# Chapter 8: Comparing two independent populations

Part 2

https://dzwang91.github.io/stat324/



## Outline



1 Permutation test

2 Comparing two independent population proportions

## What is permutation?



 Permutation refers to the arrangement of a set of objects into some specified order.

## What is permutation?



 Permutation refers to the arrangement of a set of objects into some specified order.

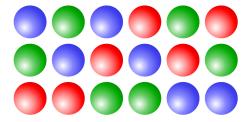


Figure: Each column is one possible permutation of three columns.

# Permuting a data set



- Given a data set of sample size n = 3:  $X_1, X_2, X_3$ , there are 6 possible permutations:
  - $X_{(1)} = (X_1, X_2, X_3)$
  - $X_{(2)} = (X_1, X_3, X_2)$
  - $X_{(3)} = (X_2, X_1, X_3)$
  - $X_{(4)} = (X_2, X_3, X_1)$
  - $X_{(5)} = (X_3, X_1, X_2)$
  - $X_{(6)} = (X_3, X_2, X_1)$

# Permuting a data set



- Given a data set of sample size n = 3:  $X_1, X_2, X_3$ , there are 6 possible permutations:
  - $X_{(1)} = (X_1, X_2, X_3)$
  - $X_{(2)} = (X_1, X_3, X_2)$
  - $X_{(3)} = (X_2, X_1, X_3)$
  - $X_{(4)} = (X_2, X_3, X_1)$
  - $X_{(5)} = (X_3, X_1, X_2)$
  - $X_{(6)} = (X_3, X_2, X_1)$
- In general, there are n! permutations for a data set with sample size n

# Why are permutations useful?



- Hypothesis testing paradigm:
  - Collect some data
  - Form the null hypothesis
  - Design the test statistic
  - ullet Derive sampling distribution of test statistic under  $H_0$

# Why are permutations useful?



- Hypothesis testing paradigm:
  - Collect some data
  - Form the null hypothesis
  - Design the test statistic
  - ullet Derive sampling distribution of test statistic under  $H_0$
- In many cases, the null hypothesis is nil hypothesis, i.e., no effect
- Under  $H_0$ , all permutations are equally likely, so permutations relate to sampling distribution



- Two independent samples from two populations, label them 1 and 2
  - $(X_1,...,X_m)$ : sample from population 1
  - $(Y_1, ..., Y_n)$ : sample from population 2
  - $\mu_1$ : true mean in population 1
  - $\mu_2$ : true mean in population 2
  - $\bar{X}$ : sample mean of the first sample
  - $\bar{Y}$ : sample mean of the second sample
- We wish to test:  $H_0: \mu_1 = \mu_2$  vs.  $H_A: \mu_1 \neq \mu_2$ .



- Two independent samples from two populations, label them 1 and 2
  - $(X_1,...,X_m)$ : sample from population 1
  - $(Y_1, ..., Y_n)$ : sample from population 2
  - $\mu_1$ : true mean in population 1
  - $\mu_2$ : true mean in population 2
  - $\bar{X}$ : sample mean of the first sample
  - $\bar{Y}$ : sample mean of the second sample
- We wish to test:  $H_0: \mu_1 = \mu_2$  vs.  $H_A: \mu_1 \neq \mu_2$ .
- Test statistic:  $T(X_1,...,X_m,Y_1,...,Y_n)=\bar{X}-\bar{Y}$



Given two original data set:  $X_1, X_2, ..., X_m$  and  $Y_1, ..., Y_n$ .

1. Compute the sample mean  $\bar{X}$  and  $\bar{Y}$ , and the realization of the test statistic:

$$T_{obs} = \bar{X} - \bar{Y}$$



Given two original data set:  $X_1, X_2, ..., X_m$  and  $Y_1, ..., Y_n$ .

1. Compute the sample mean  $\bar{X}$  and  $\bar{Y}$ , and the realization of the test statistic:

$$T_{obs} = \bar{X} - \bar{Y}$$

#### One run of permuation

- 2. Combine all data from both samples into a single group of size m+n. Take a random sample of size m, without replacement, from this group, and compute its mean, call it  $\bar{X}^*$ . Compute the mean of the remaining data points, call it  $\bar{Y}^*$ .
- 3. Compute a new realization of statistic  $T^*_{obs} = \bar{X}^* \bar{Y}^*$ .



Given two original data set:  $X_1, X_2, ..., X_m$  and  $Y_1, ..., Y_n$ .

