vacc_tests

Import data

```
Rows: 1689 Columns: 81
── Column specification ────────────────────────────────────────────────────────
Delimiter: ","
chr   (4): birthplace2_other, inpatient_other, vacc_where_other, study_comments
dbl  (75): ph3_redcap_id, ra_num, ph3_consent, unique, caregiver_sex, relati...
lgl   (1): birth_status_other
date  (1): birthdate

ℹ Use `spec()` to retrieve the full column specification for this data.
ℹ Specify the column types or set `show_col_types = FALSE` to quiet this message.
── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──
✔ dplyr     1.1.4     ✔ purrr     1.0.4
✔ forcats   1.0.0     ✔ stringr   1.5.1
✔ ggplot2   3.5.2     ✔ tibble    3.2.1
✔ lubridate 1.9.4     ✔ tidyr     1.3.1
── Conflicts ────────────────────────────────────────── tidyverse_conflicts() ──
✖ dplyr::filter() masks stats::filter()
✖ dplyr::lag()    masks stats::lag()
ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become
errors

# A tibble: 1,689 × 81
   ph3_redcap_id ra_num ph3_consent  unique caregiver_sex relationship education
           <dbl>  <dbl>       <dbl>   <dbl>         <dbl>        <dbl>     <dbl>
 1             1      6           1 6012503             0            0         2
 2             2      6           1 6102509             0            0         1
 3             3      6           1 6022505             0            0         1
 4             4      6           1 6032505             0            0         2
 5             5      6           1 6042506             0            0         0
 6             6      6           1 6052501             0            0         2
 7             7      6           1 6062512             0            0         2
 8             8      6           1 6072505             0            0         2
 9             9      6           1 6082507             0            2         1
10            10      6           1 6092504             0            0         1
# ℹ 1,679 more rows
# ℹ 74 more variables: marital <dbl>, children <dbl>, birthplace <dbl>,
#   oldest_child <dbl>, vacc_more <dbl>, vacc_healthykids <dbl>,
#   vacc_harmgood <dbl>, vacc_natimmune <dbl>, vacc_parentchoice <dbl>,
#   vacc_2for1 <dbl>, vacc_severe <dbl>, vacc_refuse <dbl>, vacc_ses <dbl>,
#   vacc_guidelines <dbl>, exp_policy <dbl>, exp_safe <dbl>, exp_protect <dbl>,
#   exp_self <dbl>, exp_seen <dbl>, exp_delay <dbl>, exp_defer <dbl>, …
```

```
# stats of aggregate beliefs and exp scores
summary(cleanvac$beliefs1)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  2.500   7.500   8.000   8.088   9.000  10.000      43 
```

```
summary(cleanvac$exp1)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
   7.00   10.50   11.00   11.32   12.00   14.00      72 
```

```
# check normality assumption
# both scores fail to meet normality assumption
shapiro.test(cleanvac$beliefs1)
```

```

	Shapiro-Wilk normality test

data:  cleanvac$beliefs1
W = 0.94202, p-value < 2.2e-16
```

```
shapiro.test(cleanvac$exp1)
```

```

	Shapiro-Wilk normality test

data:  cleanvac$exp1
W = 0.94933, p-value < 2.2e-16
```

```
# transform scores
# range = [0,1]
# interpret as proportion of questions answered favorably by diving out of total questions


# belief score, max questions = 10
cleanvac$t_beliefs <- (cleanvac$beliefs1)/10

# experience score, max questions = 14
cleanvac$t_exp   <- (cleanvac$exp1)/14
```

```
# recheck stats and normality assumption
# still fails to meet normality assumption
summary(cleanvac$t_beliefs)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
 0.2500  0.7500  0.8000  0.8088  0.9000  1.0000      43 
```

```
summary(cleanvac$t_exp)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
 0.5000  0.7500  0.7857  0.8084  0.8571  1.0000      72 
```

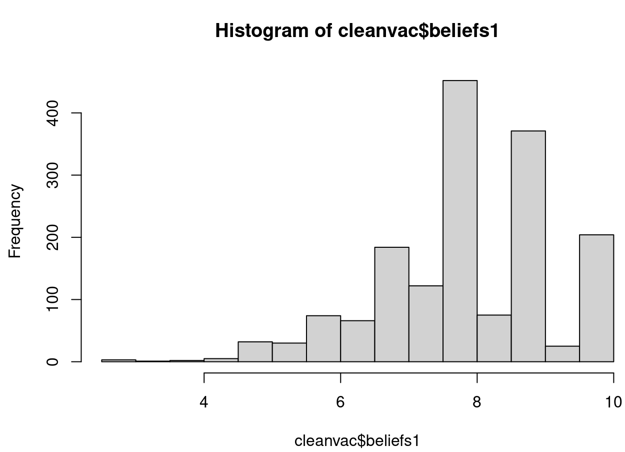
```
shapiro.test(cleanvac$t_beliefs)
```

```

	Shapiro-Wilk normality test

data:  cleanvac$t_beliefs
W = 0.94202, p-value < 2.2e-16
```

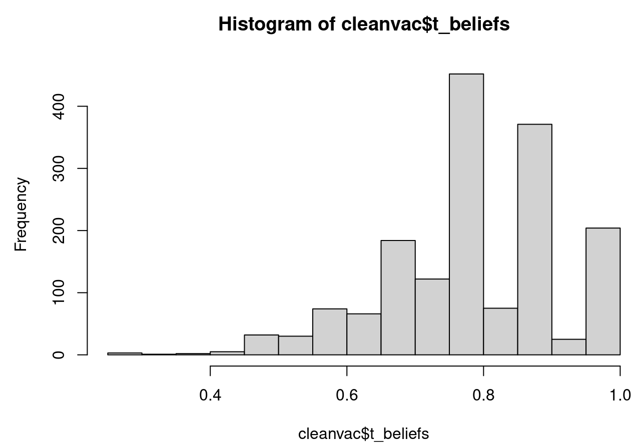
```
shapiro.test(cleanvac$t_exp)
```

```

	Shapiro-Wilk normality test

data:  cleanvac$t_exp
W = 0.94933, p-value < 2.2e-16
```

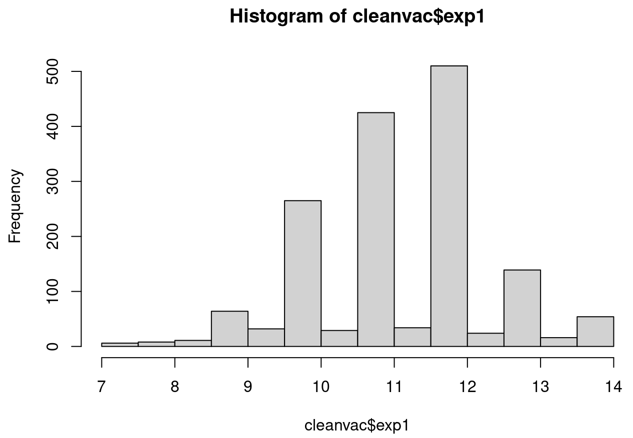
```
hist(cleanvac$beliefs1)
```



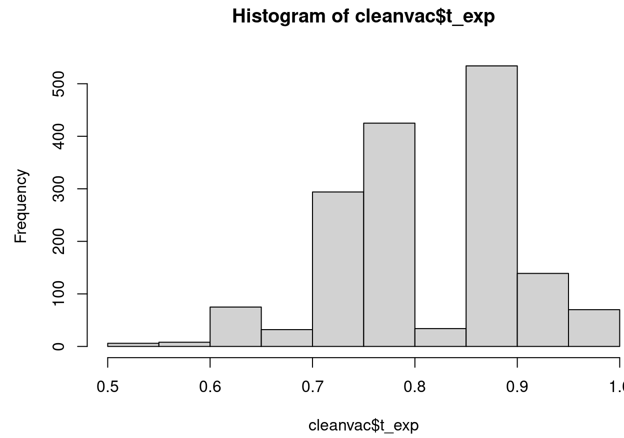

```
hist(cleanvac$t_beliefs)
```




```
hist(cleanvac$exp1)
```




```r
hist(cleanvac$t_exp)
```



Use non-parametric tests:

1. Wilcoxon rank sum test (vs. 2 groups, binary)

```r
table(cleanvac$caregiver_sex)
```

```
   0    1 
1454  231 
```

```r
class(cleanvac$caregiver_sex)
```

```
[1] "numeric"
```

```r
library(coin)
```

```
Loading required package: survival
```

```r
library(rstatix)
```

```

Attaching package: 'rstatix'

The following objects are masked from 'package:coin':

    chisq_test, friedman_test, kruskal_test, sign_test, wilcox_test

The following object is masked from 'package:stats':

    filter
```

```r
# Wilcoxon Rank Sum test, binary
wilcox.test(t_beliefs ~ caregiver_sex, data=cleanvac)
```

```

    Wilcoxon rank sum test with continuity correction

data:  t_beliefs by caregiver_sex
W = 157371, p-value = 0.8957
alternative hypothesis: true location shift is not equal to 0
```

```r
wilcox_effsize(
  cleanvac,
  t_beliefs ~ caregiver_sex,
  ref.group = "0",
  paired = FALSE,
  alternative = "two.sided"
)
```

```
# A tibble: 1 × 7
  .y.       group1 group2 effsize    n1    n2 magnitude
* <chr>     <chr>  <chr>    <dbl> <int> <int> <ord>    
1 t_beliefs 0      1      0.00324  1419   223 small    
```

```r
wilcox.test(t_beliefs ~ bednet, data=cleanvac)
```

```

    Wilcoxon rank sum test with continuity correction

data:  t_beliefs by bednet
W = 85816, p-value = 0.0003254
alternative hypothesis: true location shift is not equal to 0
```

```r
wilcox_effsize(
  cleanvac,
  t_beliefs ~ bednet,
  ref.group = "0",
  paired = FALSE,
  alternative = "two.sided"
)
```

```
# A tibble: 1 × 7
  .y.       group1 group2 effsize    n1    n2 magnitude
* <chr>     <chr>  <chr>    <dbl> <int> <int> <ord>    
1 t_beliefs 0      1       0.0886   139  1507 small    
```

```r
wilcox.test(t_beliefs ~ inpatient, data=cleanvac)
```

```

    Wilcoxon rank sum test with continuity correction

data:  t_beliefs by inpatient
W = 211464, p-value = 0.6234
alternative hypothesis: true location shift is not equal to 0
```

```r
wilcox_effsize(
  cleanvac,
  t_beliefs ~ caregiver_sex,
  ref.group = "0",
  paired = FALSE,
  alternative = "two.sided"
)
```

```
# A tibble: 1 × 7
  .y.       group1 group2 effsize    n1    n2 magnitude
* <chr>     <chr>  <chr>    <dbl> <int> <int> <ord>    
1 t_beliefs 0      1      0.00324  1419   223 small    
```

```r
wilcox.test(t_beliefs ~ child_sex, data=cleanvac)
```

```

    Wilcoxon rank sum test with continuity correction

data:  t_beliefs by child_sex
W = 323575, p-value = 0.206
alternative hypothesis: true location shift is not equal to 0
```

```r
wilcox_effsize(
  cleanvac,
  t_beliefs ~ child_sex,
  ref.group = "0",
  paired = FALSE,
  alternative = "two.sided"
)
```

```
# A tibble: 1 × 7
  .y.       group1 group2 effsize    n1    n2 magnitude
* <chr>     <chr>  <chr>    <dbl> <int> <int> <ord>
1 t_beliefs 0      1       0.0312   884   759 small
```

```r
wilcox.test(t_beliefs ~ hbv_test, data=cleanvac)
```

```
    Wilcoxon rank sum test with continuity correction

data:  t_beliefs by hbv_test
W = 4297.5, p-value = 0.02208
alternative hypothesis: true location shift is not equal to 0
```

```r
wilcox_effsize(
  cleanvac,
  t_beliefs ~ hbv_test,
  ref.group = "0",
  paired = FALSE,
  alternative = "two.sided"
)
```

```
# A tibble: 1 × 7
  .y.       group1 group2 effsize    n1    n2 magnitude
* <chr>     <chr>  <chr>    <dbl> <int> <int> <ord>
1 t_beliefs 0      1       0.0565     3  1637 small
```

```r
wilcox.test(t_beliefs ~ hbv_res, data=cleanvac)
```

```
    Wilcoxon rank sum test with continuity correction

data:  t_beliefs by hbv_res
W = 247444, p-value = 0.1414
alternative hypothesis: true location shift is not equal to 0
```

```r
wilcox_effsize(
  cleanvac,
  t_beliefs ~ hbv_res,
  ref.group = "0",
  paired = FALSE,
  alternative = "two.sided"
)
```

```
# A tibble: 1 × 7
  .y.       group1 group2 effsize    n1    n2 magnitude
* <chr>     <chr>  <chr>    <dbl> <int> <int> <ord>
1 t_beliefs 0      1       0.0364  1258   375 small
```

```r
wilcox.test(t_beliefs ~ dbs, data=cleanvac)
```

```
    Wilcoxon rank sum test with continuity correction

data:  t_beliefs by dbs
W = 14160, p-value = 0.3406
alternative hypothesis: true location shift is not equal to 0
```

```r
wilcox_effsize(
  cleanvac,
  t_beliefs ~ dbs,
  ref.group = "0",
  paired = FALSE,
  alternative = "two.sided"
)
```

```
# A tibble: 1 × 7
  .y.       group1 group2 effsize    n1    n2 magnitude
* <chr>     <chr>  <chr>    <dbl> <int> <int> <ord>
1 t_beliefs 0      1       0.0236    20  1612 small
```

```r
wilcox.test(t_exp ~ caregiver_sex, data=cleanvac)
```

```
    Wilcoxon rank sum test with continuity correction

data:  t_exp by caregiver_sex
W = 166013, p-value = 0.1999
alternative hypothesis: true location shift is not equal to 0
```

```r
wilcox_effsize(
  cleanvac,
  t_exp ~ caregiver_sex,
  ref.group = "0",
  paired = FALSE,
  alternative = "two.sided"
)
```

```
# A tibble: 1 × 7
  .y.   group1 group2 effsize    n1    n2 magnitude
* <chr> <chr>  <chr>    <dbl> <int> <int> <ord>
1 t_exp 0      1       0.0319  1385   228 small
```

```r
wilcox.test(t_exp ~ bednet, data=cleanvac)
```

```
    Wilcoxon rank sum test with continuity correction
```

```
data:  t_exp by bednet
W = 99339, p-value = 0.8076
alternative hypothesis: true location shift is not equal to 0
```

```r
wilcox_effsize(
  cleanvac,
  t_exp ~ bednet,
  ref.group = "0",
  paired = FALSE,
  alternative = "two.sided"
)
```

```
# A tibble: 1 × 7
  .y.   group1 group2 effsize    n1    n2 magnitude
* <chr> <chr>  <chr>    <dbl> <int> <int> <ord>
1 t_exp 0      1      0.00606   136  1479 small
```

```r
wilcox.test(t_exp ~ inpatient, data=cleanvac)
```

```
    Wilcoxon rank sum test with continuity correction

data:  t_exp by inpatient
W = 173683, p-value = 1.312e-07
alternative hypothesis: true location shift is not equal to 0
```

```r
wilcox_effsize(
  cleanvac,
  t_exp ~ inpatient,
  ref.group = "0",
  paired = FALSE,
  alternative = "two.sided"
)
```

```
# A tibble: 1 × 7
  .y.   group1 group2 effsize    n1    n2 magnitude
* <chr> <chr>  <chr>    <dbl> <int> <int> <ord>
1 t_exp 0      1        0.131  1284   331 small
```

```r
wilcox.test(t_exp ~ child_sex, data=cleanvac)
```

```
    Wilcoxon rank sum test with continuity correction

data:  t_exp by child_sex
W = 310010, p-value = 0.1331
alternative hypothesis: true location shift is not equal to 0
```

```r
wilcox_effsize(
  cleanvac,
  t_exp ~ child_sex,
  ref.group = "0",
  paired = FALSE,
  alternative = "two.sided"
)
```

```
# A tibble: 1 × 7
  .y.   group1 group2 effsize    n1    n2 magnitude
* <chr> <chr>  <chr>    <dbl> <int> <int> <ord>
1 t_exp 0      1       0.0374   870   744 small
```

```r
wilcox.test(t_exp ~ hbv_test, data=cleanvac)
```

```
    Wilcoxon rank sum test with continuity correction

data:  t_exp by hbv_test
W = 3305, p-value = 0.2552
alternative hypothesis: true location shift is not equal to 0
```

```r
wilcox_effsize(
  cleanvac,
  t_exp ~ hbv_test,
  ref.group = "0",
  paired = FALSE,
  alternative = "two.sided"
)
```

```
# A tibble: 1 × 7
  .y.   group1 group2 effsize    n1    n2 magnitude
* <chr> <chr>  <chr>    <dbl> <int> <int> <ord>
1 t_exp 0      1       0.0284     3  1609 small
```

```r
wilcox.test(t_exp ~ hbv_res, data=cleanvac)
```

```
    Wilcoxon rank sum test with continuity correction

data:  t_exp by hbv_res
W = 215078, p-value = 0.1605
alternative hypothesis: true location shift is not equal to 0
```

```r
wilcox_effsize(
  cleanvac,
  t_exp ~ hbv_res,
  ref.group = "0",
```

```
  paired = FALSE,
  alternative = "two.sided"
)
```

```
# A tibble: 1 × 7
  .y.   group1 group2 effsize    n1    n2 magnitude
* <chr> <chr>  <chr>    <dbl> <int> <int> <ord>
1 t_exp 0      1       0.0350  1240   364 small
```

```
wilcox.test(t_exp ~ dbs, data=cleanvac)
```

```

    Wilcoxon rank sum test with continuity correction

data:  t_exp by dbs
W = 14870, p-value = 0.9237
alternative hypothesis: true location shift is not equal to 0
```

```
wilcox_effsize(
  cleanvac,
  t_exp ~ dbs,
  ref.group = "0",
  paired = FALSE,
  alternative = "two.sided"
)
```

```
# A tibble: 1 × 7
  .y.   group1 group2 effsize    n1    n2 magnitude
* <chr> <chr>  <chr>    <dbl> <int> <int> <ord>
1 t_exp 0      1      0.00240    19  1585 small
```

```
wilcox.test(t_beliefs ~ card, data=cleanvac)
```

```

    Wilcoxon rank sum test with continuity correction

data:  t_beliefs by card
W = 295018, p-value = 0.8757
alternative hypothesis: true location shift is not equal to 0
```

```
wilcox_effsize(
  cleanvac,
  t_beliefs ~ card,
  ref.group = "0",
  paired = FALSE,
  alternative = "two.sided"
)
```

```
# A tibble: 1 × 7
  .y.       group1 group2 effsize    n1    n2 magnitude
* <chr>     <chr>  <chr>    <dbl> <int> <int> <ord>
1 t_beliefs 0      1      0.00387   531  1106 small
```

```
wilcox.test(t_exp ~ card, data=cleanvac)
```

