

6 The one-way layout

6.1.1 Example (Mucociliary efficiency)

Mucociliary efficiency from the rate of removal of dust in normal
subjects, subjects with obstructive airway disease, and subjects
with asbestosis.

x <- c(2.9, 3.0, 2.5, 2.6, 3.2) # normal subjects

y <- c(3.8, 2.7, 4.0, 2.4) # with obstructive airway disease

z <- c(2.8, 3.4, 3.7, 2.2, 2.0) # with asbestosis

Do all three groups have the same median?

What's $\alpha=0.502$ level test?

Reject H_0 if $H > 5.643$

$H = .771$

What's P-value? 0.1009

Approximate P-value? 0.64

6.1.2 Data

the data consist of $N = \sum_{j=1}^k n_j$ observations, with n_j observations from the j th treatment,
 $j=1, \dots, k$.

6.1.3 Assumptions

A1. The N random variables $\{X_{1j}, X_{2j}, \dots, X_{n_{jj}}\}$, $j=1, \dots, k$ are mutually independent.

A2. For each fixed j , the n_j random variables are a random sample from a continuous distribution with distribution function F_j .

A3. The distribution functions F_1, \dots, F_k are connected through the relationship $F_j(t) = F(t - \tau_j)$, where F is a continuous distribution function with unknown median and τ_j is the unknown treatment effect for the j th population.

6.1.4 Hypothesis

The null hypothesis is that of no differences among the treatment effects, i.e.

$H_0: [\tau_j = \dots = \tau_k]$.

6.2 Distribution-free test for general alternatives (Kruskal-Wallis)

We consider the general alternative :

$H_1: [\tau_j, \dots, \tau_k \text{ not all equal}]$

Procedure.

1. combine all N observations and order them from least to greatest
2. Let r_{ij} denote the rank of X_{ij} in this joint ranking
3. Set

$$R_j = \sum_{i=1}^{n_j} r_{ij} \text{ and } \bar{R}_j = \frac{R_j}{n_j}, j = 1, \dots, k$$

The Kruskal-Wallis statistic is given by

$$H = \frac{12}{N(N+1)} \sum_{j=1}^k n_j \left(\bar{R}_j - \frac{N+1}{2} \right)^2$$

where $N(N+1)/2$ is the average rank assigned in the joint ranking. (why?)

To test H_0 vs H_1 at the α level of significance,

Reject H_0 if $H \geq h_\alpha$ where the constant is chosen to make $P(\text{type I error}) = \alpha$. See Table A.12.

6.2.1 Large sample approximation

When H_0 is true, the statistic H has, as $\min(n_1, \dots, n_k)$ tends to infinity, an asymptotic χ^2 distribution with $k-1$ degrees of freedom. The procedure is approximated by

Reject H_0 if $H \geq \chi_{k-1, \alpha}^2$. Use Chart A.2.

* Sample size not in order? Re-order them!

6.2.2 R and Minitab Computation

It is implemented in both R and Minitab

[kruskal.test]

Using χ^2 table or chart can be tricky.

SAS: WILCOXON in the NPAR1WAY procedure

6.3 A distribution-free test for ordered alternatives (Jonckheere-Terpstra)

A nonparametric test for ordered differences among classes.

It tests the null hypothesis that the distribution of the response variable does not differ among classes.

It is designed to detect alternatives of ordered class differences, which can be expressed as

$H_2: \tau_1 \leq \tau_2 \leq \dots \leq \tau_R$ (or $\tau_1 \geq \tau_2 \geq \dots \geq \tau_R$), with at least one of the inequalities being strict, where τ_i denotes the effect of class i .

For such ordered alternatives, the Jonckheere-Terpstra test can be preferable to tests of more general class difference alternatives, such as the Kruskal - Wallis test

We calculate $k(k-1)/2$ Mann-Whitney counts

$U_{uv} = \sum_{i=1}^{n_u} \sum_{j=1}^{n_v} \phi(X_{iu}, X_{jv}), 1 \leq u < v \leq k$ and compute Jonckheere-Terpstra statistic as

$$J = \sum_{u=1}^{v-1} \sum_{v=2}^k U_{uv}$$

Reject H_0 if $J \geq j_\alpha$

Use Table A.13

Large-Sample Approximation: As $\min(n_1, \dots, n_k)$ tends to infinity, the standardized version goes to $N(0,1)$

6.3.1 Computation

Not implemented in R nor in Minitab. In R, you can run something like:

```
dat <- number
grp <- as.ordered(information)

jkstat <- function(x, g) {
  foo <- (sign(outer(x, x, "-")) + 1) / 2
  sum(foo[g[row(foo)] > g[col(foo)]])
}

print(jstat <- jkstat(dat, grp))

nsim <- 1e4 - 1
jsim <- double(nsim)
for (i in 1:nsim) {
  datsim <- sample(dat, length(dat))
  jsim[i] <- jkstat(datsim, grp)
}
phat <- mean(jsim >= jstat)
(nsim * phat + 1) / (nsim + 1)
nsim / (nsim + 1) * sqrt(phat * (1 - phat) / nsim)
proc.time()
```

6.4 A distribution-free tests for umbrella alternatives (Mack-Wolfe)

The class of umbrella alternatives:

H3: $\tau_1 \leq \tau_2 \leq \dots \leq \tau_{p-1} \leq \tau_p \geq \tau_{p+1} \geq \dots \geq \tau_k$ with at least one strict inequality

6.5 And more! (though not quite mainstream)

<http://mason.gmu.edu/~csutton/handwch6657.html>

Google Mack-Wolfe and Jonckheere-Terpstra and look at some sites.