1. Compute the sample mean  $\bar{X}$  and  $\bar{Y}$ , and the realization of the test statistic:

$$T_{obs} = \bar{X} - \bar{Y}$$

#### One run of permuation

- 2. Combine all data from both samples into a single group of size m+n. Take a random sample of size m, without replacement, from this group, and compute its mean, call it  $\bar{X}^*$ . Compute the mean of the remaining data points, call it  $\bar{Y}^*$ .
- 3. Compute a new realization of statistic  $T_{obs}^* = \bar{X}^* \bar{Y}^*$ .
- 4. Repeat steps 2-3 B times, and compute  $T_{obs}^*$  from each one. Let m be the number of values of  $T_{obs}^*$  that are less than or equal to  $-|T_{obs}|$  or greater than or equal to  $|T_{obs}|$ . Then p-value is  $\frac{m}{B}$ .

### Permutation test in R



```
> rm(list=ls())
> ## data set
> dead <- c(17.65, 20.83, 24.59, 18.52, 21.40, 23.78, 20.36, 18.83, 21.83, 20.06)
> live <- c(23.76, 21.17, 26.13, 20.18, 23.01, 24.84, 19.34, 24.94, 27.14, 25.87, 18.95, 22.61)
> all <- c(dead, live)
> m=length(dead)
> n=length(live)
> # calculate the observation of test statistic
> tobs=mean(dead)-mean(live)
```

Figure: imput data sets, merge into a single one, calculate the observation of test statistic

### Permutation test in R



```
> # build a permutation test function
> permutationtest=function(data,obs,b) {
    permutestat=NULL
    m=0
   for(i in 1:b) {
     permutationdata=all[sample.int(m+n)]
     firstsamp=permutationdata[1:m]
     secondsamp=permutationdata[(m+1):(m+n)]
     firstmean=mean(firstsamp)
      secondmean=mean(secondsamp)
     permutestat[i]=firstmean-secondmean
     if (isTRUE(permutestat[i]>=abs(obs)|permutestat[i]<=-abs(obs))){</pre>
        m=m+1
     } else {
        m=m
    pvalue=m/b
    return(pvalue)
```

Figure: make a permutation test function

### Permutation test in R



```
> # run b times
> b = 10000
> permutationtest(all,tobs,b)
[1] 0.0011
```

Figure: run permutation test for b times

## Outline



Permutation test

**2** Comparing two independent population proportions

# Example



• "Does handedness differ according to sex?"

# Example



- "Does handedness differ according to sex?"
- Let  $\pi_{FL}$  be the proportion of females that are left-handed, and  $\pi_{ML}$  be the proportion of males that are left-handed, then we want to test:

$$H_0: \pi_{FL} - \pi_{ML} = 0$$

$$H_A$$
:  $\pi_{FL} - \pi_{ML} \neq 0$ 

# Example



- "Does handedness differ according to sex?"
- Let  $\pi_{FL}$  be the proportion of females that are left-handed, and  $\pi_{ML}$  be the proportion of males that are left-handed, then we want to test:

$$H_0: \pi_{FL} - \pi_{ML} = 0$$
  
 $H_A: \pi_{FL} - \pi_{ML} \neq 0$ 

- A sample of  $n_M=54$  males and  $n_F=21$  females was taken, and each person was asked to indicate which was their dominant hand.
- The data are as follows:

Female: 12 left, 9 right Male: 23 left, 31 right



- Two separate samples from two populations, label them 1 and 2.
  - $\pi_1$  = true proportion in population 1
  - $\pi_2 = \text{true proportion in population 2}$
  - n<sub>1</sub> = sample size taken from population 1
  - $n_2$  = sample size taken from population 2
  - $P_1$  = sample proportion from first sample
  - $P_2$  = sample proportion from second sample
- We wish to test:  $H_0: \pi_1 \pi_2 = 0$  vs.  $H_A: \pi_1 \pi_2 \neq 0$ .



