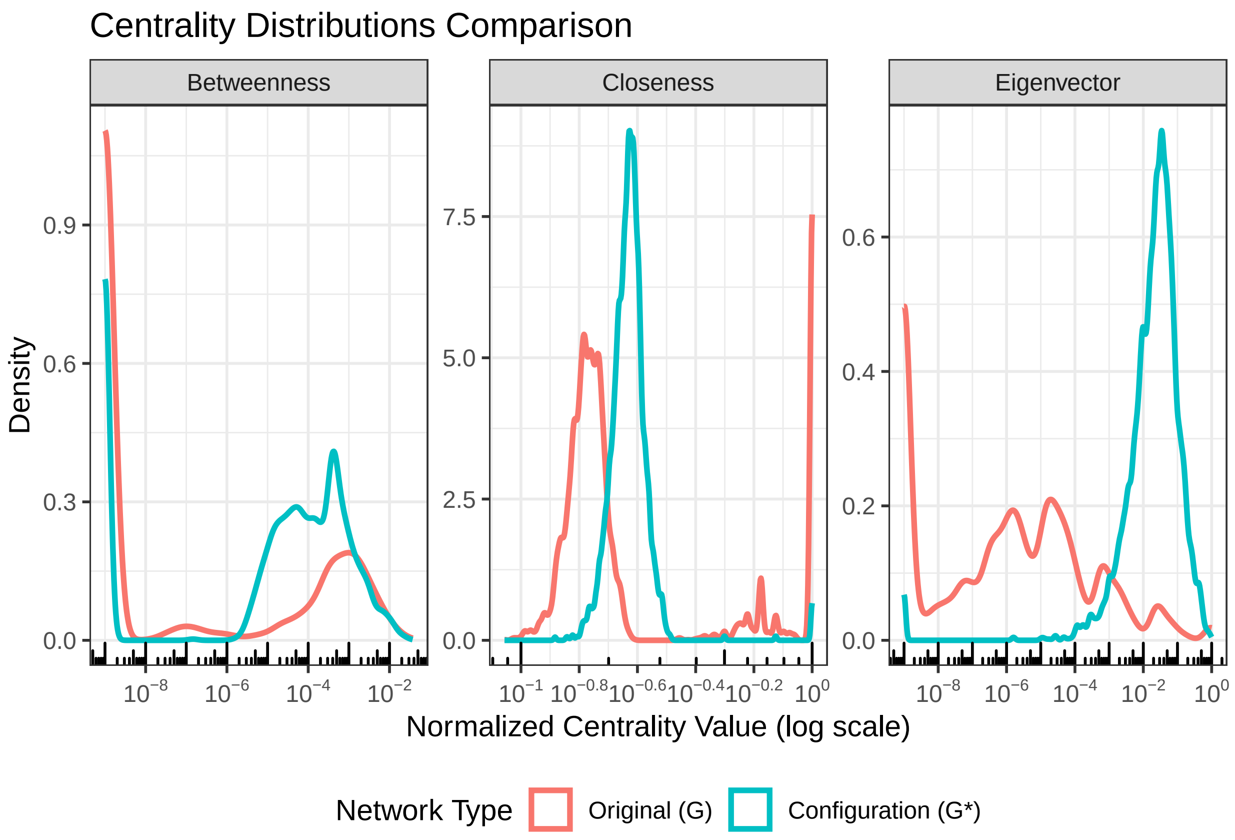
```
## Warning: The `scale` argument of `eigen_centrality()` is deprecated as of igraph 2.1.1.
## i eigen_centrality() will always behave as if scale=TRUE were used.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```r
eig_g_star_result <- eigen_centrality(G_star, directed = FALSE, scale = TRUE)
eig_g <- eig_g_result$vector
eig_g_star <- eig_g_star_result$vector


# --- Plotting Centrality Distributions ---
print("Plotting Centrality Distributions...")
