# A Handbook of Statistical Analyses Using ${\sf R}$

Brian S. Everitt and Torsten Hothorn



#### CHAPTER 3

# Conditional Inference: Guessing Lengths, Suicides, Gastrointestinal Damage, and Newborn Infants

- 3.1 Introduction
- 3.2 Conditional Test Procedures
- 3.3 Analysis Using R
- 3.3.1 Estimating the Width of a Room Revised

The unconditional analysis of the room width estimated by two groups of students in Chapter ?? lead to the conclusion that the estimates in metres are slightly larger than the estimates in feet. Here, we reanalyse these data in a conditional framework. First, we convert metres into feet and store the vector of observations in a variable y:

```
R> data("roomwidth", package = "HSAUR")
R> convert <- ifelse(roomwidth$unit == "feet", 1, 3.28)
R> feet <- roomwidth$unit == "feet"
R> metre <- !feet
R> y <- roomwidth$width * convert
The test statistic is simply the difference in means
R> T <- mean(y[feet]) - mean(y[metre])
R> T
[1] -8.858893
```

In order to approximate the conditional distribution of the test statistic T we compute 9999 test statistics for shuffled y values. A permutation of the y vector can be obtained from the sample function.

The distribution of the test statistic T under the null hypothesis of independence of room width estimates and groups is depicted in Figure 3.1. Now, the value of the test statistic T for the original unshuffled data can be compared

R> hist(meandiffs)
R> abline(v = T, lty = 2)
R> abline(v = -T, lty = 2)

# Histogram of meandiffs

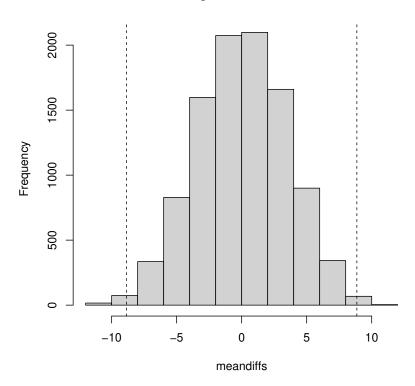


Figure 3.1 Approximated conditional distribution of the difference of mean roomwidth estimates in the feet and metres group under the null hypothesis. The vertical lines show the negative and positive absolute value of the test statistic T obtained from the original data.

with the distribution of T under the null hypothesis (the vertical lines in Figure 3.1). The p-value, i.e., the proportion of test statistics T larger than 8.859 or smaller than -8.859 is

```
R> greater <- abs(meandiffs) > abs(T)
R> mean(greater)
[1] 0.00740074
with a confidence interval of
R> binom.test(sum(greater), length(greater))$conf.int
```

```
[1] 0.005815511 0.009282160 attr(,"conf.level") [1] 0.95
```

Note that the approximated conditional p-value is roughly the same as the p-value reported by the t-test in Chapter 2.

Figure 3.2 R output of the exact permutation test applied to the roomwidth data.

Figure 3.3 R output of the exact conditional Wilcoxon rank sum test applied to the roomwidth data.

# 3.3.2 Crowds and Threatened Suicide

Figure 3.4 R output of Fisher's exact test for the suicides data.

### 3.3.3 Gastrointestinal Damages

Here we are interested in the comparison of two groups of patients, where one group received a placebo and the other one Misoprostol. In the trials shown here, the response variable is measured on an ordered scale – see Table ??. Data from four clinical studies are available and thus the observations are naturally grouped together. From the *data.frame* Lanza we can construct a three-way table as follows:

```
R> data("Lanza", package = "HSAUR")
R> xtabs(~ treatment + classification + study, data = Lanza)
, , study = I
             classification
              1 2 3 4 5
treatment
 Misoprostol 21 2 4 2 0
              2 2 4 9 13
  Placebo
, , study = II
            classification
treatment
              1 2 3 4 5
  Misoprostol 20 4 6 0 0
  Placebo
            8 4 9 4 5
, , study = III
            classification
            1 2 3 4 5
treatment
 Misoprostol 20
                 4
                    3
                       1 2
  Placebo
              0 2
                    5 5 17
, , study = IV
             classification
              1 2 3 4 5
treatment
 Misoprostol 1 4 5 0
                          0
  Placebo
               0
                 0
                    0
 For the first study, the null hypothesis of independence of treatment and
gastrointestinal damage, i.e., of no treatment effect of Misoprostol, is tested
by
R> library("coin")
R> cmh_test(classification ~ treatment, data = Lanza,
           scores = list(classification = c(0, 1, 6, 17, 30)),
+
           subset = Lanza$study == "I")
        Asymptotic Linear-by-Linear Association Test
data: classification (ordered) by treatment (Misoprostol, Placebo)
```

