

Assignment 2

Deconstruct, Reconstruct Web Report

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Antibiotic Resistance: A Comprehensive Analysis

Statement of Purpose

The aim of this study is two-fold: 1. To provide an effective visualization that educates the general public about the dangers of excessive antibiotic use. 2. To offer infectious disease doctors a quick yet comprehensive overview of antibiotic resistance in commonly encountered bacteria.

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Introduction

The following report aims to provide a detailed understanding of a dataset concerning antibiotic resistance across various bacterial species. This topic is of growing concern in the medical and scientific community.

Columns Explained

Column	Description
Bacterium Name	Scientific name of the bacteria.
Causes	Diseases or conditions that the bacteria typically cause.
Gram-negative?	Indicates whether the bacterium is Gram-negative ('yes' or 'no').
Individual Drugs	Resistance levels to specific antibiotics, represented as percentages.
Remarks	Additional comments about antibiotic resistance.
Resistance Score	A scale from 1-4 indicating the level of concern, with higher scores being more concerning.
N Antibiotics or Classes	Number of antibiotics or classes showing at least some resistance.
Average % Resistance	Calculated average resistance score across all considered antibiotics.

Key Highlights

Bacterial Species of Concern

1. **A. baumannii**
 - Nicknamed "Iraqibacter"
 - High resistance to multiple antibiotics
 - Resistance score: 4
2. **E. faecium**
 - 75% resistance to a specific antibiotic
 - Average resistance: 47%
3. **N. gonorrhoeae**
 - Causes gonorrhea
 - Resistance score: 3

- 14.35% average resistance
4. **M. tuberculosis**
 - Extremely drug-resistant variants
 - Resistance score: 3
 5. **S. aureus**
 - 25.90% average resistance but to only one antibiotic class
 6. **Note After 1992**
 - No major new antibiotics have been developed for over 20 years.
 7. **Gram-negative Bacteria**
 - Typically more resistant due to their cell wall structure.
-

Key Concerns

1. **Rising Resistance:** Resistance is stable or increasing for many bacteria.
 2. **Multi-drug Resistance:** Resistance to multiple classes of antibiotics.
 3. **Gram-negative Bacteria:** More resistant and increasing so over time.
 4. **Data Gaps:** Unquantified resistances could underrepresent actual resistance levels.
-

Conclusion

This dataset serves as a snapshot that underlines the urgency for new antibiotics and effective strategies to manage antibiotic resistance. It calls for immediate action from both the medical community and policymakers.

References

- [Original data visualization source](#)
- [Data](#)
- Centre for Disease Dynamics
- World Health Organisation
- CDC (US data)

Deconstruct

Original

The original data visualisation selected for the assignment was as follows:

Source: ACMA Research and Analysis Section (2015).

Objective and Audience

The objective and audience of the original data visualisation chosen can be summarised as follows:

Objective

Audience

Critique

The visualisation chosen had the following three main issues:

- Briefly explain issue 1
- Briefly explain issue 2

- Briefly explain issue 3

Reconstruct

Code

The following code was used to fix the issues identified in the original.

```
# Read and preprocess libraries
library(readxl)
library(dplyr)
library(stringr)
library(writexl)
```

```
# Load necessary libraries
library(ggplot2)
library(tidyr)
```

Pre-processing

```
# Comment: Read Excel data from the first sheet
data <- read_excel("../data/antibiotic_data.xlsx", sheet = 1)

# Comment: Rename Columns
# Assuming the first row has column names that need renaming
names(data) <- str_replace_all(names(data), c(" " = "_", "%" = "percent", "-" = "_"))

# Comment: Save the cleaned data into a new CSV file
write.csv(data, "../data/cleaned_antibiotic_data.csv", row.names = FALSE)

data
```

```
## # A tibble: 20 x 49
##   Antibiotic~1 by_In~2 Antib~3 Penic~4 Penic~5 Amino~6 Amino~7 Other~8 Macro~9
##   <chr>         <chr>   <chr>   <chr>   <chr>   <chr>   <chr>   <chr>   <chr>
## 1 Adding up dr "data ~ Indivi~ all   Penici~ all   Strept~ Chlora~ all
## 2 Bacterium na "Cause~ Gram n~ <NA>   <NA>   <NA>   <NA>   <NA>   <NA>
## 3 A. baumanii  "\"Ira~ yes    x      x      0.46   <NA>   <NA>   x
## 4 K. pneumoniae "pneum~ yes    <NA>   <NA>   0.08   <NA>   <NA>   <NA>
## 5 E. faecium    "urina~ <NA>   <NA>   <NA>   <NA>   <NA>   <NA>   <NA>
## 6 N. gonorrhoe~ "gonor~ yes    0.3    x      <NA>   <NA>   <NA>   <NA>
## 7 Shigella      "dysen~ yes    <NA>   <NA>   <NA>   0.56   0.14   <NA>
## 8 M. tuberculo~ "tuber~ <NA>   <NA>   <NA>   <NA>   <NA>   <NA>   <NA>
## 9 P. mirabilis  "kidne~ <NA>   <NA>   <NA>   0.09   <NA>   <NA>   <NA>
## 10 CoNS         "food ~ <NA>   <NA>   x      <NA>   <NA>   x      <NA>
## 11 C. difficile "sever~ <NA>   <NA>   <NA>   <NA>   <NA>   <NA>   <NA>
## 12 P. aeruginosa "lung,~ yes    <NA>   <NA>   0.15   <NA>   <NA>   <NA>
## 13 S. pneumoniae "pneum~ <NA>   <NA>   0.08   <NA>   <NA>   <NA>   0.41
## 14 E. coli       "food ~ yes    <NA>   <NA>   0.09   <NA>   <NA>   <NA>
## 15 S. aureus     "boils~ <NA>   <NA>   <NA>   <NA>   <NA>   <NA>   <NA>
## 16 <NA>         <NA>   <NA>   <NA>   <NA>   <NA>   <NA>   <NA>
## 17 gram-negativ "stron~ <NA>   <NA>   <NA>   <NA>   <NA>   <NA>   <NA>
## 18 <NA>         <NA>   <NA>   <NA>   <NA>   <NA>   <NA>   <NA>
## 19 <NA>         <NA>   <NA>   <NA>   <NA>   <NA>   <NA>   <NA>
## 20 <NA>         <NA>   Date i~ <NA>   1942.0 <NA>   1944.0 1949.0 <NA>
```

```

## # ... with 40 more variables: Macrolides...10 <chr>, Other...11 <chr>,
## #   Glycopeptides <chr>, Tetracyclines <chr>, Aminoglycosides...14 <chr>,
## #   Penicillins...15 <chr>, `Penicillins_(Aminopenicillins)...16` <chr>,
## #   Penicillins...17 <chr>, Nitroimidazoles <chr>,
## #   `Penicillins_(Aminopenicillins)...19` <chr>, Sulfonamides <chr>,
## #   `Cephalosporins_(First_generation)P` <chr>,
## #   `Cephalosporins_(First_generation)` <chr>, Aminoglycosides...23 <chr>, ...
## # i Use `colnames()` to see all variable names

# Load data (assuming it's saved in a file called "data.csv")
df <- read.csv("../data/cleaned_antibiotic_data.csv", stringsAsFactors = FALSE, header = TRUE)

# Handle missing values:
# Replace "x" with NA and convert to numeric
df[df == "x"] <- NA
df[4:ncol(df)] <- lapply(df[4:ncol(df)], as.numeric)

# Handle columns:
# The first three columns seem to be about the bacterium name, its common diseases, and its gram-negative
# For better clarity, we will rename them.
colnames(df)[1:3] <- c("BacteriumName", "Causes", "GramNegative")

# Removing rows that are not relevant to our analysis:
# Rows that contain only NAs or meta-information are removed.
df <- df %>% filter(!is.na(BacteriumName))

# As a suggestion, you might want to separate the antibiotics based on their family/group.
# However, this would require domain knowledge about which antibiotic belongs to which group.

# You can save the cleaned data to a new CSV file if desired.
write.csv(df, "../data/cleaned_data.csv", row.names = FALSE)

# The data is now cleaned and saved as "cleaned_data.csv".
df

##           BacteriumName
## 1 Adding up drug resistance
## 2           Bacterium name
## 3             A. baumanii
## 4             K. pneumoniae
## 5             E. faecium
## 6             N. gonorrhoeae
## 7             Shigella
## 8             M. tuberculosis
## 9             P. mirabilis
## 10            CoNS
## 11            C. difficile
## 12            P. aeruginosa
## 13            S. pneumoniae
## 14             E. coli
## 15            S. aureus
## 16 gram-negative bacteria
##
## Causes
## 1 data are % of bacteria that are resistant, US\nx = resistance, but unquantified
## 2 Causes