```

```
## [1] "Plotting Centrality Distributions..."
```

```r
# Combine data for plotting
centrality_df <- data.frame(
  Value = c(btw_g, btw_g_star, close_g, close_g_star, eig_g, eig_g_star),
  Centrality = factor(rep(c("Betweenness", "Closeness", "Eigenvector"),
                         each = length(btw_g) + length(btw_g_star))),
  Network = factor(rep(rep(c("Original (G)", "Configuration (G*)"), each = length(btw_g)), 3),
                  levels = c("Original (G)", "Configuration (G*)"))
)

# Plotting (using density plots, add + small constant for log scale if needed)
plot_centrality <- ggplot(centrality_df, aes(x = Value + 1e-9, color = Network)) + # Add small value fo
  geom_density(alpha = 0.7, linewidth=1.0, adjust=0.5) +
  scale_x_log10(breaks = scales::trans_breaks("log10", function(x) 10^x),
               labels = scales::trans_format("log10", scales::math_format(10^.x))) +
  facet_wrap(~ Centrality, scales = "free") +
  labs(
    title = "Centrality Distributions Comparison",
    x = "Normalized Centrality Value (log scale)",
    y = "Density",
    color = "Network Type"
  ) +
  theme_bw() +
  theme(legend.position = "bottom") +
  annotation_logticks(sides = "b")

print(plot_centrality)
```

```
## Warning: Removed 2 rows containing non-finite outside the scale range
## (`stat_density()`).
```



```
print("---------------------------------")
```

```
## [1] "---------------------------------"
```

```
# --- 5. Community Detection ---
print("--- Performing Community Detection (Louvain) ---")
```

```
## [1] "--- Performing Community Detection (Louvain) ---"
```

```
# Run Louvain algorithm
comm_g <- cluster_louvain(g_undir)
comm_g_star <- cluster_louvain(G_star)

# Compare Modularity
mod_g <- modularity(comm_g)
mod_g_star <- modularity(comm_g_star)
print(paste("Modularity (G):", sprintf("%.4f", mod_g)))
```

```
## [1] "Modularity (G): 0.8613"
```

```r
print(paste("Modularity (G*):", sprintf("%.4f", mod_g_star)))
```

```
## [1] "Modularity (G*): 0.4089"
```

```r
print("Higher modularity suggests stronger community structure.")
```

```