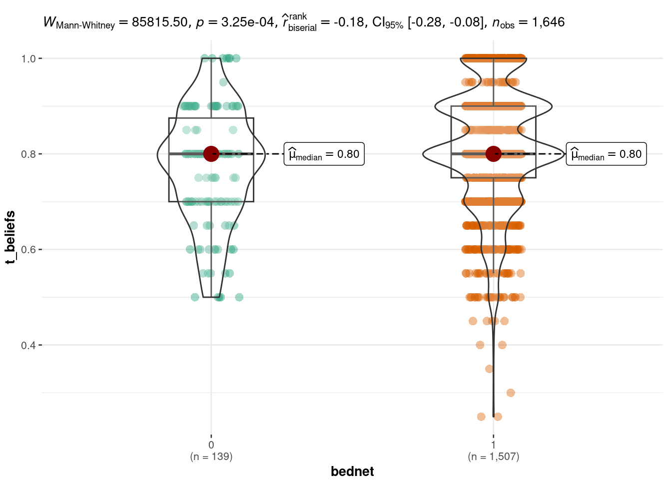
```

    Wilcoxon rank sum test with continuity correction

data:  t_exp by card
W = 262752, p-value = 0.01225
alternative hypothesis: true location shift is not equal to 0
```

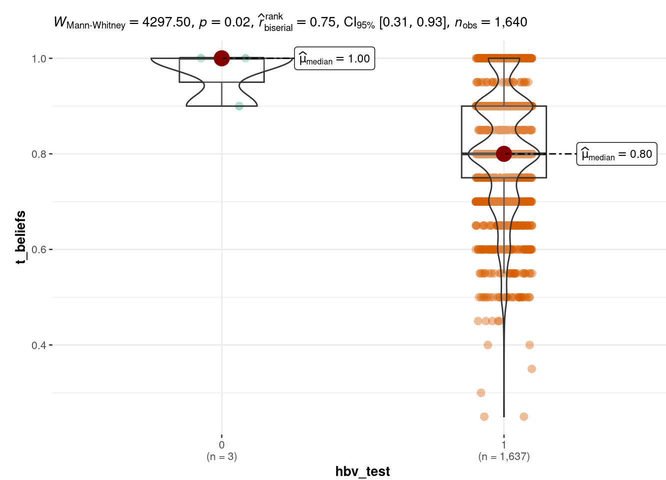
```
wilcox_effsize(
  cleanvac,
  t_exp ~ card,
  ref.group = "0",
  paired = FALSE,
  alternative = "two.sided"
)
```

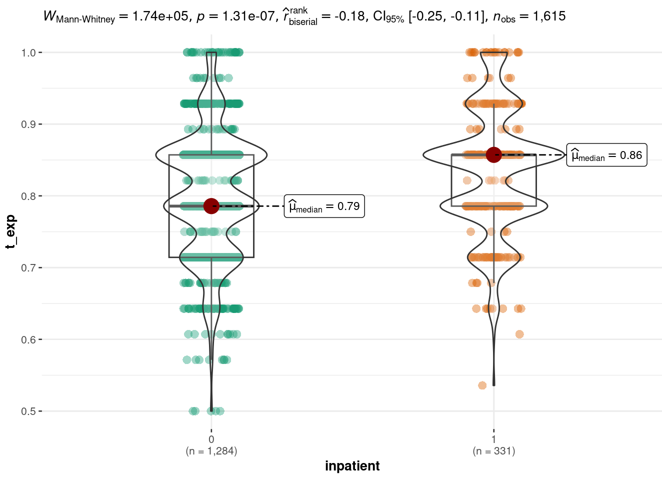
```
# A tibble: 1 × 7
  .y.   group1 group2 effsize    n1    n2 magnitude
* <chr> <chr>  <chr>    <dbl> <int> <int> <ord>
1 t_exp 0      1       0.0625   524  1084 small
```

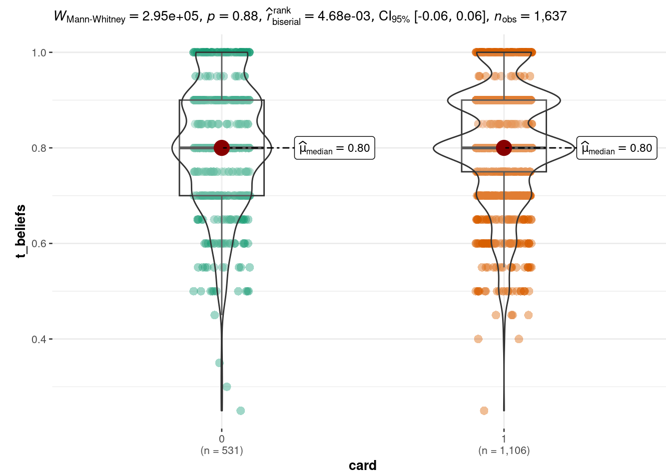
Wilcoxon boxplots, sig. associations

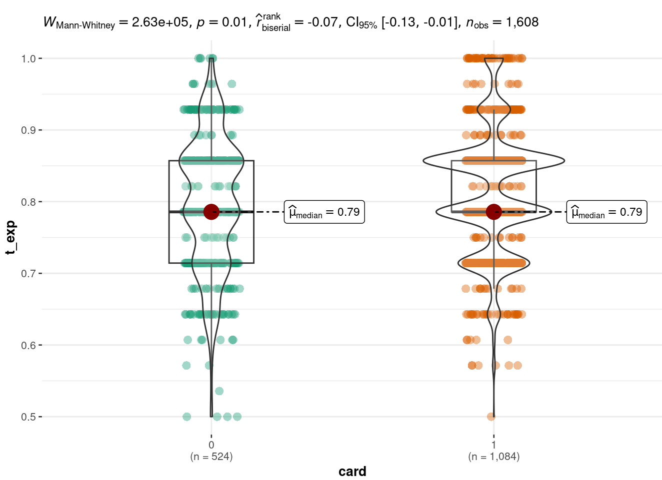
```
You can cite this package as:
     Patil, I. (2021). Visualizations with statistical details: The 'ggstatsplot' approach.
     Journal of Open Source Software, 6(61), 3167, doi:10.21105/joss.03167
```











