

```

E. coli
  Df Sum Sq Mean Sq F value    Pr(>F)
df1$Treatment  4   68.83   17.208    36.88 5.86e-06
Residuals     10    4.67    0.467

df1$Treatment ***
Residuals
---
Signif. codes:
  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
$statistics
      MSerror Df Mean      CV  t.value      LSD
0.4666667 10 13.5 5.060223 2.228139 1.242796

$parameters
      test p.adjusted      name.t ntr alpha
Fisher-LSD      none df1$Treatment  5 0.05

$means
      df1$Ecoli      std r      LCL      UCL
Ag20      13.33333 0.2886751 3 12.45454 14.21212
AgNP30     11.83333 0.2886751 3 10.95454 12.71212
AgNP60     12.16667 0.2886751 3 11.28788 13.04546
AgNP90     12.50000 1.3228757 3 11.62121 13.37879
Positive   17.66667 0.5773503 3 16.78788 18.54546
      Min  Max   Q25  Q50   Q75
Ag20     13.0 13.5 13.25 13.5 13.50
AgNP30    11.5 12.0 11.75 12.0 12.00
AgNP60    12.0 12.5 12.00 12.0 12.25
AgNP90    11.5 14.0 11.75 12.0 13.00
Positive  17.0 18.0 17.50 18.0 18.00

$comparison
NULL

$groups
      df1$Ecoli groups
Positive 17.66667      a
Ag20     13.33333      b
AgNP90   12.50000     bc
AgNP60   12.16667     bc
AgNP30   11.83333      c

attr(,"class")
[1] "group"

```

S. typhi

```
              Df Sum Sq Mean Sq F value Pr(>F)
df1$Treatment  4 116.77  29.192    5.197 0.0158 *
Residuals     10   56.17   5.617
```

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

\$statistics

```
      MSerror Df      Mean      CV  t.value
5.616667 10 13.93333 17.00922 2.228139
      LSD
4.311575
```

\$parameters

```
      test p.adjusted      name.t ntr alpha
Fisher-LSD      none df1$Treatment  5  0.05
```

\$means

```
              df1$Styphi      std r      LCL
Ag20          12.33333 0.2886751 3  9.284589
AgNP30         11.33333 1.1547005 3  8.284589
AgNP60         12.50000 0.5000000 3  9.451256
AgNP90         19.16667 5.1071845 3 16.117923
Positive       14.33333 0.5773503 3 11.284589
              UCL  Min  Max   Q25  Q50  Q75
Ag20          15.38208 12.0 12.5 12.25 12.5 12.50
AgNP30         14.38208 10.0 12.0 11.00 12.0 12.00
AgNP60         15.54874 12.0 13.0 12.25 12.5 12.75
AgNP90         22.21541 15.5 25.0 16.25 17.0 21.00
Positive       17.38208 14.0 15.0 14.00 14.0 14.50
```

\$comparison

NULL

\$groups

```
              df1$Styphi groups
AgNP90         19.16667      a
Positive       14.33333      b
AgNP60         12.50000      b
Ag20           12.33333      b
AgNP30         11.33333      b
```

attr(,"class")

[1] "group"

S. aureus

```
              Df Sum Sq Mean Sq F value    Pr(>F)
df1$Treatment  4  197.1   49.28    19.71 9.82e-05
Residuals     10   25.0    2.50
---
df1$Treatment ***
Residuals
---
Signif. codes:
  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
$statistics
      MSerror Df Mean      CV  t.value      LSD
      2.5 10 14.6 10.82972 2.228139 2.876515

$parameters
      test p.adjusted      name.t ntr alpha
Fisher-LSD      none df1$Treatment  5  0.05

$means
      df1$Saureus      std r      LCL      UCL
Ag20      12.33333 0.5773503 3 10.299330 14.36734
AgNP30     11.83333 0.7637626 3  9.799330 13.86734
AgNP60     12.00000 0.8660254 3  9.965997 14.03400
AgNP90     15.50000 1.3228757 3 13.465997 17.53400
Positive   21.33333 3.0138569 3 19.299330 23.36734
      Min  Max   Q25  Q50   Q75
Ag20     12.0 13.0 12.00 12.0 12.50
AgNP30    11.0 12.5 11.50 12.0 12.25
AgNP60    11.0 12.5 11.75 12.5 12.50
AgNP90    14.5 17.0 14.75 15.0 16.00
Positive  18.5 24.5 19.75 21.0 22.75

$comparison
NULL

$groups
      df1$Saureus groups
Positive   21.33333      a
AgNP90     15.50000      b
Ag20       12.33333      c
AgNP60     12.00000      c
AgNP30     11.83333      c

attr(,"class")
[1] "group"
```

P. aeruginosa

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
df1\$Treatment	4	378.6	94.64	227.1	9.09e-10
Residuals	10	4.2	0.42		

df1\$Treatment ***

Residuals

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

\$statistics

MSerror	Df	Mean	CV	t.value
0.4166667	10	10.03333	6.433527	2.228139

LSD

1.174332

\$parameters

test	p.adjusted	name.t	ntr	alpha
Fisher-LSD	none	df1\$Treatment	5	0.05

\$means

	df1\$Paeruginosa	std	r	LCL
Ag20	13.00000	0.0000000	3	12.1696217
AgNP30	12.50000	0.5000000	3	11.6696217
AgNP60	12.16667	0.2886751	3	11.3362883
AgNP90	12.50000	1.3228757	3	11.6696217
Positive	0.00000	0.0000000	3	-0.8303783

	UCL	Min	Max	Q25	Q50	Q75
Ag20	13.8303783	13	13.0	13.00	13.0	13.00
AgNP30	13.3303783	12	13.0	12.25	12.5	12.75
AgNP60	12.9970450	12	12.5	12.00	12.0	12.25
AgNP90	13.3303783	11	13.5	12.00	13.0	13.25
Positive	0.8303783	0	0.0	0.00	0.0	0.00

\$comparison

NULL

\$groups

	df1\$Paeruginosa	groups
Ag20	13.00000	a
AgNP30	12.50000	a
AgNP90	12.50000	a
AgNP60	12.16667	a
Positive	0.00000	b

attr(,"class")

[1] "group"