

Cochrane Armitage to Assess Overall Trends in MDR Resistant Isolates

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```
install.packages("rmarkdown")

## Installing package into '/cloud/lib/x86_64-pc-linux-gnu-library/4.3'
## (as 'lib' is unspecified)

library(rmarkdown)
install.packages("knitr")

## Installing package into '/cloud/lib/x86_64-pc-linux-gnu-library/4.3'
## (as 'lib' is unspecified)

library(knitr)

# Total Gram Negative Isolates

if (!requireNamespace("DescTools", quietly = TRUE)) {
  install.packages("DescTools")
}

library(DescTools)

# MDR Gram Negative vs Not MDR Gram Negative

data_matrix <- matrix(c(
  12, 13,
  22, 12,
  27, 8,
  17, 5,
  15, 5,
  17, 5,
  8, 1,
  21, 9,
  8, 8,
  8, 5,
  14, 4
), byrow = TRUE, ncol = 2)

# Perform the Cochran-Armitage test for trend
result <- CochranArmitageTest(data_matrix)

# View the test result
print(result)

##
## Cochran-Armitage test for trend
```

```

##
## data: data_matrix
## Z = 0.72675, dim = 11, p-value = 0.4674
## alternative hypothesis: two.sided

# Total Gram Positive Isolates

if (!requireNamespace("DescTools", quietly = TRUE)) {
  install.packages("DescTools")
}

library(DescTools)

# MDR Gram Positive vs Not MDR Gram Positive

data_matrix <- matrix(c(
29, 81,
22, 86,
25, 72,
14, 43,
11, 24,
28, 45,
9, 37,
2, 25,
19, 27,
13, 29,
5, 13
), byrow = TRUE, ncol = 2)

# Perform the Cochran-Armitage test for trend
result <- CochranArmitageTest(data_matrix)

# View the test result
print(result)

##
## Cochran-Armitage test for trend
##
## data: data_matrix
## Z = 1.4185, dim = 11, p-value = 0.156
## alternative hypothesis: two.sided

# Total Isolates MDR

if (!requireNamespace("DescTools", quietly = TRUE)) {
  install.packages("DescTools")
}

library(DescTools)

# MDR TOTAL vs Not MDR TOTAL

data_matrix <- matrix(c(
41, 94,
44, 98,

```

```

52, 80,
31, 48,
26, 29,
45, 50,
17, 38,
23, 34,
27, 35,
21, 34,
19, 17
), byrow = TRUE, ncol = 2)

# Perform the Cochran-Armitage test for trend
result <- CochranArmitageTest(data_matrix)

# View the test result
print(result)

##
## Cochran-Armitage test for trend
##
## data: data_matrix
## Z = 2.641, dim = 11, p-value = 0.008266
## alternative hypothesis: two.sided

```