2. Kruskal-Wallis test (vs. 3 or more groups, nominal)

```
    Kruskal-Wallis rank sum test

data:  t_beliefs by relationship
Kruskal-Wallis chi-squared = 5.0936, df = 4, p-value = 0.2778


    Kruskal-Wallis rank sum test

data:  t_beliefs by marital
Kruskal-Wallis chi-squared = 2.9695, df = 3, p-value = 0.3964


    Kruskal-Wallis rank sum test

data:  t_beliefs by vacc_where
Kruskal-Wallis chi-squared = 38.388, df = 4, p-value = 9.317e-08


    Kruskal-Wallis rank sum test

data:  t_beliefs by birthplace2
Kruskal-Wallis chi-squared = 22.633, df = 4, p-value = 0.0001499

    Kruskal-Wallis rank sum test

data:  t_beliefs by birth_status
Kruskal-Wallis chi-squared = 1.9894, df = 2, p-value = 0.3698


    Kruskal-Wallis rank sum test

data:  t_beliefs by muac_color
Kruskal-Wallis chi-squared = 6.2667, df = 2, p-value = 0.04357


    Kruskal-Wallis rank sum test

data:  t_beliefs by education
Kruskal-Wallis chi-squared = 12.388, df = 3, p-value = 0.006166


    Kruskal-Wallis rank sum test

data:  t_exp by relationship
Kruskal-Wallis chi-squared = 4.4359, df = 4, p-value = 0.3502


    Kruskal-Wallis rank sum test

data:  t_exp by marital
Kruskal-Wallis chi-squared = 15.307, df = 3, p-value = 0.001572


    Kruskal-Wallis rank sum test

data:  t_exp by vacc_where
Kruskal-Wallis chi-squared = 17.362, df = 4, p-value = 0.001644


    Kruskal-Wallis rank sum test

data:  t_exp by birthplace2
Kruskal-Wallis chi-squared = 1.4651, df = 4, p-value = 0.8328


    Kruskal-Wallis rank sum test

data:  t_exp by birth_status
Kruskal-Wallis chi-squared = 1.2026, df = 2, p-value = 0.5481
```

```
    Kruskal-Wallis rank sum test

data:  t_exp by muac_color
Kruskal-Wallis chi-squared = 4.218, df = 2, p-value = 0.1214


    Kruskal-Wallis rank sum test

data:  t_exp by education
Kruskal-Wallis chi-squared = 9.9152, df = 3, p-value = 0.0193
```

Dunn test

```r
# Multiple comparison tests after sig. association in kruskal-wallis

options(tibble.print_max = Inf)

library(rstatix)
dunn_test(data=cleanvac, t_beliefs ~ vacc_where, p.adjust.method = "holm", detailed = TRUE)
```

```
# A tibble: 10 × 13
   .y.       group1 group2    n1    n2 estimate estimate1 estimate2 statistic
 * <chr>     <chr>  <chr>  <int> <int>    <dbl> <dbl[1d]> <dbl[1d]>     <dbl>
 1 t_beliefs 0      1        419   653    -27.3      876.      849.    -0.938
 2 t_beliefs 0      2        419   434   -157.       876.      719.    -4.94
 3 t_beliefs 0      3        419    85     66.4      876.      942.     1.20
 4 t_beliefs 0      4        419    51   -176.       876.      700.    -2.55
 5 t_beliefs 1      2        653   434   -130.       849.      719.    -4.51
 6 t_beliefs 1      3        653    85     93.7      849.      942.     1.75
 7 t_beliefs 1      4        653    51   -148.       849.      700.    -2.19
 8 t_beliefs 2      3        434    85    224.       719.      942.     4.05
 9 t_beliefs 2      4        434    51    -18.3      719.      700.    -0.265
10 t_beliefs 3      4         85    51   -242.       942.      700.    -2.94
# ℹ 4 more variables: p <dbl>, method <chr>, p.adj <dbl>, p.adj.signif <chr>
```

```r
dunn_test(data=cleanvac, t_beliefs ~ birthplace2, p.adjust.method = "holm", detailed = TRUE)
```

```
# A tibble: 10 × 13
   .y.       group1 group2    n1    n2 estimate estimate1 estimate2 statistic
 * <chr>     <chr>  <chr>  <int> <int>    <dbl> <dbl[1d]> <dbl[1d]>     <dbl>
 1 t_beliefs 0      1        256   666     11.1      859.      870.     0.325
 2 t_beliefs 0      2        256    88    -34.1      859.      825.    -0.592
 3 t_beliefs 0      3        256   631   -102.       859.      757.    -2.96
 4 t_beliefs 0      4        256     4    251.       859.     1110      1.07
 5 t_beliefs 1      2        666    88    -45.2      870.      825.    -0.855
 6 t_beliefs 1      3        666   631   -114.       870.      757.    -4.38
 7 t_beliefs 1      4        666     4    240.       870.     1110      1.03
```

```
# A tibble: 6 × 13
  .y.   group1 group2    n1    n2 estimate estimate1 estimate2 statistic        p
* <chr> <chr>  <chr>  <int> <int>    <dbl> <dbl[1d]> <dbl[1d]>     <dbl>    <dbl>
1 t_exp 0      1         80  1473   182.        639.      821.    3.50   4.57e-4
2 t_exp 0      2         80    53    63.0       639.      702.    0.784  4.33e-1
3 t_exp 0      3         80     9   178.        639.      817.    1.12   2.64e-1
4 t_exp 1      2       1473    53  -119.        821.      702.   -1.88   5.95e-2
5 t_exp 1      3       1473     9    -4.20      821.      817.   -0.0277 9.78e-1
6 t_exp 2      3         53     9   115.        702.      817.    0.705  4.81e-1
# ℹ 3 more variables: method <chr>, p.adj <dbl>, p.adj.signif <chr>
```

```r
dunn_test(data=cleanvac, t_exp ~ education, p.adjust.method = "holm", detailed = TRUE)
```

```
# A tibble: 6 × 13
  .y.   group1 group2    n1    n2 estimate estimate1 estimate2 statistic       p
* <chr> <chr>  <chr>  <int> <int>    <dbl> <dbl[1d]> <dbl[1d]>     <dbl>   <dbl>
1 t_exp 0      1        157   979   -103.       907.      804.    -2.64  0.00834
2 t_exp 0      2        157   441   -129.       907.      778.    -3.07  0.00217
3 t_exp 0      3        157    38    -52.3      907.      855.    -0.638 0.523
4 t_exp 1      2        979   441    -26.4      804.      778.    -1.01  0.310
5 t_exp 1      3        979    38     50.5      804.      855.     0.674 0.500
6 t_exp 2      3        441    38     76.9      778.      855.     1.00  0.316
# ℹ 3 more variables: method <chr>, p.adj <dbl>, p.adj.signif <chr>
```

K-W plots

```
 8 t_beliefs 2      3         88   631    -68.3      825.      757.    -1.29
 9 t_beliefs 2      4         88     4    285.       825.     1110      1.20
10 t_beliefs 3      4        631     4    353.       757.     1110      1.51
# ℹ 4 more variables: p <dbl>, method <chr>, p.adj <dbl>, p.adj.signif <chr>
```

```r
dunn_test(data=cleanvac, t_beliefs ~ muac_color, p.adjust.method = "holm", detailed = TRUE)
```

```
# A tibble: 3 × 13
  .y.    group1 group2    n1    n2 estimate estimate1 estimate2 statistic      p
* <chr>  <chr>  <chr>  <int> <int>    <dbl> <dbl[1d]> <dbl[1d]>     <dbl>  <dbl>
1 t_bel… 0      1       1568    56   -158.       827.      670.    -2.49  0.0128
2 t_bel… 0      2       1568    18    -34.4      827.      793.    -0.312 0.755
3 t_bel… 1      2         56    18    123.       670.      793.     0.977 0.329
# ℹ 3 more variables: method <chr>, p.adj <dbl>, p.adj.signif <chr>
```

