

# Cochran Armitage Measuring Trends for MDR

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```
# S pneumoniae
# Install the DescTools package
if (!requireNamespace("DescTools", quietly = TRUE)) {
  install.packages("DescTools")
}

library(DescTools)

# Input the data into a matrix, with rows corresponding to time points
# MDR and Not MDR counts
data_matrix <- matrix(c(
  25, 71,
  21, 79,
  21, 59,
  11, 40,
  9, 20,
  26, 44,
  6, 32,
  2, 11,
  10, 16,
  7, 15,
  5, 10
), 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 = 1.3927, dim = 11, p-value = 0.1637
## alternative hypothesis: two.sided

# S Typhimurium
# Install the DescTools package
if (!requireNamespace("DescTools", quietly = TRUE)) {
  install.packages("DescTools")
}
```

```

library(DescTools)

# Input the data into a matrix, with rows corresponding to time points
# and columns to MDR and Not MDR counts
data_matrix <- matrix(c(
  10, 3,
  14, 1,
  18, 1,
  5, 0,
  3, 0,
  4, 0,
  1, 0,
  2, 1,
  1, 0,
  2, 0,
  0, 0
), 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 = 0.73927, dim = 11, p-value = 0.4597
## alternative hypothesis: two.sided
# H influenzae MDR Incidence

(!requireNamespace("DescTools", quietly = TRUE))

```

```
## [1] FALSE
```

```
install.packages("DescTools")
```

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

```

library(DescTools)

# Input the data into a matrix, with rows corresponding to time points
# MDR and Not MDR counts
data_matrix <- matrix(c(
  1, 7,
  5, 7,
  5, 3,
  8, 3,
  4, 1,
  6, 2,
  3, 0,
  1, 1,
  1, 0,

```

```

0, 1,
1, 0
), byrow = TRUE, ncol = 2)

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

print(result)

##
## Cochran-Armitage test for trend
##
## data: data_matrix
## Z = 2.5527, dim = 11, p-value = 0.01069
## alternative hypothesis: two.sided

# K pneumoniae
# Install the DescTools package
if (!requireNamespace("DescTools", quietly = TRUE)) {
  install.packages("DescTools")
}

library(DescTools)

# Input the data into a matrix, with rows corresponding to time points
# and columns to MDR and Not MDR counts
data_matrix <- matrix(c(
  0, 0,
  1, 4,
  1, 0,
  2, 0,
  4, 0,
  2, 2,
  1, 0,
  7, 3,
  1, 0,
  3, 0,
  9, 0
), 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 = 2.6765, dim = 11, p-value = 0.00744
## alternative hypothesis: two.sided

```