**Questions**

1. Overall structure of the plant-pollinator network?
   1. Function plotweb() creates the bipartite network plot
      1. Rectangles: species
         1. Top rectangles: higher trophic level (pollinators)
         2. Bottom rectangles: lower trophic level (plants)
      2. Line widths
         1. Strength of interactions/frequency of visits
2. Which pollinator species are most important?

**Figures:**

1. Bipartite Network Plot
   1. plotweb()
2. Interaction Matrix Visualization
   1. visweb()
3. Bar Plot of Pollinator Importance
   1. barplot()

**Example Code**

# Install and load required package

if (!requireNamespace("bipartite", quietly = TRUE)) {

install.packages("bipartite")

}

library(bipartite)

# Load and prepare data

data <- read.csv("Cleaned\_Plant-Pollinator\_Dataset.csv", row.names = 1) # Replace with your file path

interaction\_matrix <- as.matrix(data)

# --- Question 1: Overall Network Structure ---

# Visualize the network

plotweb(interaction\_matrix)

# Calculate and display network-level metrics

network\_metrics <- networklevel(interaction\_matrix)

print(network\_metrics)

# Visualize interaction diversity

visweb(interaction\_matrix, type = "diagonal")

# --- Question 2: Key Pollinator Species ---

# Calculate species-level metrics

species\_metrics <- specieslevel(interaction\_matrix)

# Extract pollinator metrics (higher level)

pollinator\_metrics <- species\_metrics$`higher level` # Pollinators are columns

important\_pollinators <- pollinator\_metrics[order(-pollinator\_metrics$`dependence`), ] # Sort by importance

# Print sorted metrics

print(important\_pollinators)

# Visualize pollinator importance with a barplot

barplot(important\_pollinators$`dependence`,

names.arg = rownames(important\_pollinators),

las = 2,

main = "Pollinator Dependence",

ylab = "Dependence")