6.5.1 Computer implementation

Very rarely implemented in standard statistical computer packages

7 The two-way layout

```
## Hollander & Wolfe (1973), p. 140ff.
## Comparison of three methods ("round out", "narrow angle", and
## "wide angle") for rounding first base. For each of 18 players
## and the three method, the average time of two runs from a point on
## the first base line 35ft from home plate to a point 15ft short of
## second base is recorded.
> RoundingTimes
  Round Out Narrow Angle Wide Angle
1      5.40          5.50      5.55
2      5.85          5.70      5.75
3      5.20          5.60      5.50
4      5.55          5.50      5.40
5      5.90          5.85      5.70
6      5.45          5.55      5.60
7      5.40          5.40      5.35
8      5.45          5.50      5.35
9      5.25          5.15      5.00
10     5.85          5.80      5.70
11     5.25          5.20      5.10
12     5.65          5.55      5.45
13     5.60          5.35      5.45
14     5.05          5.00      4.95
15     5.50          5.50      5.40
16     5.45          5.55      5.50
17     5.55          5.55      5.35
18     5.45          5.50      5.55
19     5.50          5.45      5.25
20     5.65          5.60      5.40
21     5.70          5.65      5.55
22     6.30          6.30      6.25
>
friedman.test(RoundingTimes)
boxplot(data.frame(RoundingTimes))
boxplot(data.frame(t(RoundingTimes)))
kruskal.test(data.frame(RoundingTimes))

      Friedman rank sum test

data:  RoundingTimes
Friedman chi-squared = 11.1429, df = 2, p-value = 0.003805
>
```

An experimental design involving two factors, each with at two or more levels

Treatment factor vs blocking factor

A randomized block design

All treatments; treatment(s) vs control (baseline)

of bservations in each 'cell' (treatment-block combination) with 0, 1 (complete), >1 (replications)

Data:

The data consist of $N = \sum_{i=1}^n \sum_{j=1}^k c_{ij}$ observations, with c_{ij} observations from the combination of i 'th block and j 'th treatment [(i,j)th cell] for $i=1,\dots,n$ and $j=1,\dots,k$.

$$X_{ijt}, \alpha=1,\dots,c_{ij}$$

Assumptions:

A1. The N random variables are mutually independent

A2. For each fixed (i,j), the c_{ij} random variables X_{ijt} are a random sample from a continuous distribution F_{ij}

A3. The distribution functions are connected through:

$$F_{ij}(u) = F(u - \beta_i - \tau_j), \text{ i.e.}$$

$$X_{ijt} = \theta + \beta_i + \tau_j + e_{ijt}$$

overall mean + block effect + treatment effect + noise (from a distribution with median 0)

Hypothesis:

$$H_0: \tau_1 = \dots = \tau_k$$

Underlying distributions within each block are the same.

A randomized complete block design: one obs per treatment-block combination

What's the treatment and block in the example dataset?

7.1 A distribution-free test for general alternatives in a randomized complete block design (Friedman)

$H_1: \tau_1, \dots, \tau_k$ are not all equal

7.1.1 Procedure

Order the k observations within each block and let r_{ij} be the rank of X_{ij} in the joint ranking in the i 'th block. Set R_i and R_j as before.

$$R_j = \sum_{i=1}^n r_{ij} \text{ and } R_i = \frac{R_j}{n}, j = 1, \dots, k$$

Then Friedman statistic is

$$S = \frac{12n}{k(k+1)} \sum_{j=1}^k \left(R_j - \frac{k+1}{2} \right)^2$$

The test of significance level α rejects H_0 if $S \geq s_\alpha$. (Use Table A.22)

* Compute S for the following subset of the data:

```
> RoundingTimes
  Round Out Narrow Angle Wide Angle
1      5.40      5.50      5.55
2      5.85      5.70      5.75
3      5.20      5.60      5.50
4      5.55      5.50      5.40
5      5.90      5.85      5.70
```

* Don't confuse with Kruskal-Wallis statistic

$$H = \frac{12}{N(N+1)} \sum_{j=1}^k n_j \left(R_{.j} - \frac{N+1}{2} \right)^2$$

* What's the value of **Kruskal statistic and P-value** (if we don't consider this block effect)?

* Experimental design : make an effort to '*randomize*' (**how?**)

7.1.2 Large-sample approximation

When H_0 is true, as n tends to infinity, $S \sim \chi^2(k-1)$ approximately.

Using the approximation, we reject H_0 if $S \geq \chi_{k-1, \alpha}^2$ (Chart A.2)

* Why consider **blocks**?

- To compare apples and apples.

* The method works under a slightly weaker condition

* Connection to normal theory test: if we apply the usual two-way layout F test to the ranks instead of the actual observations, we get something proportional to S .

* In the special case of $k=2$ treatments, the procedures are identical to the two-sided sign test of section 3.4 (**why?**)

7.2 And more

* Extensions to the cases when we have replications, missing values, etc.

* Extensions when we considered ordered alternatives etc.