Z = -5.371, p-value = 7.83e-08

```
alternative hypothesis: two.sided
and, by default, the conditional distribution is approximated by the corre-
sponding limiting distribution. The p-value indicates a strong treatment effect.
For the second study, the asymptotic p-value is a little bit larger
R> cmh_test(classification ~ treatment, data = Lanza,
            scores = list(classification = c(0, 1, 6, 17, 30)),
            subset = Lanza$study == "II")
        Asymptotic Linear-by-Linear Association Test
data: classification (ordered) by treatment (Misoprostol, Placebo)
Z = -3.4733, p-value = 0.000514
alternative hypothesis: two.sided
and we make sure that the implied decision is correct by calculating a confi-
dence interval for the exact p-value
R> p <- cmh_test(classification ~ treatment, data = Lanza,</pre>
            scores = list(classification = c(0, 1, 6, 17, 30)),
            subset = Lanza$study == "II", distribution =
            approximate(B = 19999))
R> pvalue(p)
[1] <5.00025e-05
99 percent confidence interval:
 0.000000000 0.000264894
The third and fourth study indicate a strong treatment effect as well
R> cmh_test(classification ~ treatment, data = Lanza,
            scores = list(classification = c(0, 1, 6, 17, 30)),
+
            subset = Lanza$study == "III")
        Asymptotic Linear-by-Linear Association Test
data: classification (ordered) by treatment (Misoprostol, Placebo)
Z = -5.3065, p-value = 1.118e-07
alternative hypothesis: two.sided
R> cmh_test(classification ~ treatment, data = Lanza,
            scores = list(classification = c(0, 1, 6, 17, 30)),
            subset = Lanza$study == "IV")
        Asymptotic Linear-by-Linear Association Test
data: classification (ordered) by treatment (Misoprostol, Placebo)
Z = -3.9675, p-value = 7.262e-05
alternative hypothesis: two.sided
```

At the end, a separate analysis for each study is unsatisfactory. Because the design of the four studies is the same, we can use study as a block variable and perform a global linear-association test investigating the treatment effect

of Misoprostol in all four studies. The block variable can be incorporated into the *formula* by the | symbol.

Based on this result, a strong treatment effect can be established.

## 3.3.4 Teratogenesis

In this example, the medical doctor (MD) and the research assistant (RA) assessed the number of anomalies (0,1,2 or 3) for each of 395 babies:

```
R> anomalies <- c(235, 23, 3, 0, 41, 35, 8, 0,
                   20, 11, 11, 1, 2, 1, 3, 1)
R> anomalies <- as.table(matrix(anomalies,</pre>
       ncol = 4, dimnames = list(MD = 0:3, RA = 0:3)))
R> anomalies
MD
      0
              20
  0 235
          41
          35
     23
              11
                   7
                   3
      3
           8
              11
      0
                   1
           0
               7
```

We are interested in testing whether the number of anomalies assessed by the medical doctor differs structurally from the number reported by the research assistant. Because we compare *paired* observations, i.e., one pair of measurements for each newborn, a test of marginal homogeneity (a generalisation of McNemar's test, see Chapter 2) needs to be applied:

### R> mh\_test(anomalies)

Asymptotic Marginal Homogeneity Test

The p-value indicates a deviation from the null hypothesis. However, the levels of the response are not treated as ordered. Similar to the analysis of the gastrointestinal damage data above, we can take this information into account by the definition of an appropriate score. Here, the number of anomalies is a natural choice:

```
R> mh_test(anomalies, scores = list(response = c(0, 1, 2, 3)))

Asymptotic Marginal Homogeneity Test for Ordered Data

data: response (ordered) by

conditions (MD, RA)

stratified by block

Z = -4.5847, p-value = 4.545e-06

alternative hypothesis: two.sided
```

In our case, one can conclude that the assessment of the number of anomalies differs between the medical doctor and the research assistant.