```

```

## 3          "Iraqibacter" - pneumonia, meningitis
## 4          pneumonia, bronchitis, urinary infections
## 5          urinary infections
## 6          gonorrhoea
## 7          dysentery
## 8          tuberculosis
## 9          kidney stones, proteus
## 10         food poisoning
## 11         severe diarrhoea, colitis
## 12         lung, urinary, skin, wound & blood infections
## 13         pneumonia, meningitis & many other infections
## 14         food poisoning
## 15         boils, sinusitis, food poisoning
## 16         strong membrane, more resistant
##      GramNegative Penicillins...4 Penicillins...5 Aminoglycosides...6
## 1 Individual drug      NA      NA      NA
## 2   Gram negative?      NA      NA      NA
## 3         yes      NA      NA      0.46
## 4         yes      NA      NA      0.08
## 5         <NA>      NA      NA      NA
## 6         yes      0.3      NA      NA
## 7         yes      NA      NA      NA
## 8         <NA>      NA      NA      NA
## 9         <NA>      NA      NA      0.09
## 10        <NA>      NA      NA      NA
## 11        <NA>      NA      NA      NA
## 12        yes      NA      NA      0.15
## 13        <NA>      NA      0.08      NA
## 14        yes      NA      NA      0.09
## 15        <NA>      NA      NA      NA
## 16        <NA>      NA      NA      NA
##      Aminoglycosides...7 Other...8 Macrolides...9 Macrolides...10 Other...11
## 1          NA      NA      NA      NA      NA
## 2          NA      NA      NA      NA      NA
## 3          NA      NA      NA      NA      NA
## 4          NA      NA      NA      NA      NA
## 5          NA      NA      NA      NA      NA
## 6          NA      NA      NA      NA      NA
## 7          0.56      0.14      NA      NA      NA
## 8          NA      NA      NA      NA      0.09
## 9          NA      NA      NA      NA      NA
## 10         NA      NA      NA      NA      NA
## 11         NA      NA      NA      NA      NA
## 12         NA      NA      NA      NA      NA
## 13         NA      NA      0.41      NA      NA
## 14         NA      NA      NA      NA      NA
## 15         NA      NA      NA      NA      NA
## 16         NA      NA      NA      NA      NA
##      Glycopeptides Tetracyclines Aminoglycosides...14 Penicillins...15
## 1          NA      NA      NA      NA
## 2          NA      NA      NA      NA
## 3          NA      NA      NA      NA
## 4          NA      NA      NA      NA
## 5          0.75      NA      NA      NA

```

## 6	NA	NA	NA	NA
## 7	NA	0.45	0.009	NA
## 8	NA	NA	NA	NA
## 9	NA	NA	NA	NA
## 10	0.00	0.16	NA	0.63
## 11	0.11	0.03	NA	NA
## 12	NA	NA	NA	NA
## 13	NA	NA	NA	NA
## 14	NA	NA	NA	NA
## 15	NA	NA	NA	NA
## 16	NA	NA	NA	NA
##	Penicillins_.Aminopenicillins....16 Penicillins...17 Nitroimidazoles			
## 1		NA	NA	NA
## 2		NA	NA	NA
## 3		NA	NA	NA
## 4		NA	NA	NA
## 5		NA	NA	NA
## 6		NA	NA	NA
## 7		NA	NA	NA
## 8		NA	NA	NA
## 9		0.22	NA	NA
## 10		NA	NA	NA
## 11		NA	NA	0
## 12		NA	NA	NA
## 13		NA	NA	NA
## 14		0.45	NA	NA
## 15		NA	0.51	NA
## 16		NA	NA	NA
##	Penicillins_.Aminopenicillins....19 Sulfonamides			
## 1		NA	NA	
## 2		NA	NA	
## 3		NA	NA	
## 4		NA	NA	
## 5		NA	NA	
## 6		NA	NA	
## 7		0.78	0.47	
## 8		NA	NA	
## 9		NA	NA	
## 10		NA	NA	
## 11		NA	NA	
## 12		NA	NA	
## 13		NA	NA	
## 14		NA	NA	
## 15		NA	NA	
## 16		NA	NA	
##	Cephalosporins_.First_generation.P Cephalosporins_.First_generation.			
## 1		NA		NA
## 2		NA		NA
## 3		NA		NA
## 4		NA		NA
## 5		NA		NA
## 6		NA		NA
## 7		NA		0.06
## 8		NA		NA