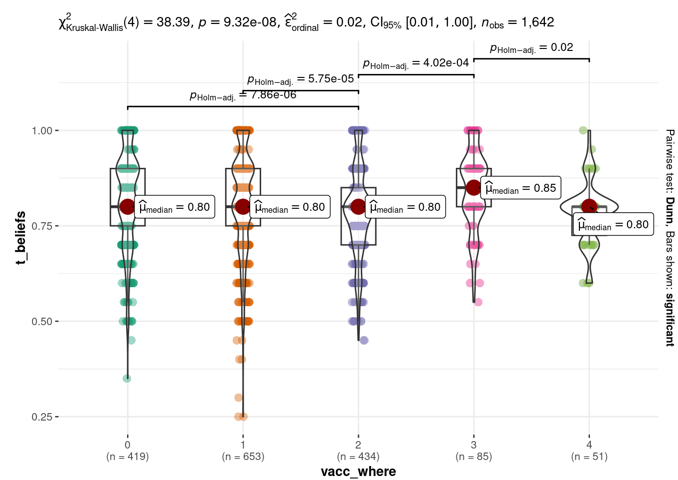
```r
dunn_test(data=cleanvac, t_beliefs ~ education, p.adjust.method = "holm", detailed = TRUE)
```

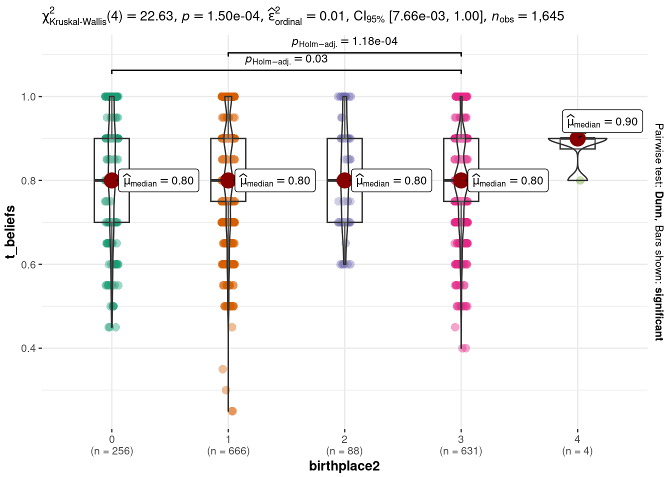
```
# A tibble: 6 × 13
  .y.    group1 group2    n1    n2 estimate estimate1 estimate2 statistic       p
* <chr>  <chr>  <chr>  <int> <int>    <dbl> <dbl[1d]> <dbl[1d]>     <dbl>   <dbl>
1 t_be… 0      1        160   995   138.        700.      838.     3.46  5.37e-4
2 t_be… 0      2        160   453   132.        700.      832.     3.08  2.08e-3
3 t_be… 0      3        160    37   150.        700.      850.     1.77  7.73e-2
4 t_be… 1      2        995   453    -5.48      838.      832.    -0.207 8.36e-1
5 t_be… 1      3        995    37    12.8       838.      850.     0.164 8.70e-1
6 t_be… 2      3        453    37    18.3       832.      850.     0.229 8.19e-1
# ℹ 3 more variables: method <chr>, p.adj <dbl>, p.adj.signif <chr>
```

```r
dunn_test(data=cleanvac, t_exp ~ vacc_where, p.adjust.method = "holm", detailed = TRUE)
```

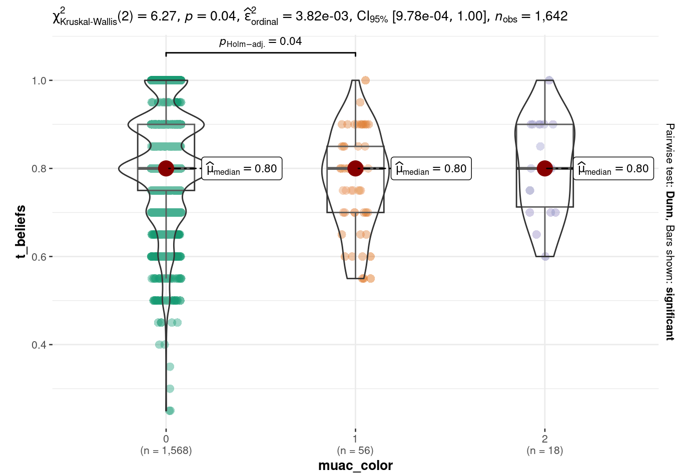
```
# A tibble: 10 × 13
   .y.   group1 group2    n1    n2 estimate estimate1 estimate2 statistic
 * <chr> <chr>  <chr>  <int> <int>    <dbl> <dbl[1d]> <dbl[1d]>     <dbl>
 1 t_exp 0      1        413   643    109.       752.      861.     3.82
 2 t_exp 0      2        413   422     40.2      752.      793.     1.28
 3 t_exp 0      3        413    83     -6.25     752.      746.    -0.115
 4 t_exp 0      4        413    52     31.9      752.      784.     0.479
 5 t_exp 1      2        643   422    -68.8      861.      793.    -2.43
 6 t_exp 1      3        643    83   -115.       861.      746.    -2.18
 7 t_exp 1      4        643    52    -77.1      861.      784.    -1.18
 8 t_exp 2      3        422    83    -46.5      793.      746.    -0.855
 9 t_exp 2      4        422    52     -8.29     793.      784.    -0.125
10 t_exp 3      4         83    52     38.2      746.      784.     0.477
# ℹ 4 more variables: p <dbl>, method <chr>, p.adj <dbl>, p.adj.signif <chr>
```

```r
dunn_test(data=cleanvac, t_exp ~ marital, p.adjust.method = "holm", detailed = TRUE)
```

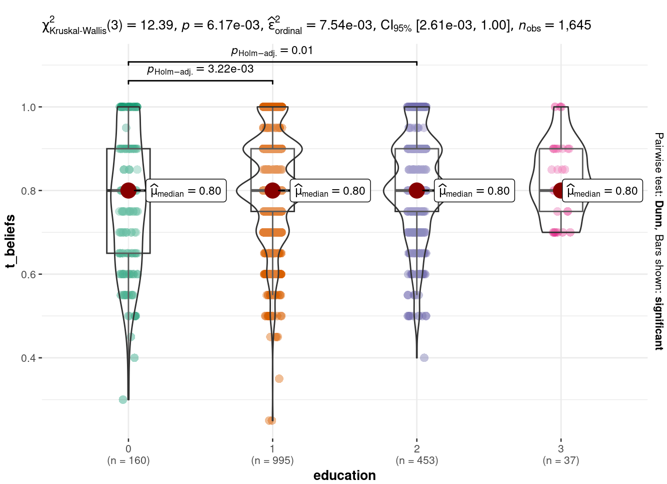




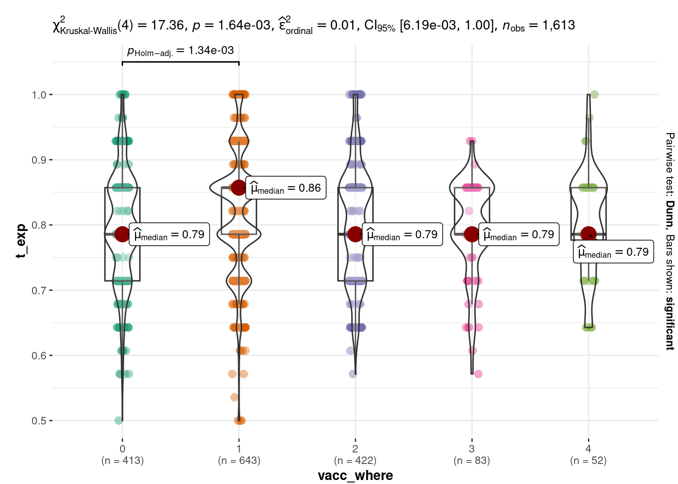
$\chi^2_{\text{Kruskal-Wallis}}(4) = 22.63$, $p = 1.50\text{e-}04$, $\widehat{\epsilon}^2_{\text{ordinal}} = 0.01$, $\text{CI}_{95\%}$ [7.66e-03, 1.00], $n_{\text{obs}} = 1,645$
$p_{\text{Holm-adj.}} = 1.18\text{e-}04$
$p_{\text{Holm-adj.}} = 0.03$
$\widehat{\mu}_{\text{median}} = 0.80$
$\widehat{\mu}_{\text{median}} = 0.90$
t_beliefs
birthplace2
0 (n = 256)
1 (n = 666)
2 (n = 88)
3 (n = 631)
4 (n = 4)
Pairwise test: Dunn, Bars shown: significant