## [1] "Higher modularity suggests stronger community structure."
```

```r
# Compare Number of Communities
num_comm_g <- length(sizes(comm_g))
num_comm_g_star <- length(sizes(comm_g_star))
print(paste("Number of Communities (G):", num_comm_g))
```

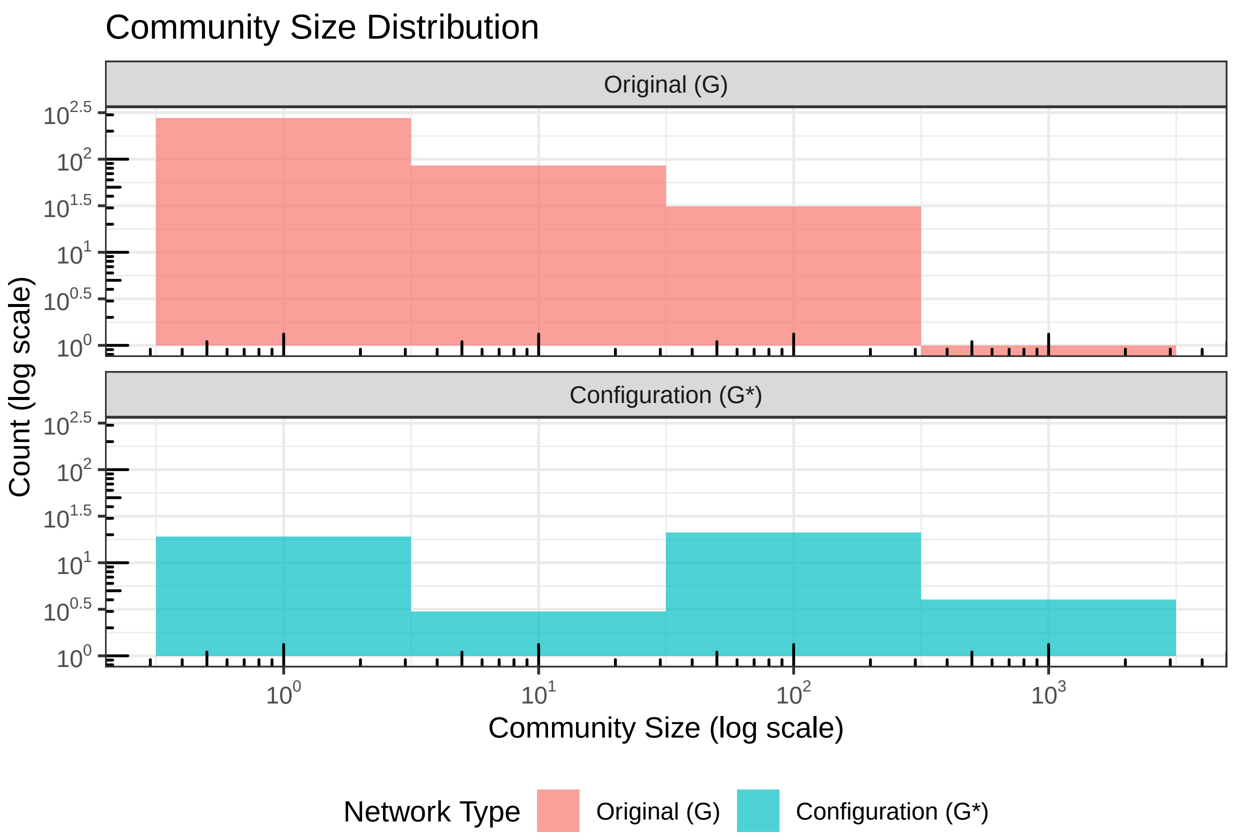
```
## [1] "Number of Communities (G): 392"
```

```r
print(paste("Number of Communities (G*):", num_comm_g_star))
```

```
## [1] "Number of Communities (G*): 47"
```

```r
# Compare Community Size Distributions
sizes_g <- sizes(comm_g)
sizes_g_star <- sizes(comm_g_star)

community_size_df <- data.frame(
  Size = c(as.numeric(sizes_g), as.numeric(sizes_g_star)),
  Network = factor(rep(c("Original (G)", "Configuration (G*)"),
                       times = c(length(sizes_g), length(sizes_g_star))),
                   levels = c("Original (G)", "Configuration (G*)"))
)

# Plotting community size distributions (histogram often works well)
plot_comm_sizes <- ggplot(community_size_df, aes(x = Size, fill = Network)) +
  geom_histogram(binwidth = 1, position = "identity", alpha = 0.7) + # Adjust binwidth as needed
  scale_x_log10(breaks = scales::trans_breaks("log10", function(x) 10^x),
                labels = scales::trans_format("log10", scales::math_format(10^.x))) +
  scale_y_log10(breaks = scales::trans_breaks("log10", function(x) 10^x),
                labels = scales::trans_format("log10", scales::math_format(10^.x))) +
  labs(
    title = "Community Size Distribution",
    x = "Community Size (log scale)",
    y = "Count (log scale)",
    fill = "Network Type"
  ) +
  theme_bw() +
  theme(legend.position = "bottom") +
  annotation_logticks() +
  facet_wrap(~Network, ncol=1) # Separate panels often clearer for histograms

print(plot_comm_sizes)
```

```
## Warning in scale_y_log10(breaks = scales::trans_breaks("log10", function(x)
## 10^x), : log-10 transformation introduced infinite values.
```


Community Size Distribution
Original (G)
Configuration (G*)
Count (log scale)
$10^{2.5}$
$10^{2}$
$10^{1.5}$
$10^{1}$
$10^{0.5}$
$10^{0}$
$10^{0}$
$10^{1}$
$10^{2}$
$10^{3}$
Community Size (log scale)
Network Type
Original (G)
Configuration (G*)