## 9		NA		NA
## 10		NA		NA
## 11		NA		NA
## 12		NA		NA
## 13		NA		NA
## 14		NA		NA
## 15		NA		NA
## 16		NA		NA
##	Aminoglycosides...23	Fluoroquinolones	Fluroquinolones...25	Rifamycin
## 1	NA	NA	NA	NA
## 2	NA	NA	NA	NA
## 3	NA	0.58	NA	0.000
## 4	NA	0.11	NA	NA
## 5	0.190	NA	NA	NA
## 6	NA	NA	NA	NA
## 7	0.002	0.02	0.01	NA
## 8	NA	NA	NA	NA
## 9	NA	0.28	NA	NA
## 10	NA	0.50	NA	NA
## 11	NA	NA	NA	0.100
## 12	NA	0.27	NA	NA
## 13	NA	NA	NA	NA
## 14	NA	0.33	NA	NA
## 15	NA	NA	NA	0.008
## 16	NA	NA	NA	NA
##	Lincosamides	Sulfonamides_._other.	Aminoglycosides...29	Penicillins...30
## 1	NA	NA	NA	NA
## 2	NA	NA	NA	NA
## 3	NA	NA	0e+00	NA
## 4	NA	0.15	NA	NA
## 5	NA	NA	NA	NA
## 6	NA	NA	NA	NA
## 7	NA	0.46	6e-04	0.02
## 8	NA	NA	NA	NA
## 9	NA	0.27	NA	NA
## 10	0.33	0.34	NA	NA
## 11	0.28	NA	NA	NA
## 12	NA	NA	NA	NA
## 13	NA	NA	NA	NA
## 14	NA	0.25	NA	NA
## 15	NA	NA	NA	NA
## 16	NA	NA	NA	NA
##	Cephalosporins_.	Third_generation...	31	
## 1		NA		
## 2		NA		
## 3		NA		
## 4		0.23		
## 5		NA		
## 6		NA		
## 7		NA		
## 8		NA		
## 9		0.02		
## 10		NA		
## 11		NA		

## 12			NA
## 13			NA
## 14			0.15
## 15			NA
## 16			NA
##	Cephalosporins_Third_generation...	32	
## 1			NA
## 2			NA
## 3			NA
## 4			NA
## 5			NA
## 6			0.004
## 7			0.000
## 8			NA
## 9			NA
## 10			NA
## 11			NA
## 12			NA
## 13			NA
## 14			NA
## 15			NA
## 16			NA
##	Cephalosporins_Third_generation...	33	Carbapenems...34 Carbapenems...35
## 1			NA NA NA
## 2			NA NA NA
## 3			0.52 0.41 NA
## 4			NA 0.11 NA
## 5			NA NA NA
## 6			NA NA NA
## 7			NA NA NA
## 8			NA NA NA
## 9			NA NA NA
## 10			NA NA NA
## 11			NA NA NA
## 12			0.10 0.14 NA
## 13			NA NA NA
## 14			NA NA NA
## 15			NA NA NA
## 16			NA NA NA
##	Penicillins...36 ...37 Fluroquinolones...38 Fluroquinolones...39		
## 1	NA NA		NA NA
## 2	NA NA		NA NA
## 3	0.25 NA		NA NA
## 4	NA NA		NA NA
## 5	NA NA		NA NA
## 6	0.13 NA		0.1400 NA
## 7	NA 6e-04		0.0006 NA
## 8	NA NA		NA NA
## 9	NA NA		NA NA
## 10	NA NA		NA NA
## 11	NA NA		NA 0.39
## 12	NA NA		NA NA
## 13	NA NA		NA NA
## 14	NA NA		NA NA

## 15	NA	NA		NA		NA
## 16	NA	NA		NA		NA
##	Penicillins...	40	...	41 Multi_drug	Remarks	Resistance_score ...45
## 1	NA	NA		NA		NA
## 2	NA	NA		NA		NA
## 3	NA	NA		0.510	NA	4
## 4	NA	NA		0.060	NA	2
## 5	NA	NA		NA	NA	1
## 6	NA	NA		0.300	NA	3
## 7	NA	NA		0.640	NA	4
## 8	NA	NA		0.600	NA	3
## 9	NA	NA		0.006	NA	2
## 10	NA	NA		0.130	NA	3
## 11	NA	NA		NA	NA	3
## 12	0.12	NA		0.100	NA	2
## 13	NA	NA		0.080	NA	1
## 14	NA	NA		0.015	NA	2
## 15	NA	NA		NA	NA	1
## 16	NA	NA		NA	NA	NA
##	N_antibiotics_or_classes			Average_percent_resistance	...	48 Sources
## 1		NA		NA	NA	NA
## 2		NA		NA	NA	NA
## 3		18		0.3171429	NA	NA
## 4		5		0.1360000	NA	NA
## 5		2		0.4700000	NA	NA
## 6		6		0.1435000	NA	NA
## 7		16		0.1864250	NA	NA
## 8		7		0.0900000	NA	NA
## 9		5		0.1760000	NA	NA
## 10		9		0.3266667	NA	NA
## 11		7		0.1516667	NA	NA
## 12		5		0.1560000	NA	NA
## 13		2		0.2450000	NA	NA
## 14		5		0.2540000	NA	NA
## 15		1		0.2590000	NA	NA
## 16		NA		NA	NA	NA

Reconstruction

The following plot fixes the main issues in the original.

```
library(ggplot2)
library(tidyr)

# Updated data
antibiotic_resistance_df <- data.frame(
  Bacterium_name = c('A. baumannii', 'K. pneumoniae', 'E. coli', 'E. faecium', 'S. aureus', 'P. aeruginosa'),
  Causes = c('pneumonia, meningitis', 'pneumonia, bronchitis', 'gastrointestinal infections', 'urinary tract infections'),
  Gram_negative = c('yes', 'yes', 'yes', 'no', 'no', 'yes', 'no'),
  Penicillin = c(46, 8, 12, NA, 90, 23, NA),
  Streptomycin = c(NA, NA, 75, 85, 15, 26, 50),
  Erythromycin = c(58, 11, 19, 30, 45, 40, 38)
)

# Reshape data for plotting
```

