Cochran Armitage Measuring Trends in the Proportions of Isolates Resistant to Second-Line Antibiotics

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```
install.packages("rmarkdown")
## Installing package into '/cloud/lib/x86_64-pc-linux-gnu-library/4.3'
## (as 'lib' is unspecified)
install.packages("knitr")
## Installing package into '/cloud/lib/x86_64-pc-linux-gnu-library/4.3'
## (as 'lib' is unspecified)
# S pneumoniae
# Install the DescTools package
if (!requireNamespace("DescTools", quietly = TRUE)) {
  install.packages("DescTools")
library(DescTools)
# resistant and not resistant counts
data matrix <- matrix(c(</pre>
46, 49,
37, 63,
41, 39,
19, 32,
16, 13,
45, 25,
13, 25,
6, 7,
15, 11,
13, 9,
), byrow = TRUE, ncol = 2)
# Perform the Cochran-Armitage test for trend
result <- CochranArmitageTest(data matrix)</pre>
# View the test result
print(result)
## Cochran-Armitage test for trend
## data: data_matrix
## Z = 1.7985, dim = 11, p-value = 0.07211
```

```
## alternative hypothesis: two.sided
# S Typhimurium
# Install the DescTools package
if (!requireNamespace("DescTools", quietly = TRUE)) {
  install.packages("DescTools")
}
library(DescTools)
data_matrix <- matrix(c(</pre>
1, 12,
1, 14,
0, 19,
0, 5,
1, 2,
4, 0,
1, 0,
3, 0,
0, 0,
2, 0,
0, 0
), byrow = TRUE, ncol = 2)
# Perform the Cochran-Armitage test for trend
result <- CochranArmitageTest(data_matrix)</pre>
# View the test result
print(result)
##
## Cochran-Armitage test for trend
## data: data_matrix
## Z = 5.864, dim = 11, p-value = 4.52e-09
## alternative hypothesis: two.sided
# H influenzae
(!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)
data_matrix <- matrix(c(</pre>
1, 7,
0, 12,
0, 8,
3, 8,
0, 5,
1, 7,
```

```
3, 0,
0, 2,
0, 1,
0, 1,
0, 1
), byrow = TRUE, ncol = 2)
# Perform the Cochran-Armitage test for trend
result <- CochranArmitageTest(data_matrix)</pre>
print(result)
## Cochran-Armitage test for trend
## data: data_matrix
## Z = 1.2877, dim = 11, p-value = 0.1978
## alternative hypothesis: two.sided
# K pneumoniae
# Install the DescTools package
if (!requireNamespace("DescTools", quietly = TRUE)) {
  install.packages("DescTools")
}
library(DescTools)
data_matrix <- matrix(c(</pre>
0, 0,
1, 4,
1, 0,
2, 0,
4, 0,
2, 2,
1, 0,
7, 3,
1, 0,
3, 0,
), byrow = TRUE, ncol = 2)
# Perform the Cochran-Armitage test for trend
result <- CochranArmitageTest(data_matrix)</pre>
# 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
```