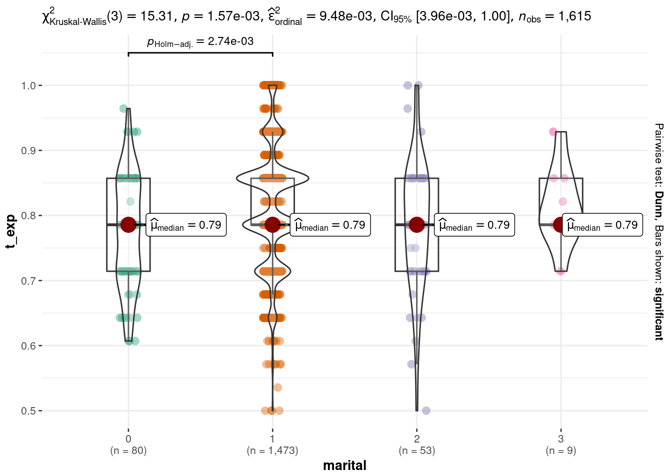
$\chi^2_{\text{Kruskal-Wallis}}(2) = 6.27$, $p = 0.04$, $\widehat{\epsilon}^2_{\text{ordinal}} = 3.82\text{e-}03$, $\text{CI}_{95\%}$ [9.78e-04, 1.00], $n_{\text{obs}} = 1,642$
$p_{\text{Holm-adj.}} = 0.04$
$\widehat{\mu}_{\text{median}} = 0.80$
t_beliefs
muac_color
0 (n = 1,568)
1 (n = 56)
2 (n = 18)
Pairwise test: Dunn, Bars shown: significant

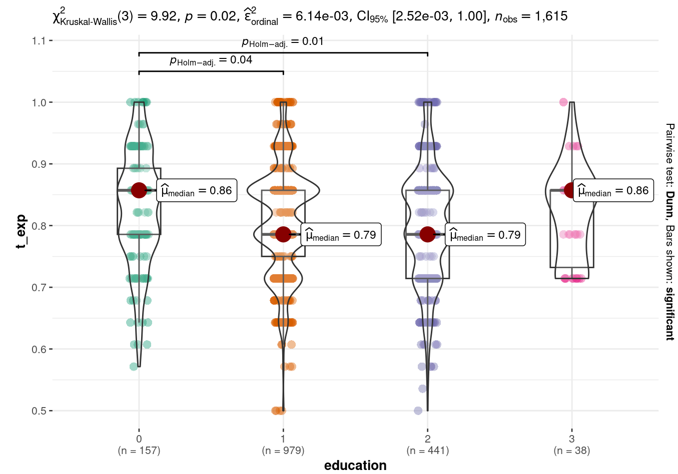


$\chi^2_{\text{Kruskal-Wallis}}(3) = 12.39$, $p = 6.17\text{e-}03$, $\widehat{\epsilon}^2_{\text{ordinal}} = 7.54\text{e-}03$, $\text{CI}_{95\%}$ [2.61e-03, 1.00], $n_{\text{obs}} = 1,645$
$p_{\text{Holm-adj.}} = 0.01$
$p_{\text{Holm-adj.}} = 3.22\text{e-}03$
$\widehat{\mu}_{\text{median}} = 0.80$
t_beliefs
education
0 (n = 160)
1 (n = 995)
2 (n = 453)
3 (n = 37)
Pairwise test: Dunn, Bars shown: significant

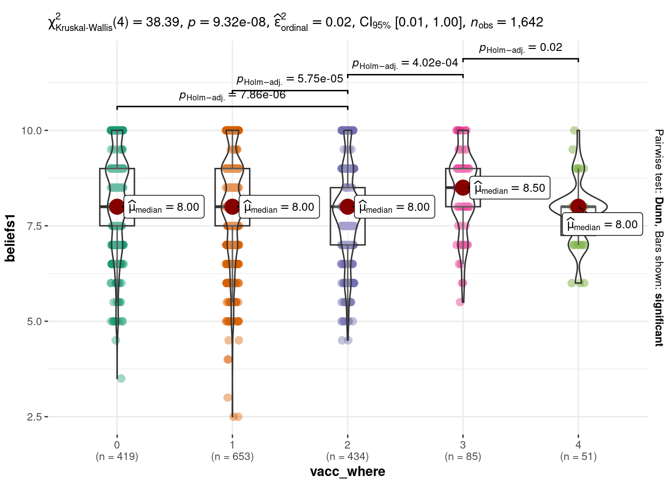


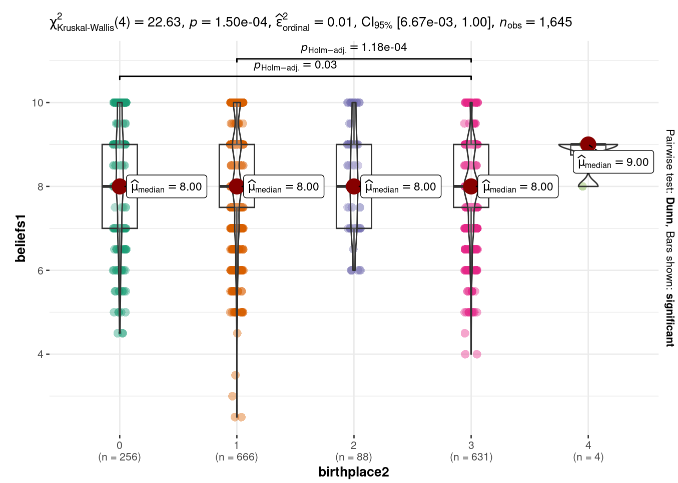
$\chi^2_{\text{Kruskal-Wallis}}(4) = 17.36$, $p = 1.64\text{e-}03$, $\widehat{\epsilon}^2_{\text{ordinal}} = 0.01$, $\text{CI}_{95\%}$ [6.19e-03, 1.00], $n_{\text{obs}} = 1,613$
$p_{\text{Holm-adj.}} = 1.34\text{e-}03$
$\widehat{\mu}_{\text{median}} = 0.79$
$\widehat{\mu}_{\text{median}} = 0.86$
t_exp
vacc_where
0 (n = 413)
1 (n = 643)
2 (n = 422)
3 (n = 83)
4 (n = 52)
Pairwise test: Dunn, Bars shown: significant

