Lecture 11: Permutation tests

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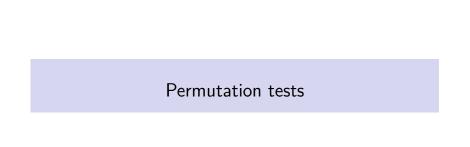


- ▶ One sample sign test, Wilcoxon signed rank test, large-sample approximation, median, Hodges-Lehman estimator, distribution-free confidence interval.
- Jackknife for bias and standard error of an estimator.
- Bootstrap samples, bootstrap replicates.
- Bootstrap standard error of an estimator.
- Bootstrap percentile confidence interval. Hypothesis testing with the bootstrap (one-sample problem.)
- Assessing the error in bootstrap estimates. ▶ Example: inference on ratio of heart attack rates in the
- aspirin-intake group to the placebo group. ▶ The exhaustive bootstrap distribution

- Discrete data problems (one-sample, two-sample proportion)
- tests, test of homogeneity, test of independence) ► Two-sample problems (location problem - equal variance, unequal variance, exact test or Monte Carlo, large-sample

approximation, H-L estimator, dispersion problem, general

distribution)



Permutation tests

- The Mann-Whitney/Wilcoxon test is actually a special case of a permutation test.
 - Re-assignment of combined ranks with probability of each re-assignment is $\frac{1}{\binom{N}{2}}$ under H_0 .
- Permutation test are computationally-intensive but exists before computers.
- R. A Fisher (1930's) introduced to support theoretical argument of Student's t-test.

Permutation test

- ► Two-sample problem
 - ▶ $X = (X_1, \dots, X_m)$ and $Y = (X_1, \dots, X_m)$ are drawn from $F(\cdot)$ and $G(\cdot)$, respectively.
- ▶ Test H_0 : F = G.
 - ► If H₀ is true, any of the observations could have come equally well from either F or G.

Permutation test recipe (two-sample problem)

- Decide a test statistic T.
- ▶ Compute the test statistic for the given data t_0 .
- ► H₀ assigns equal probabilities to all possible re-assignments of combined observations.
- ▶ P-value is defined to be the probability of observing at least that large a value when the null hypothesis is true.

p-value =
$$P_{H_0} (T^* \ge t_0)$$
,

where t_0 is fixed and the random variable T^* has the null hypothesis distirbution, the distribution of T if H_0 is true.

► The smaller value of p-value, the stronger the evidence against H₀.

Example (Permutation test)

- ▶ The mouse data in **ET** page 11, table 2.1.
 - Sixteen mice were randomly assigned to a treatment group or a control group.
 - Measured their survival times, in days, following a test surgery.
 - Did the treatment prolong survival?

```
ET.table.2.1 = list(treatment = c(94, 197, 16, 38, 99, 141,23), control = c(52, 104, 146, 10, 51, 30, 40, 27, 46))
ET.table.2.1
```

```
## $treatment
## [1] 94 197 16 38 99 141 23
##
## $control
## [1] 52 104 146 10 51 30 40 27 46
```

Example (Permutation test)

- ▶ Let *X* be survival times of mice in treatment group and *Y* be survival times of mice in control group.
- Observed small amount of data

```
lapply(ET.table.2.1, function(x){length(x)})
```

```
## $treatment
## [1] 7
##
## $control
## [1] 9
```

Example (Wilcoxon rank sum test)

Use Wilcoxon test (dispersion is equal)

```
wilcox.test(x = ET.table.2.1$treatment,
  ET.table.2.1$control, alternative = "greater",
  paired = FALSE, exact = TRUE)
```

```
##
## Wilcoxon rank sum test
##
## data: ET.table.2.1$treatment and ET.table.2.1$control
## W = 36, p-value = 0.3403
## alternative hypothesis: true location shift is greater
```

Example (Wilcoxon rank sum test)

- ▶ Use permutation to find the null distribution of Wilcoxon rank sum test statistic.
- ▶ The exact p-value is computed using this null distribution.

- ▶ Permutation test for the general hypothesis F = G.
 - Assume F and G only differ in location.
- ▶ $T = \bar{X} \bar{Y}$. Test statistic is mean difference.
- ▶ t₀

```
t.0 = round(mean(ET.table.2.1$treatment) -
  mean(ET.table.2.1$control), digits = 2); t.0
```

```
## [1] 30.63
```

- ▶ This indicates treatment distribution *F* gives longer survival times than does control distribution *G*.
- ▶ Is it significant?

- ► Find the all possible re-assignments of combined observations under H₀.
 - ▶ Combine all the N = m + n observations from both treatment and control.
 - ► Take a sample of size *m* without replacement to treatment group.
 - Assign remaining n observations to control.
 - ► There are $\binom{N}{n}$ possible re-assignments with $\frac{1}{\binom{N}{n}}$ probability.

Order statistic representation

```
library(dplyr)
combined.sample = data.frame(group = c(rep("treatment",
  length(ET.table.2.1$treatment)),
  rep("control",
    length(ET.table.2.1$control))),
  value = c(ET.table.2.1$treatment,
    ET.table.2.1$control))
combined.sample = mutate(combined.sample,
  rank.combined = rank(value))
combined.sample =
  combined.sample[order(combined.sample$rank.combined,
    decreasing = FALSE), ]
```

group walue rank combined

combined.sample

##

| ## | | group | varue | rank.combined | |
|----|----|-------------------|-------|---------------|--|
| ## | 11 | control | 10 | 1 | |
| ## | 3 | ${\tt treatment}$ | 16 | 2 | |
| ## | 7 | ${\tt treatment}$ | 23 | 3 | |
| ## | 15 | control | 27 | 4 | |
| ## | 13 | control | 30 | 5 | |
| ## | 4 | ${\tt treatment}$ | 38 | 6 | |
| ## | 14 | control | 40 | 7 | |
| ## | 16 | control | 46 | 8 | |
| ## | 12 | control | 51 | 9 | |
| ## | 8 | control | 52 | 10 | |
| ## | 1 | ${\tt treatment}$ | 94 | 11 | |
| ## | 5 | ${\tt treatment}$ | 99 | 12 | |
| ## | 9 | control | 104 | 13 | |
| ## | 6 | ${\tt treatment}$ | 141 | 14 | |
| | | | | | |