• Assume  $\pi_1 n_1, (1 - \pi_1) n_1, \pi_2 n_2, (1 - \pi_2) n_2$  are all greater than 5:

$$P_1 pprox \mathcal{N}(\pi_1, rac{\pi_1(1-\pi_1)}{n_1})$$

$$P_2 \approx N(\pi_2, \frac{\pi_2(1-\pi_2)}{n_2})$$



• Assume  $\pi_1 n_1, (1 - \pi_1) n_1, \pi_2 n_2, (1 - \pi_2) n_2$  are all greater than 5:

$$P_1 pprox \mathcal{N}(\pi_1, rac{\pi_1(1-\pi_1)}{n_1})$$

$$P_2 \approx N(\pi_2, \frac{\pi_2(1-\pi_2)}{n_2})$$

 Assume all of the data points are independent, both within and between populations:

$$P_1 - P_2 \approx N(\pi_1 - \pi_2, \frac{\pi_1(1 - \pi_1)}{n_1} + \frac{\pi_2(1 - \pi_2)}{n_2})$$



• Therefore under  $H_0$ :  $\pi_1 = \pi_2 = \pi$ , we have

$$P_1 - P_2 \approx N(0, \ \pi(1-\pi)(\frac{1}{n_1} + \frac{1}{n_2}))$$



• Therefore under  $H_0$ :  $\pi_1 = \pi_2 = \pi$ , we have

$$P_1 - P_2 \approx N(0, \ \pi(1-\pi)(\frac{1}{n_1} + \frac{1}{n_2}))$$

Equivalently,

$$rac{P_1 - P_2}{\sqrt{\pi(1-\pi)(rac{1}{n_1} + rac{1}{n_2})}} pprox N(0,1)$$



• Therefore under  $H_0$ :  $\pi_1 = \pi_2 = \pi$ , we have

$$P_1 - P_2 \approx N(0, \ \pi(1-\pi)(\frac{1}{n_1} + \frac{1}{n_2}))$$

Equivalently,

$$rac{P_1 - P_2}{\sqrt{\pi(1 - \pi)(rac{1}{n_1} + rac{1}{n_2})}} pprox N(0, 1)$$

• But  $\pi$  is unknown,



• Therefore under  $H_0$ :  $\pi_1 = \pi_2 = \pi$ , we have

$$P_1 - P_2 \approx N(0, \ \pi(1-\pi)(\frac{1}{n_1} + \frac{1}{n_2}))$$

Equivalently,

$$rac{P_1 - P_2}{\sqrt{\pi(1-\pi)(rac{1}{n_1} + rac{1}{n_2})}} pprox N(0,1)$$

• But  $\pi$  is unknown, so we estimate  $\pi$  using a weighted average of the two individual sample proportions:

$$P = \frac{P_1 n_1 + P_2 n_2}{n_1 + n_2}.$$



• Therefore under  $H_0$ :  $\pi_1 = \pi_2 = \pi$ , we have

$$P_1 - P_2 \approx N(0, \ \pi(1-\pi)(\frac{1}{n_1} + \frac{1}{n_2}))$$

Equivalently,

$$rac{P_1 - P_2}{\sqrt{\pi(1-\pi)(rac{1}{n_1} + rac{1}{n_2})}} pprox N(0,1)$$

• But  $\pi$  is unknown, so we estimate  $\pi$  using a weighted average of the two individual sample proportions:

$$P = \frac{P_1 n_1 + P_2 n_2}{n_1 + n_2}.$$

Then the test statistic is:

$$Z = \frac{P_1 - P_2}{\sqrt{P(1 - P)(\frac{1}{n_1} + \frac{1}{n_2})}}.$$

## Recap



- We need to check:
  - All of the data points are independent, both within and between populations
  - The sample sizes are large enough  $(\pi n_1, (1-\pi)n_1, \pi n_2, \text{ and } (1-\pi)n_2$  are all greater than 5)
- Under  $H_0$ , the test statistic

$$Z = \frac{P_1 - P_2}{\sqrt{P(1-P)(\frac{1}{n_1} + \frac{1}{n_2})}} \approx N(0,1)$$

• Calculate the p-value or rejection region based on the given significance level  $\alpha$  to make a conclusion

# Back to example



- $P_{FL} = 0.571$ ,  $P_{ML} = 0.426$ , and  $P_L = \frac{12+23}{21+54} = 0.467$ .
- The realization of test statistic:

$$Z_{obs} = \frac{0.571 - 0.426 - 0}{\sqrt{0.467(1 - 0.467)(\frac{1}{21} + \frac{1}{54})}} = 1.13.$$

• p-value =  $2 \times P(Z > 1.13) = 0.258$ . If  $\alpha = 0.05$ , we conclude that there is not enough evidence to say that males and females have a different proportion of left-handed individuals.

## What's the next?



We'll discuss how to compare two paired populations in next lecture.