

STAT 423 Review Guide

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Chapter 1

Paired Two-Sample Tests

Data for paired two-sample tests have the following properties:

- each subject i has two observations X_i and Y_i to give a paired observation (X_i, Y_i)
- $(X_1, Y_1), \dots, (X_n, Y_n)$ are independent

Our general strategy is to perform one-sample tests on the paired difference $Z_i = Y_i - X_i$

For this section, we will use the R dataset `sleep`. In this data, each subject was given both drug 1 and drug 2, and the change in their sleep was measured. The column `group` indicates which drug the subject took, and the column `extra` indicates the change in sleep.

```
data("sleep")

# X: effect on sleep from drug 1
x <- sleep$extra[sleep$group == 1]

# Y: effect on sleep from drug 2
y <- sleep$extra[sleep$group == 2]

# Z: paired difference between X and Y
z <- y - x
```

For each of these tests, we will be testing the hypotheses $H_0: \mu = 0$ vs $H_a: \mu \neq 0$, where μ is the mean of Z .

1.1 Paired t -test

- Parametric test

- One-sample t -test on the mean μ of Z
- Assumption: $Z_i \stackrel{\text{iid}}{\sim} N(\mu, \sigma^2)$
- Hypotheses: $H_0: \mu = \mu_0$ vs $H_a: \mu \neq \mu_0$ (or $<$, $>$)
- Test statistic:

$$T_{\text{obs}} = \frac{\bar{Z} - \mu_0}{s_Z / \sqrt{n}},$$

where \bar{Z} and s_Z are the sample mean and sample standard deviation of Z

- Null distribution: Under H_0 , $T_{\text{obs}} \sim t_{n-1}$

There are three ways to do this test in R using the function `t.test`.

If the observations for group X and group Y are stored in separate vectors `x` and `y`, then we use `t.test` with the argument `paired = TRUE`.

```
t.test(x, y, paired = TRUE, alternative = "two.sided")

##
## Paired t-test
##
## data: x and y
## t = -4.0621, df = 9, p-value = 0.002833
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.4598858 -0.7001142
## sample estimates:
## mean of the differences
## -1.58
```

If the paired differences $Z = Y - X$ are stored in one vector `z`, then we use a one-sample `t.test`.

```
t.test(z, alternative = "two.sided")

##
## One Sample t-test
##
## data: z
## t = 4.0621, df = 9, p-value = 0.002833
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## 0.7001142 2.4598858
## sample estimates:
## mean of x
## 1.58
```

If the data is stored in one matrix or dataframe where one column contains the observations and another column contains the groups, we can use the following syntax. For this data, `extra` contains the observations, and `group` indicates which group each observation comes from.

```
t.test(extra ~ group, paired = TRUE, data = sleep, alternative = "two.sided")

##
## Paired t-test
##
## data: extra by group
## t = -4.0621, df = 9, p-value = 0.002833
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.4598858 -0.7001142
## sample estimates:
## mean of the differences
## -1.58
```

The result for all three values is the same: p -value = 0.002833.

1.2 Sign test

- Also called binomial test
- Nonparametric test on the median θ of Z
- Assumption: Z_i are iid
- Hypotheses: $H_0: \theta = \theta_0$ vs $H_a: \theta \neq \theta_0$ (or $<$, $>$)
- Test statistic:

$$X = I\{Z_i > \theta_0\},$$

where $I\{Z_i > \theta_0\}$ is the number of observations Z_i that are greater than θ_0 .

- Null distribution: Under H_0 , $X \sim \text{Binom}(n, p = 0.5)$

The alternative hypothesis $H_a: \theta < 0$ is equivalent to $H_a: p < 0.5$, where $p = P(Z_i > 0)$. This is because, under $H_0: \theta = 0$, the probability of Z_i being less than the median θ is 0.5.