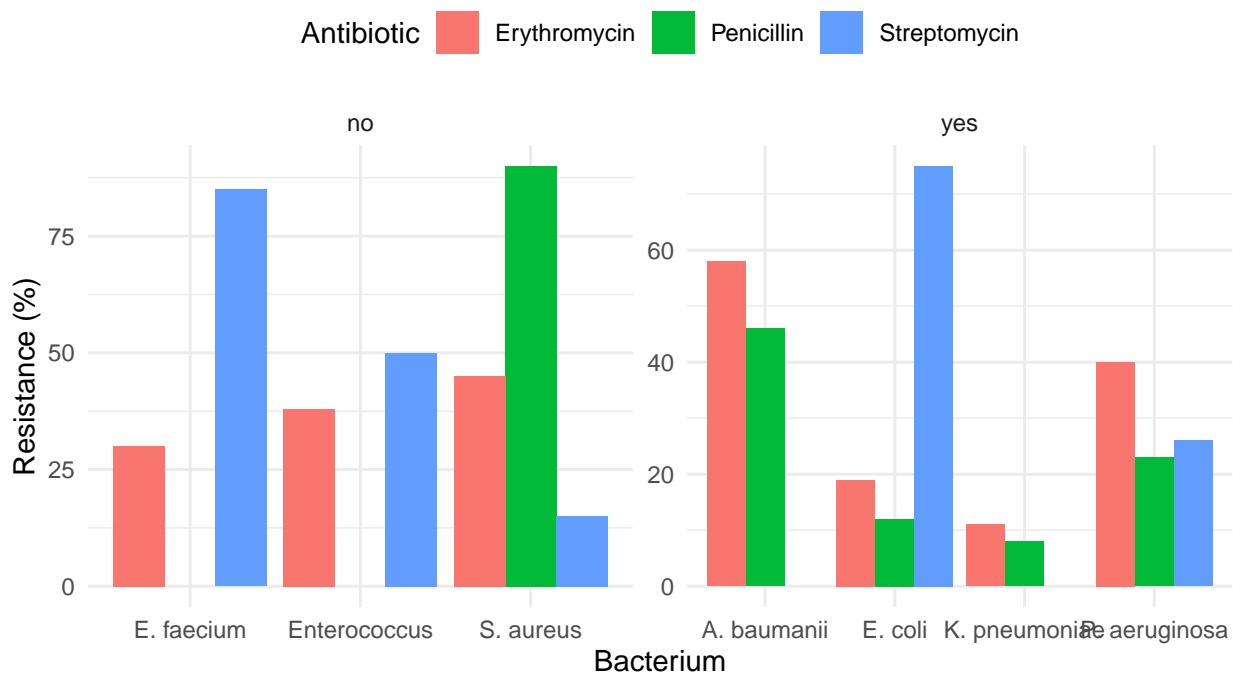
```
df_long <- antibiotic_resistance_df %>%
  gather(key = 'Antibiotic', value = 'Resistance', Penicillin, Streptomycin, Erythromycin)

# Comprehensive Visualization
plot <- ggplot(df_long, aes(x = Bacterium_name, y = Resistance, fill = Antibiotic)) +
  geom_bar(stat = "identity", position = "dodge") +
  facet_wrap(~Gram_negative, scales = "free", ncol = 2) +
  labs(
    title = "Antibiotic Resistance Across Different Bacteria",
    subtitle = "Faceted by Gram-negative Status",
    x = "Bacterium",
    y = "Resistance (%)",
    caption = "Sources: Centre for Disease Dynamics, World Health Organisation, CDC (US data)\nInspiration from: https://informationisbeautiful.net/visualizations/antibiotic-resistance/"
  ) +
  theme_minimal() +
  theme(legend.position = "top", plot.caption = element_text(hjust = 1, color = "gray"))

# Display the plot
print(plot)
```

Antibiotic Resistance Across Different Bacteria

Faceted by Gram-negative Status



Sources: Centre for Disease Dynamics, World Health Organisation, CDC (US data)
Inspiration from: <https://informationisbeautiful.net/visualizations/antibiotic-resistance/>

```
# Save the plot to the ../images directory
ggsave(filename = "../images/antibiotic_resistance_plot.png", plot = plot, width = 20, height = 15)

library(RColorBrewer)

# Colorblind-friendly palette for 3 groups
cb_palette <- brewer.pal(n = 3, name = "Set2")
```

```

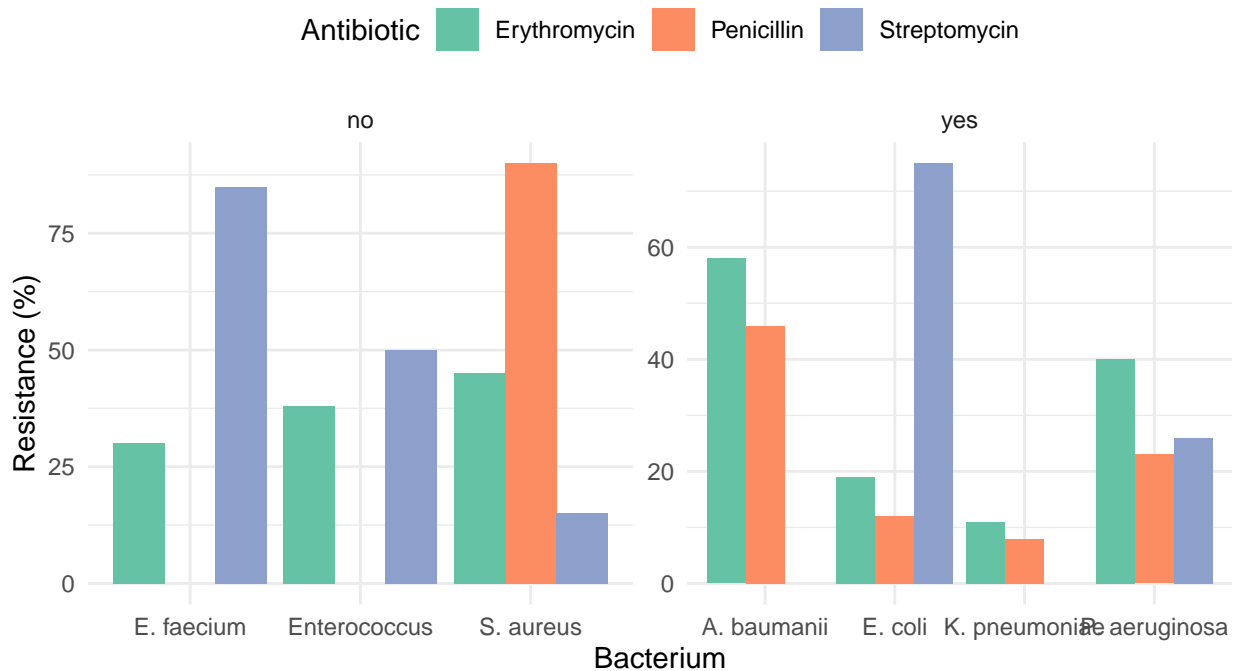
plot <- ggplot(df_long, aes(x = Bacterium_name, y = Resistance, fill = Antibiotic)) +
  geom_bar(stat = "identity", position = "dodge") +
  facet_wrap(~Gram_negative, scales = "free", ncol = 2) +
  labs(
    title = "Antibiotic Resistance Across Different Bacteria",
    subtitle = "Faceted by Gram-negative Status",
    x = "Bacterium",
    y = "Resistance (%)",
    caption = "Sources: Centre for Disease Dynamics, World Health Organisation, CDC (US data)\nInspiration from: https://informationisbeautiful.net/visualizations/antibiotic-resistance/"
  ) +
  scale_fill_manual(values = cb_palette) +
  theme_minimal() +
  theme(legend.position = "top", plot.caption = element_text(hjust = 1, color = "gray"))

print(plot)

