

AMRFinder Heatmaps & Graphs Documentation

This document includes the full visualization script and expected output files.

Script:

```
# =====
# STEP 2 - PLOTTING AMR RESULTS
# =====

library(tibble)
library(dplyr)
library(tidyr)
library(readr)
library(ggplot2)
library(pheatmap)

# -----
# Load files
# -----
presence_abs <- read_tsv("AMR_class_presence_absence.tsv")
class_summary <- read_tsv("AMR_class_summary.tsv")
beta_lactams <- read_tsv("beta_lactam_subclasses_summary.tsv")

# =====
# 1. BAR PLOT - AMR CLASS FREQUENCY
# =====
png("AMR_class_distribution.png", width = 1600, height = 1000, res = 200)

ggplot(class_summary,
  aes(x = reorder(AMR_class, -No_of_isolates),
    y = No_of_isolates)) +
  geom_bar(stat = "identity", fill = "steelblue") +
  theme_bw() +
  labs(title = "Distribution of AMR Classes Across Isolates",
    x = "AMR Class", y = "Number of Isolates with AMR Genes") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))

dev.off()

# =====
# 2. HEATMAP - AMR PRESENCE/ABSENCE
# =====
heatmap_data <- presence_abs %>%
  column_to_rownames("isolate") %>%
  as.matrix()

png("AMR_presence_absence_heatmap.png", width = 1800, height = 2000, res = 200)

pheatmap(heatmap_data,
  cluster_rows = TRUE,
  cluster_cols = TRUE,
  color = colorRampPalette(c("white", "red"))(50),
  main = "Presence/Absence of AMR Classes Across Isolates")

dev.off()

# =====
# 3. BETA-LACTAM SUBCLASSES PLOT
# =====
png("beta_lactam_subclasses_distribution.png",
  width = 1600, height = 1000, res = 200)

ggplot(beta_lactams,
  aes(x = reorder(Type, -No_of_isolates),
    y = No_of_isolates)) +
  geom_bar(stat = "identity", fill = "darkgreen") +
  theme_bw() +
  labs(title = "Distribution of Beta-lactam Subclasses",
    x = "Subclass Type", y = "Number of Isolates") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))

dev.off()
```

Expected Output Files:

AMR_class_distribution.png
AMR_presence_absence_heatmap.png
beta_lactam_subclasses_distribution.png