The test is conducted as follows.

```
# calculate paired differences
z <- y - x

# calculate the number of observations greater than 0
X <- sum(z > 0)

# calculate p-value
2 * min(pbinom(X, size = length(z), prob = 0.5),
        1 - pbinom(X, size = length(z), prob = 0.5))

## [1] 0.001953125
```

1.3 Wilcoxon Signed-Rank Test

- Nonparametric test on the median θ of Z
- Assumptions: Z_i are iid and symmetric
- Hypotheses: $H_0: \theta = \theta_0$ vs $H_a: \theta \neq \theta_0$ (or $<$, $>$)
- Test statistic:

$$V = \sum_{i=1}^n I\{Z_i > \theta_0\} \text{rank}(|Z_i - \theta_0|)$$

Like with the paired t -test, there are three ways to conduct the Wilcoxon test using `wilcox.test`.

```
wilcox.test(x, y, paired = TRUE, alternative = "two.sided")
```

```
## Warning in wilcox.test.default(x, y, paired = TRUE, alternative = "two.sided"):
## cannot compute exact p-value with ties
```

```
## Warning in wilcox.test.default(x, y, paired = TRUE, alternative = "two.sided"):
## cannot compute exact p-value with zeroes
```

```
##
```

```
## Wilcoxon signed rank test with continuity correction
```

```
##
```

```
## data: x and y
```

```
## V = 0, p-value = 0.009091
```

```
## alternative hypothesis: true location shift is not equal to 0
```

```
wilcox.test(z, alternative = "two.sided")
```

```
## Warning in wilcox.test.default(z, alternative = "two.sided"): cannot compute
## exact p-value with ties
```

```
## Warning in wilcox.test.default(z, alternative = "two.sided"): cannot compute
## exact p-value with zeroes
```

```
##
```

```
## Wilcoxon signed rank test with continuity correction
```

```
##
```

```
## data: z
```

```
## V = 45, p-value = 0.009091
```

```
## alternative hypothesis: true location is not equal to 0
```

```
wilcox.test(extra ~ group, paired = TRUE, data = sleep, alternative = "two.sided")
```

```
## Warning in wilcox.test.default(x = c(0.7, -1.6, -0.2, -1.2, -0.1, 3.4, 3.7, :
## cannot compute exact p-value with ties
```

```
## Warning in wilcox.test.default(x = c(0.7, -1.6, -0.2, -1.2, -0.1, 3.4, 3.7, :
## cannot compute exact p-value with zeroes
```

```
##
```



```
## Wilcoxon signed rank test with continuity correction
##
## data:  extra by group
## V = 0, p-value = 0.009091
## alternative hypothesis: true location shift is not equal to 0
```

Using all three methods, p -value = 0.009091.

1.4 Permutation Test

- Paired data (X_i, Y_i) , where X_i and Y_i are correlated
- Assumption: $(X_1, Y_1), \dots, (X_n, Y_n)$ are iid
- For n subjects, there are $R = 2^n$ equally likely permutation outcomes
- For each possible outcome $\ell \in \{1, \dots, R\}$, we calculate the sample mean of differences

$$z_\ell = \frac{1}{n} \sum_{i=1}^n (Y_{\ell i} - X_{\ell i}),$$

where $(X_{\ell i}, Y_{\ell i})$ is the i th observation of the ℓ th permutation outcome.

The p -value depends on the direction of H_a .

H_a	p -value
$\mu > 0$	$I\{z_\ell \geq \bar{Z}\}/R$
$\mu < 0$	$I\{z_\ell \leq \bar{Z}\}/R$
$\mu \neq 0$	$I\{ z_\ell \geq \bar{Z} \}/R$

1.4.1 Exact permutation test

The exact permutation test for $H_a: \mu \neq 0$ is performed as follows.

```
# paired differences
z <- y - x
# sample size
n <- length(z)

# create permutation matrix
lists <- split(matrix(c(-1, 1), n, 2, byrow=TRUE), 1:n)
all.outcomes <- as.matrix(expand.grid(lists))

# observed test statistic
zbar <- mean(z)

# test statistic for permutation samples
z1 <- apply(all.outcomes, 1, function(u) mean(u*abs(z)))
```

```
# p-value
mean(abs(z1) >= abs(zbar))
```

```
## [1] 0.00390625
```

In this example, we used the sample mean as our test statistic, but the choice of test statistic for the permutation test is flexible.

1.4.2 Large-sample approximation for permutation test

Instead of using all $R = 2^n$ possible permutation outcomes, we can randomly select R permutation outcomes and calculate the approximate p -value.

```
R <- 1000
z <- y - x
n <- length(z)

# generate permutation matrix
outcomes <- replicate(R, sample(c(-1, 1), n, replace = TRUE))

# observed test statistic
zbar <- mean(z)

# test statistic for permutation samples
z1 <- apply(outcomes, 2, function(u) mean(u*abs(z)))

# p-value
mean(abs(z1) >= abs(zbar))

## [1] 0.004
```