```

Antibiotic Resistance Across Different Bacteria

Faceted by Gram-negative Status



Sources: Centre for Disease Dynamics, World Health Organisation, CDC (US data)
Inspiration from: <https://informationisbeautiful.net/visualizations/antibiotic-resistance/>

```

library(ggplot2)
library(tidyr)

# Updated data
antibiotic_resistance_df <- data.frame(
  Bacterium_name = c('A. baumannii', 'K. pneumoniae', 'E. coli', 'E. faecium', 'S. aureus', 'P. aeruginosa'),
  Causes = c('pneumonia, meningitis', 'pneumonia, bronchitis', 'gastrointestinal infections', 'urinary tract infections', 'skin infections', 'respiratory infections'),
  Gram_negative = c('yes', 'yes', 'yes', 'no', 'no', 'yes', 'no'),
  Penicillin = c(46, 8, 12, NA, 90, 23, NA),
  Streptomycin = c(NA, NA, 75, 85, 15, 26, 50),
  Erythromycin = c(58, 19, 11, 30, 45, 40, NA)
)

```

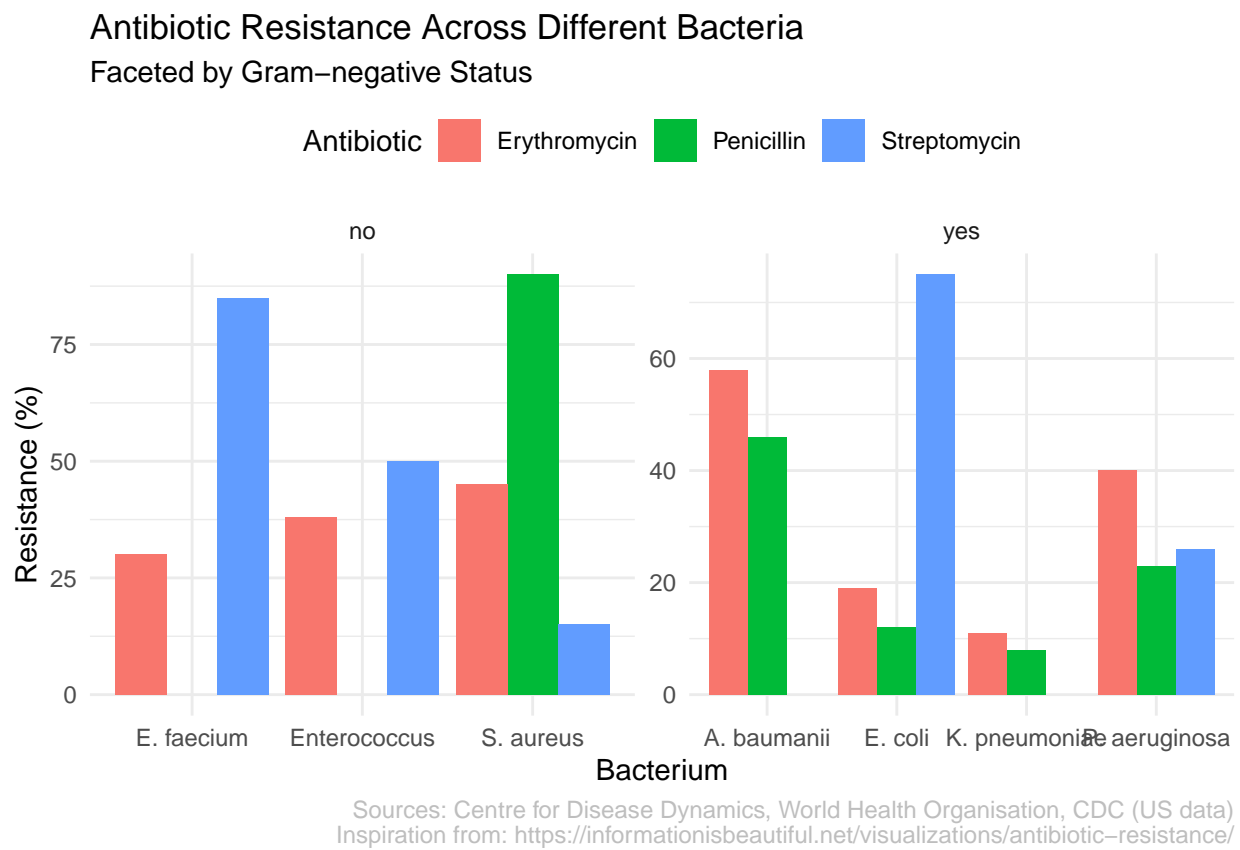


Figure 1: Reconstructed plot.

```

Erythromycin = c(58, 11, 19, 30, 45, 40, 38)
)

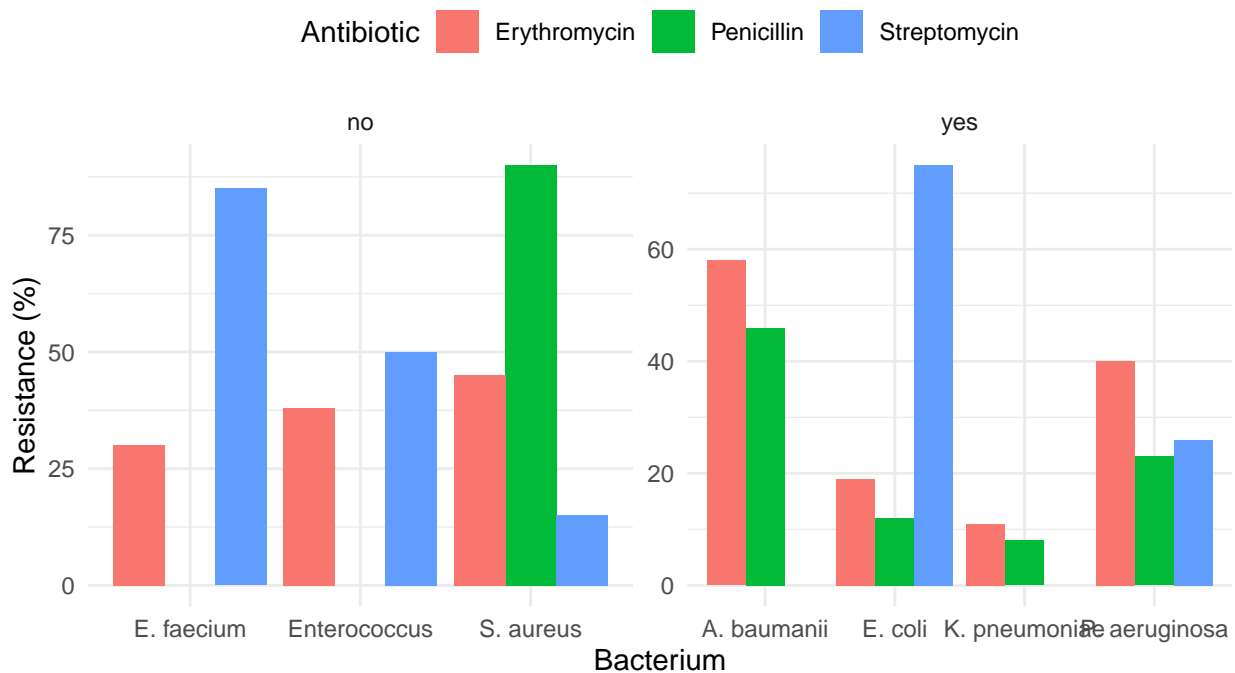
# Reshape data for plotting
df_long <- antibiotic_resistance_df %>%
  gather(key = 'Antibiotic', value = 'Resistance', Penicillin, Streptomycin, Erythromycin)

# Comprehensive Visualization
ggplot(df_long, aes(x = Bacterium_name, y = Resistance, fill = Antibiotic)) +
  geom_bar(stat = "identity", position = "dodge") +
  facet_wrap(~Gram_negative, scales = "free", ncol = 2) +
  labs(
    title = "Antibiotic Resistance Across Different Bacteria",
    subtitle = "Faceted by Gram-negative Status",
    x = "Bacterium",
    y = "Resistance (%)",
    caption = "Sources: Centre for Disease Dynamics, World Health Organisation, CDC (US data)\nInspiration from: https://informationisbeautiful.net/visualizations/antibiotic-resistance/"
  ) +
  theme_minimal() +
  theme(legend.position = "top", plot.caption = element_text(hjust = 1))