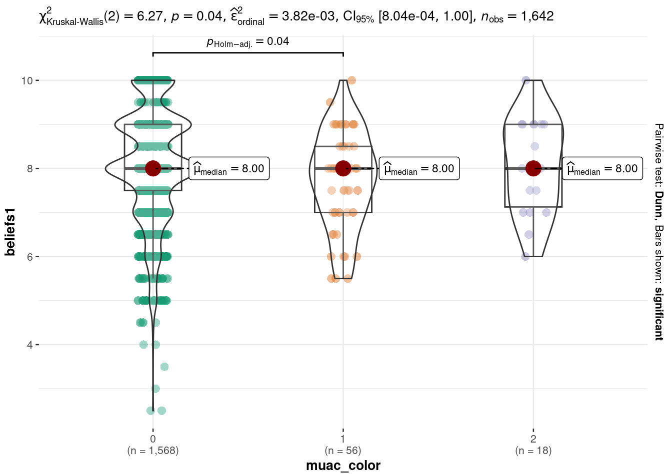


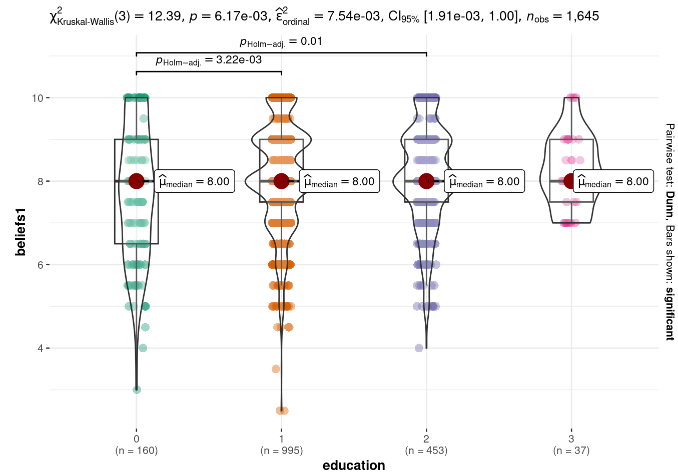


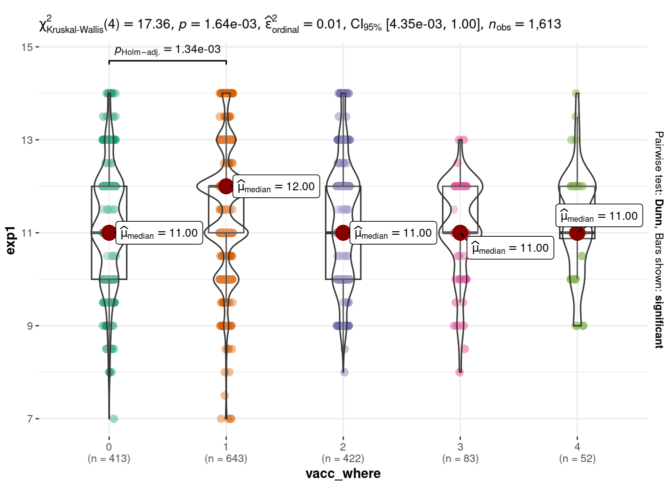
Untransformed scores

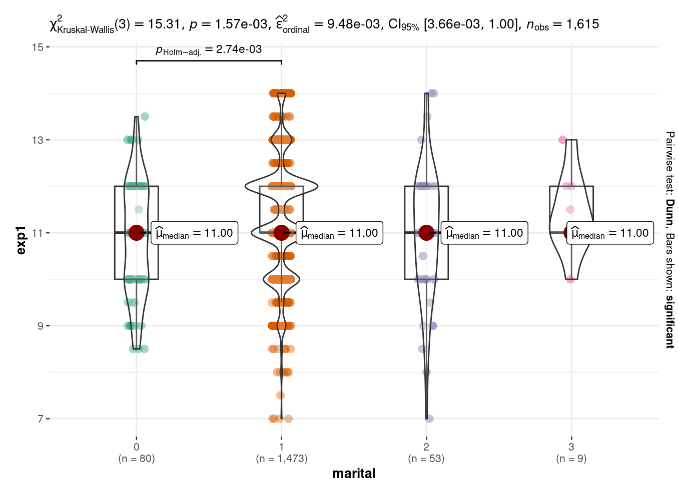


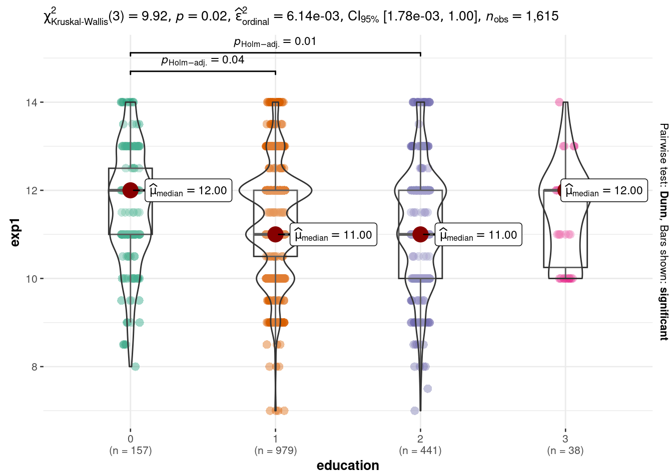



$\chi^2_{\text{Kruskal-Wallis}}(2) = 6.27$, $p = 0.04$, $\widehat{\epsilon}^2_{\text{ordinal}} = 3.82\text{e-}03$, $\text{CI}_{95\%}$ [8.04e-04, 1.00], $n_{\text{obs}} = 1{,}642$
$p_{\text{Holm-adj.}} = 0.04$
$\widehat{\mu}_{\text{median}} = 8.00$
$\widehat{\mu}_{\text{median}} = 8.00$
$\widehat{\mu}_{\text{median}} = 8.00$
beliefs1
muac_color
0 (n = 1,568)
1 (n = 56)
2 (n = 18)
Pairwise test: **Dunn**, Bars shown: **significant**


$\chi^2_{\text{Kruskal-Wallis}}(3) = 12.39$, $p = 6.17\text{e-}03$, $\widehat{\epsilon}^2_{\text{ordinal}} = 7.54\text{e-}03$, $\text{CI}_{95\%}$ [1.91e-03, 1.00], $n_{\text{obs}} = 1{,}645$
$p_{\text{Holm-adj.}} = 0.01$
$p_{\text{Holm-adj.}} = 3.22\text{e-}03$
$\widehat{\mu}_{\text{median}} = 8.00$
$\widehat{\mu}_{\text{median}} = 8.00$
$\widehat{\mu}_{\text{median}} = 8.00$
$\widehat{\mu}_{\text{median}} = 8.00$
beliefs1
education
0 (n = 160)
1 (n = 995)
2 (n = 453)
3 (n = 37)
Pairwise test: **Dunn**, Bars shown: **significant**


$\chi^2_{\text{Kruskal-Wallis}}(4) = 17.36$, $p = 1.64\text{e-}03$, $\widehat{\epsilon}^2_{\text{ordinal}} = 0.01$, $\text{CI}_{95\%}$ [4.35e-03, 1.00], $n_{\text{obs}} = 1{,}613$
$p_{\text{Holm-adj.}} = 1.34\text{e-}03$
$\widehat{\mu}_{\text{median}} = 11.00$
$\widehat{\mu}_{\text{median}} = 12.00$
$\widehat{\mu}_{\text{median}} = 11.00$
$\widehat{\mu}_{\text{median}} = 11.00$
$\widehat{\mu}_{\text{median}} = 11.00$
exp1
vacc_where
0 (n = 413)
1 (n = 643)
2 (n = 422)
3 (n = 83)
4 (n = 52)
Pairwise test: **Dunn**, Bars shown: **significant**


$\chi^2_{\text{Kruskal-Wallis}}(3) = 15.31$, $p = 1.57\text{e-}03$, $\widehat{\epsilon}^2_{\text{ordinal}} = 9.48\text{e-}03$, $\text{CI}_{95\%}$ [3.66e-03, 1.00], $n_{\text{obs}} = 1{,}615$
$p_{\text{Holm-adj.}} = 2.74\text{e-}03$
$\widehat{\mu}_{\text{median}} = 11.00$
$\widehat{\mu}_{\text{median}} = 11.00$
$\widehat{\mu}_{\text{median}} = 11.00$
$\widehat{\mu}_{\text{median}} = 11.00$
exp1
marital
0 (n = 80)
1 (n = 1,473)
2 (n = 53)
3 (n = 9)
Pairwise test: **Dunn**, Bars shown: **significant**



3. Kendall's tau (vs. continuous)

```
# Kendall's tau corr, continuous

cor.test(cleanvac$t_beliefs, cleanvac$t_exp, method = "kendall")
```

```

	Kendall's rank correlation tau

data:  cleanvac$t_beliefs and cleanvac$t_exp
z = -0.28982, p-value = 0.772
alternative hypothesis: true tau is not equal to 0
sample estimates:
         tau 
-0.005710061 
```

```
cor.test(cleanvac$t_beliefs, cleanvac$age_months, method = "kendall")
```

```

	Kendall's rank correlation tau

```

```
data:  cleanvac$t_beliefs and cleanvac$birthplace
z = 0.17765, p-value = 0.859
alternative hypothesis: true tau is not equal to 0
sample estimates:
        tau 
0.003574578 
```

```
cor.test(cleanvac$t_exp, cleanvac$age_months, method = "kendall")
```

```

	Kendall's rank correlation tau

data:  cleanvac$t_exp and cleanvac$age_months
z = -1.0836, p-value = 0.2785
alternative hypothesis: true tau is not equal to 0
sample estimates:
        tau 
-0.02025126 
```

```
cor.test(cleanvac$t_exp, cleanvac$oldest_child, method = "kendall")
```

```

	Kendall's rank correlation tau

data:  cleanvac$t_exp and cleanvac$oldest_child
z = 3.7558, p-value = 0.0001728
alternative hypothesis: true tau is not equal to 0
sample estimates:
       tau 
0.07080068 
```

```
cor.test(cleanvac$t_exp, cleanvac$muac, method = "kendall")
```

```

	Kendall's rank correlation tau

data:  cleanvac$t_exp and cleanvac$muac
z = -3.1997, p-value = 0.001376
alternative hypothesis: true tau is not equal to 0
sample estimates:
        tau 
-0.05897766 
```

```
cor.test(cleanvac$t_exp, cleanvac$children, method = "kendall")
```

```

	Kendall's rank correlation tau