► Find all possible re-assignments.

```
library(gtools)
all.possible.assignments = combinations(n = dim(combined.s
r = length(ET.table.2.1$treatment),
v = combined.sample$rank.combined)
saveRDS(all.possible.assignments, "all.possible.assignments")
```

```
all.possible.assignments = readRDS("all.possible.assignments
compute.T.star = function(combined.sample,
  all.possible.assignments){
  T.star = apply(all.possible.assignments, 1,
    function(x){
    x.star = combined.sample$value[x]
    y.star = combined.sample$value[-x]
    mean(x.star) - mean(y.star)
  })
  return(T.star)
T.star = compute.T.star(combined.sample = combined.sample,
  all.possible.assignments = all.possible.assignments)
```

Exact p-value

```
p.value.exact = mean(T.star >= t.0)
round(p.value.exact, digits = 3)
```

```
## [1] 0.141
```

Example (Permutation test in practice)

▶ Choose B possible re-assignments, each being randomly selected from the set of all $\binom{N}{n}$ possible re-assignments [B] usually be at least 1000].

```
B = 1000
compute.T.star.Monte.Carlo = function(x,
  combined.sample){
  re.assignment.index = sample(combined.sample$rank.combine
    size = length(combined.sample$rank.combined),
    replace = FALSE)
 x.star = combined.sample$value[re.assignment.index[1:lenger]
  y.star = combined.sample$value[re.assignment.index[(leng
  T.star = mean(x.star) - mean(y.star)
  return(T.star)
```

```
T.star = lapply(seq_along(1:B),
  FUN = compute.T.star.Monte.Carlo,
  combined.sample = combined.sample)
```

T.star = unlist(T.star)

Example (Permutation test in practice)

▶ P-value using Monte Carlo method

```
P.value.MC = mean(T.star >= t.0)
round(P.value.MC, digits = 3)
```

```
## [1] 0.148
```

T =
$$\frac{X - Y}{\sigma \sqrt{\frac{1}{m} + \frac{1}{n}}}$$
. - We don't know σ and an estimate for σ is $\bar{\sigma}$, the standard deviation of combined sample.

```
student.t.0 = (mean(ET.table.2.1$treatment) - mean(ET.table
round(student.t.0, digits = 2)
```

1.11

[1] 54.7

```
B = 1000
compute.T.star.Monte.Carlo = function(x,
  combined.sample){
  re.assignment.index = sample(combined.sample$rank.combined
    size = length(combined.sample$rank.combined),
    replace = FALSE)
  x.star = combined.sample$value[re.assignment.index[1:leng
  y.star = combined.sample$value[re.assignment.index[(leng
  sigma.bar.star = sd(c(x.star, y.star))
  student.t.star = (mean(x.star) - mean(y.star))/(sigma.bar)
  T.star = student.t.star
  return(T.star)
```

```
T.star = lapply(seq_along(1:B),
  FUN = compute.T.star.Monte.Carlo,
  combined.sample = combined.sample)
T.star = unlist(T.star)
```

```
p.value.student.t.test.MC = mean(T.star >= student.t.0)
round(p.value.student.t.test.MC, digits = 3)
```

```
## [1] 0.141
```

Example (Compare the permutation test results using different test statistics)

- ▶ Rank-based permutation test: exact p-value with T = W is .340. (Rank-based permutation test)
- Exact p-value with $T = \bar{X} \bar{Y}$ is .141.
- lacksquare P-value with $T=ar{X}-ar{Y}$ and using Monte Carlo method is

P-value with $T=\frac{\bar{X}-\bar{Y}}{\sigma\sqrt{\frac{1}{m}+\frac{1}{n}}}$ and using Monte Carlo method is

Permutation and bootstrap hypothesis tests

Permutation tests

- ▶ Define *F*₀ the null distirbution of test statistics using the possible re-assginments of observations.
- ▶ Use for more general test of F(t) = G(t).
- Important aspect of permutation test is its accuracy.
 - ▶ If $H_0: F = G$ is true, $P_{H_0}\{\text{p-value}_{\text{perm}} < \alpha\} = \alpha$.
- Bootstrap testing.
 - Uses plug-in estimator for F_0 . Denote the combined sample z and let its empirical distirbution be \hat{F}_0 , putting probability $\frac{1}{(n+m)}$ on each member of z.
 - Can be used for many statistical problems when there is nothing to permute.
 - Bootstrap p-value is approximate.

Exchangeability

- A sufficient condition for permutation test is exchangeable of observations.
 - ▶ Consider random sample $X_1, \dots X_n$.
 - ▶ If their joint distribution are equal under permuations Π $P_{X_1, \dots X_n}(x_1, \dots, x_n) = P_{X_{\Pi(1)}, \dots X_{\Pi(n)}}(x_{\Pi(1)}, \dots, x_{\Pi(n)})$, then $X_1, \dots X_n$ are exchangable.
- This is a weaker assumption than indepdendence of observations.

References for this lecture

ET Chapter 15

Li:H1997: Holmes (1997). Lecture Notes on Computer Intensive Methods in Statistics.