```

Antibiotic Resistance Across Different Bacteria

Faceted by Gram-negative Status



Sources: Centre for Disease Dynamics, World Health Organisation, CDC (US data)
Inspiration from: <https://informationisbeautiful.net/visualizations/antibiotic-resistance/>

```

library(ggplot2)
library(tidyr)
library(grid)

# Updated data
antibiotic_resistance_df <- data.frame(

```

```

Bacterium_name = c('A. baumannii', 'K. pneumoniae', 'E. coli', 'E. faecium', 'S. aureus', 'P. aeruginosa')
Causes = c('pneumonia, meningitis', 'pneumonia, bronchitis', 'gastrointestinal infections', 'urinary tract infections')
Gram_negative = c('yes', 'yes', 'yes', 'no', 'no', 'yes', 'no'),
Penicillin = c(46, 8, 12, NA, 90, 23, NA),
Streptomycin = c(NA, NA, 75, 85, 15, 26, 50),
Erythromycin = c(58, 11, 19, 30, 45, 40, 38)
)

# Reshape data for plotting
df_long <- antibiotic_resistance_df %>%
  gather(key = 'Antibiotic', value = 'Resistance', Penicillin, Streptomycin, Erythromycin)

# Create the plot and save it to an object
p <- ggplot(df_long, aes(x = Bacterium_name, y = Resistance, fill = Antibiotic)) +
  geom_bar(stat = "identity", position = "dodge") +
  facet_wrap(~Gram_negative, scales = "free", ncol = 2) +
  labs(
    title = "Antibiotic Resistance Across Different Bacteria",
    subtitle = "Faceted by Gram-negative Status",
    x = "Bacterium",
    y = "Resistance (%)"
  ) +
  theme_minimal() +
  theme(legend.position = c(1, 1), legend.justification = c(1, 1))

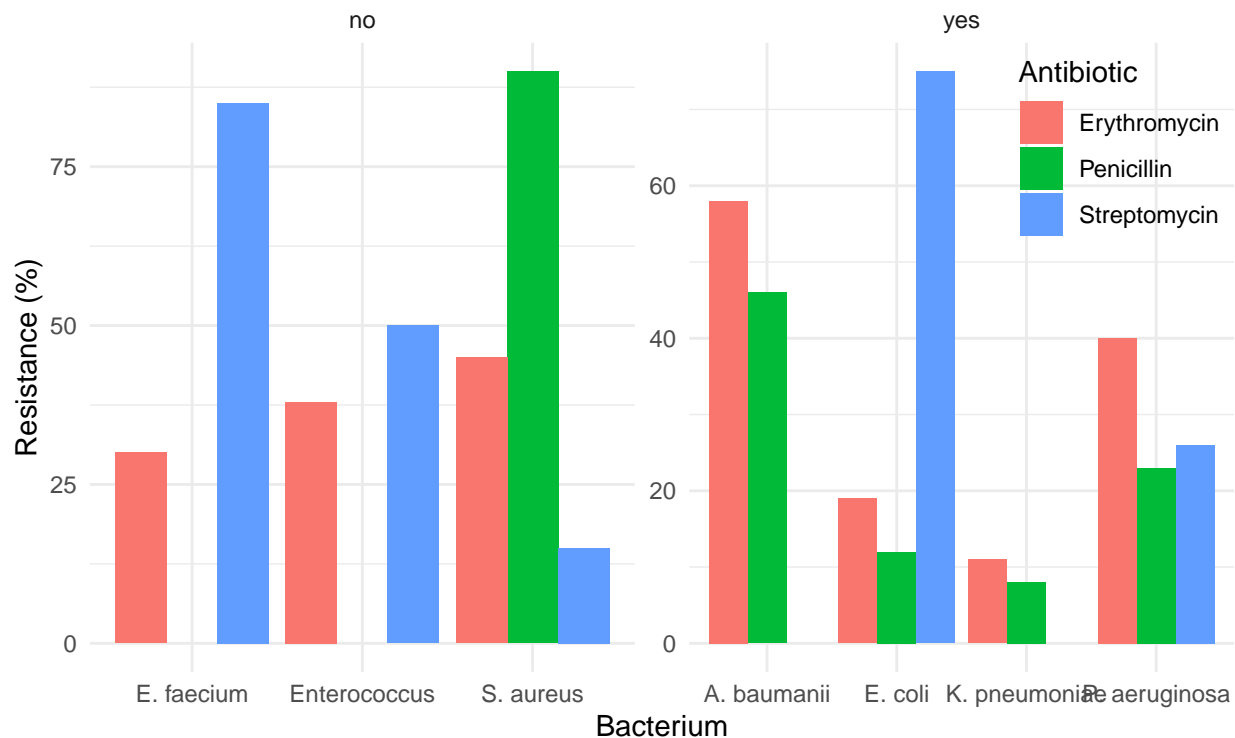
# Print the plot
print(p)

# Add the source text using grid package
grid.text("Sources: Centre for Disease Dynamics, World Health Organisation, CDC (US data)\nInspiration: Antibiotic Resistance",
  x = 1, y = 1.03, hjust = 1, gp = gpar(col = "darkgray", fontsize = 8))