```

```
data:  cleanvac$t_beliefs and cleanvac$age_months
z = 1.2058, p-value = 0.2279
alternative hypothesis: true tau is not equal to 0
sample estimates:
       tau 
0.02198937 
```

```
cor.test(cleanvac$t_beliefs, cleanvac$oldest_child, method = "kendall")
```

```

	Kendall's rank correlation tau

data:  cleanvac$t_beliefs and cleanvac$oldest_child
z = -0.74839, p-value = 0.4542
alternative hypothesis: true tau is not equal to 0
sample estimates:
        tau 
-0.01377575 
```

```
cor.test(cleanvac$t_beliefs, cleanvac$muac, method = "kendall")
```

```

	Kendall's rank correlation tau

data:  cleanvac$t_beliefs and cleanvac$muac
z = 2.4608, p-value = 0.01386
alternative hypothesis: true tau is not equal to 0
sample estimates:
       tau 
0.04425442 
```

```
cor.test(cleanvac$t_beliefs, cleanvac$children, method = "kendall")
```

```

	Kendall's rank correlation tau

data:  cleanvac$t_beliefs and cleanvac$children
z = -0.067604, p-value = 0.9461
alternative hypothesis: true tau is not equal to 0
sample estimates:
        tau 
-0.00127626 
```

```
cor.test(cleanvac$t_beliefs, cleanvac$birthplace, method = "kendall")
```

```

	Kendall's rank correlation tau

```

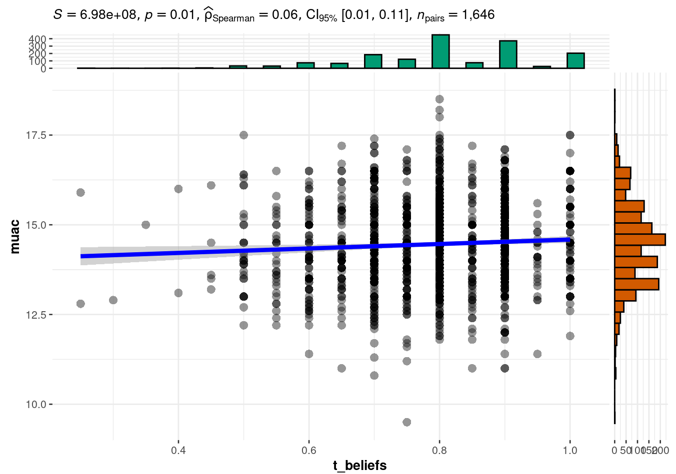
```
data:  cleanvac$t_exp and cleanvac$children
z = 3.6371, p-value = 0.0002757
alternative hypothesis: true tau is not equal to 0
sample estimates:
      tau 
0.0703592 
```

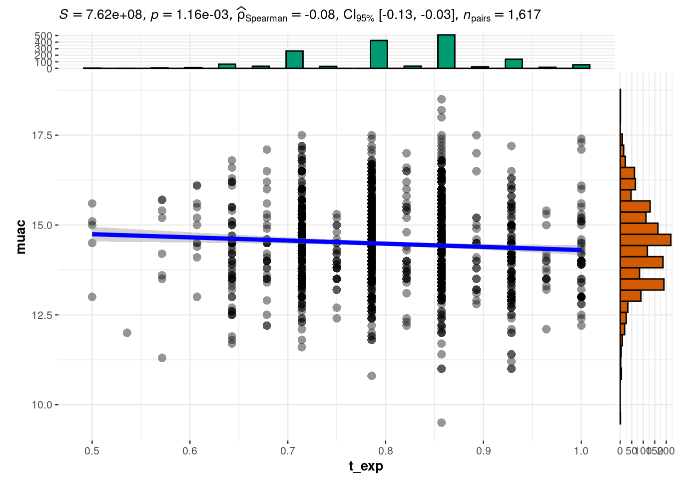
```
cor.test(cleanvac$t_exp, cleanvac$birthplace, method = "kendall")
```

```

	Kendall's rank correlation tau

data:  cleanvac$t_exp and cleanvac$birthplace
z = 1.6537, p-value = 0.09819
alternative hypothesis: true tau is not equal to 0
sample estimates:
       tau 
0.03414482 
```

Corr plots, sig. associations

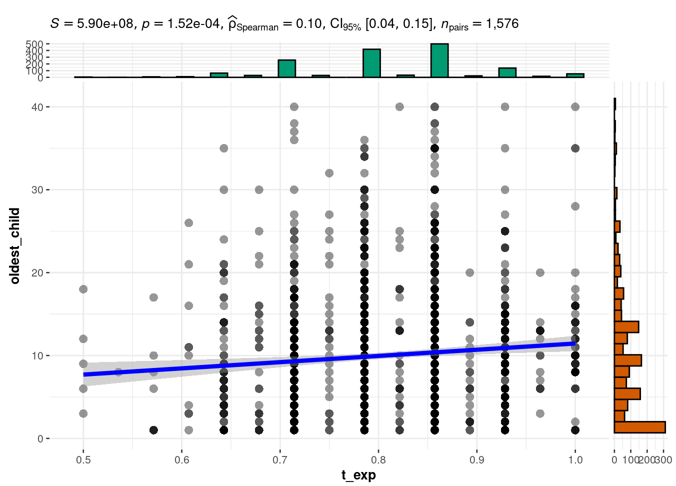
```
Registered S3 method overwritten by 'ggside':
  method from   
  +.gg   ggplot2

`stat_xsidebin()` using `bins = 30`. Pick better value with `binwidth`.
`stat_ysidebin()` using `bins = 30`. Pick better value with `binwidth`.
```

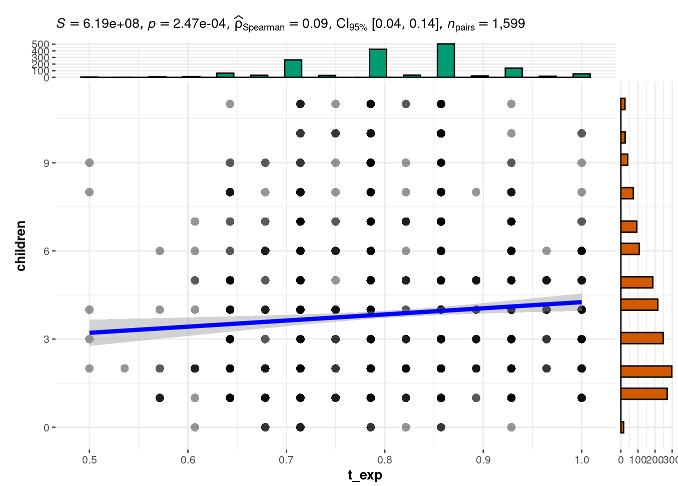





```
`stat_xsidebin()` using `bins = 30`. Pick better value with `binwidth`.
`stat_ysidebin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
`stat_xsidebin()` using `bins = 30`. Pick better value with `binwidth`.
`stat_ysidebin()` using `bins = 30`. Pick better value with `binwidth`.
```






```
`stat_xsidebin()` using `bins = 30`. Pick better value with `binwidth`.
`stat_ysidebin()` using `bins = 30`. Pick better value with `binwidth`.
```

Brief Results

Caregivers who brought their child to government health facilities 2, 3, or Immunization Program Visits to receive vaccinations over private healthcare were associated with a higher aggregate belief score (Table S1). Caregivers who did not complete school compared to those who completed primary or secondary school, and children born in private healthcare facilities over government health facilities or at home were associated with a lower aggregate belief score (Table S1). Children who slept under a bed net in the previous night were associated with a higher aggregate belief score, although with minimal effect (Cohen's d = 0.089, p-value = <0.001, Table 3).

Caregivers taking care of more children were associated with a marginally higher aggregate experience score (Kendall's tau = 0.070, p-value = < 0.001, Table 3). Caregivers who brought their child to government health facility 2 over facility 3 to receive vaccinations were associated with a higher aggregate experience score (Table S1). In contrast to belief scores, caregivers who did not complete school compared to those who completed primary and secondary school, and married caregivers over those unmarried were associated with a higher aggregate experience score (Table S1). Children who stayed overnight in a hospital or clinic at least once in their lifetime were associated with a higher aggregate experience score, although with small effect (Cohen's d = 0.131, p-value = <0.001, Table 3).