```

Antibiotic Resistance Across Different Bacteria

Faceted by Gram-negative Status



```
library(ggplot2)
library(tidyr)

# Updated data
antibiotic_resistance_df <- data.frame(
  Bacterium_name = c('A. baumannii', 'K. pneumoniae', 'E. coli', 'E. faecium', 'S. aureus', 'P. aeruginosa'),
  Causes = c('pneumonia, meningitis', 'pneumonia, bronchitis', 'gastrointestinal infections', 'urinary infections'),
  Gram_negative = c('yes', 'yes', 'yes', 'no', 'no', 'yes', 'no'),
  Penicillin = c(46, 8, 12, NA, 90, 23, NA),
  Streptomycin = c(NA, NA, 75, 85, 15, 26, 50),
  Erythromycin = c(58, 11, 19, 30, 45, 40, 38)
)

# Reshape data for plotting
df_long <- antibiotic_resistance_df %>%
  gather(key = 'Antibiotic', value = 'Resistance', Penicillin, Streptomycin, Erythromycin)

# Comprehensive Visualization
ggplot(df_long, aes(x = Bacterium_name, y = Resistance, fill = Antibiotic)) +
  geom_bar(stat = "identity", position = "dodge") +
  facet_wrap(~Gram_negative, scales = "free", ncol = 2) +
  labs(
    title = "Antibiotic Resistance Across Different Bacteria",
    subtitle = "Faceted by Gram-negative Status",
    x = "Bacterium",
    y = "Resistance (%)"
  ) +
```

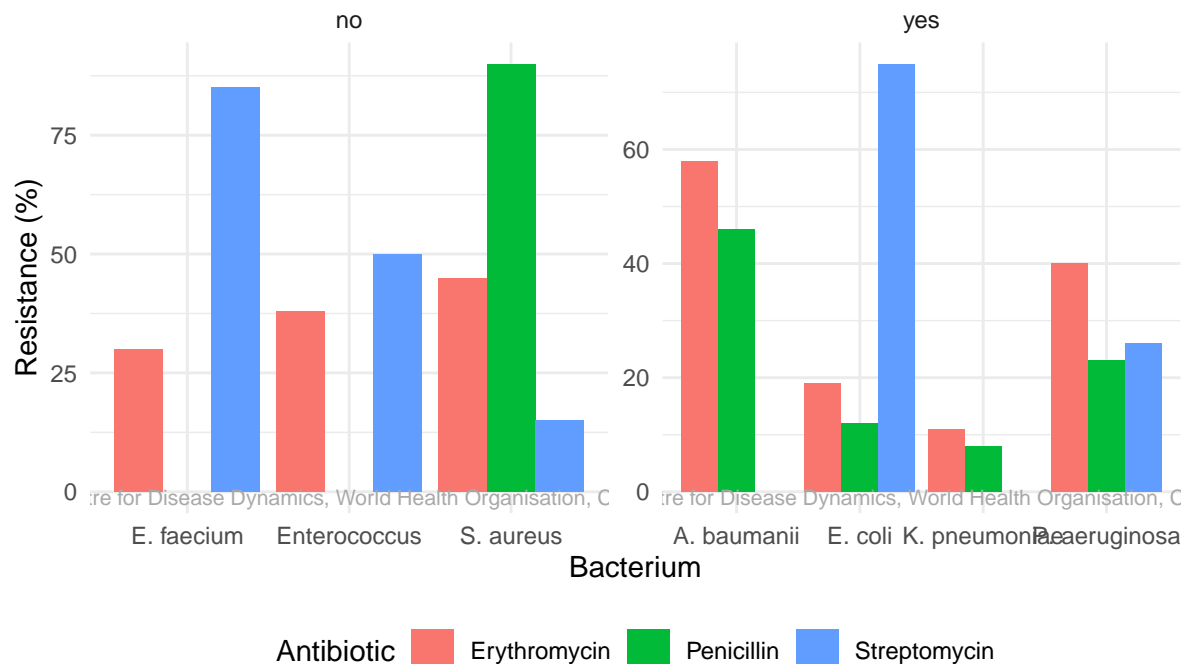


```

theme_minimal() +
theme(
  legend.position = "bottom",
  plot.margin = margin(5.5, 5.5, 5.5, 5.5, "mm") # Add a bit more margin to the bottom to accommodate
) +
annotation_custom(
  grob = grid::textGrob(label = "Sources: Centre for Disease Dynamics, World Health Organisation, CDC",
    gp = grid::gpar(col = "darkgray", fontsize = 8)),
  xmin = -Inf, xmax = Inf, ymin = -Inf, ymax = -Inf
)

```

Antibiotic Resistance Across Different Bacteria Faceted by Gram-negative Status



```

library(ggplot2)
library(tidyr)

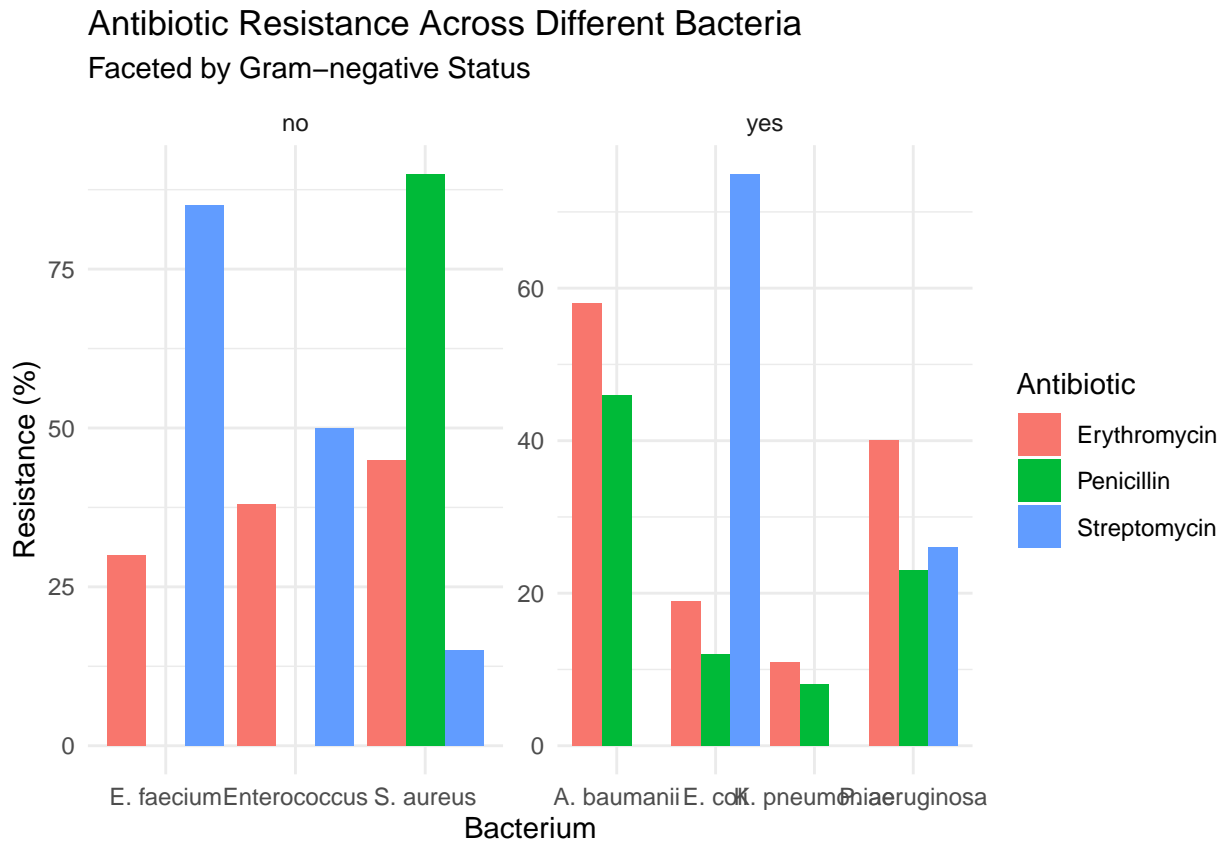
# Updated data
antibiotic_resistance_df <- data.frame(
  Bacterium_name = c('A. baumannii', 'K. pneumoniae', 'E. coli', 'E. faecium', 'S. aureus', 'P. aeruginosa'),
  Causes = c('pneumonia, meningitis', 'pneumonia, bronchitis', 'gastrointestinal infections', 'urinary tract infections', 'skin infections', 'respiratory infections'),
  Gram_negative = c('yes', 'yes', 'yes', 'no', 'no', 'yes', 'no'),
  Penicillin = c(46, 8, 12, NA, 90, 23, NA),
  Streptomycin = c(NA, NA, 75, 85, 15, 26, 50),
  Erythromycin = c(58, 11, 19, 30, 45, 40, 38)
)

# Reshape data for plotting
df_long <- antibiotic_resistance_df %>%
  gather(key = 'Antibiotic', value = 'Resistance', Penicillin, Streptomycin, Erythromycin)

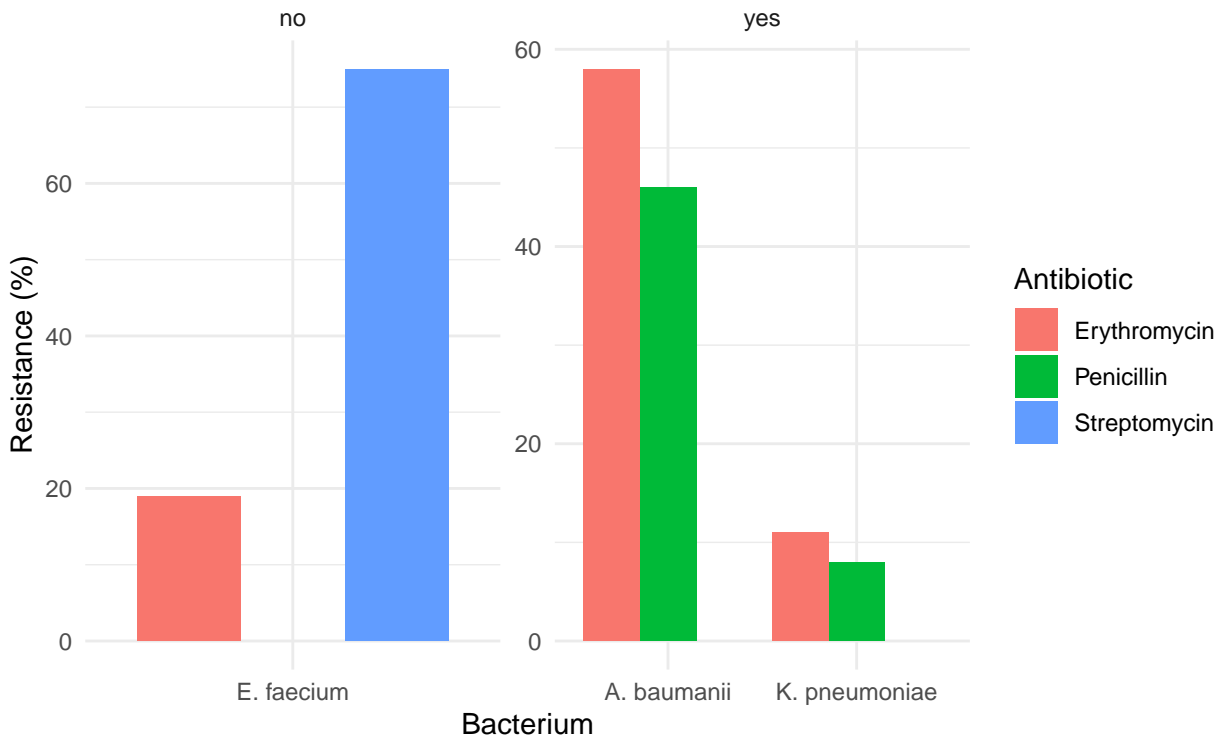
# Comprehensive Visualization

```

```
ggplot(df_long, aes(x = Bacterium_name, y = Resistance, fill = Antibiotic)) +
  geom_bar(stat = "identity", position = "dodge") +
  facet_wrap(~Gram_negative, scales = "free", ncol = 2) +
  labs(
    title = "Antibiotic Resistance Across Different Bacteria",
    subtitle = "Faceted by Gram-negative Status",
    x = "Bacterium",
    y = "Resistance (%)"
  ) +
  theme_minimal()
```



Antibiotic Resistance Across Different Bacteria Faceted by Gram-negative Status



References

The reference to the original data visualisation choose, the data source(s) used for the reconstruction and any other sources used for this assignment are as follows:

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