#### **Announcement: Mid-term Exam**

- Scope: All materials provided by Week 7
- Preparation: 완충 휴대폰 + Laptop
  - 휴대폰: Webex 접속 → 본인화면 찍기
    - 컴퓨터화면, 키보드, 본인의 모습이 나타나도록 촬영
  - Laptop: 이러닝 사이트 접속 → 문제 풀기 & 제출
    - 8주차의 퀴즈 클릭 → 문제 별 답안 작성 → 제출

#### NOTICE

- Closed book
- No cheating → Zero tolerance
- 최종 제출 후 조기 퇴실 (접속종료) 가능 (재 접속 불가)
- 자세한 내용은 공지사항 참조



#### **Announcement: Intermediate Presentation**

- It's graded (0-100)
- Prepare 10 mins presentation including:
  - Brief description of your research idea/design
    - Motivation + model + dataset + ...
  - What you have done & What you will do more
  - (extra credit) share your troubleshooting during research!
- Q&A (5 mins)
- NOTES
  - Your progress should be reasonable for you to finish off by this semester
  - Attendance will be checked
  - Presentation order will be announced



# Week 7: Statistics 2 (Quantitative Analysis Method)

Instructor: Daejin Choi (djchoi@inu.ac.kr)



#### **Goals & Contents**

 Goal: Understanding Statistical Methods (Quant. Analysis)

#### Contents

- Terminologies
- Central Tendency
- Probability
- Distribution & Information Theory
- Computing Association between Distributions
- Hyphothesis Testing



## **Association between Distributions**

#### **Pearson Correlation Coeff.**

 A measure of the strength of the linear relation between two variables x and y

• 1 is total positive correlation, 0 is no correlation, and -1 is total negative correlation

$$r = \frac{\sum_{i=1}^{n} (X_i - \bar{X})(Y_i - \bar{Y})}{\sqrt{\sum_{i=1}^{n} (X_i - \bar{X})^2} \sqrt{\sum_{i=1}^{n} (Y_i - \bar{Y})^2}}$$

```
>>> from scipy import stats
>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> rvs6 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> stats.pearsonr(rvs1,rvs6)
(-0.028991426987572115, 0.5177734067731351)
     Lo correlation
```



#### Spearman's correlation

- The Spearman correlation is a nonparametic → ™ × measure of the monotonicity of the relationship between two datasets

```
>>> from scipy import stats
>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> rvs6 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> stats.spearmanr(rvs1,rvs6)
(-0.045163188652754614, 0.31351864108864802)
```



#### Kendall's Tau

- A measure of the correspondence between two rankings. → בּן זוֹ אוּרָ
- Close to 1 if strong agreement, -1 indicates strong disagreement

```
>>> from scipy import stats
>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> rvs6 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> stats.kendalltau(rvs1,rvs6)
(-0.0319198396793587, 0.28602201432226193)

$\frac{\tau_1 \tau_2 \tau_3 \tau_3 \tau_4 \tau_4
```

- What if two sets have different elements?
  - Or, what if two sets have different #elements?



### **Hyphothesis Testing**

#### **Hyphothesis Testing**

- Hyphothesis: A statement about some characteristic of a variable or a collection of variables. (Agresti & Finlay, 1997)
- When a hyphothesis relates to **characteristics of a population**, such as population parameters, one can use statistical methods with sample data to test its validity
- Example: Are female and male Twitter users distinct in terms of visit counts for the sites?



#### **Hyphothesis Testing (cont'd)**

- A way of statistically testing a hyphothesis by comparing the data to values predicted by the hyphothesis
- Data that fall from the predicted values provide evidence against the hyphothesis
- All significance tests have five elements:
   Assumptions, hyphotheses, test statistic, p-value, and conclusion



#### **Hyphothesis Testing: Hyphothesis**

- Considering two hyphotheses about the value of a population parameter
  - Null hyphothesis: A hyphothesis to directly test = H.
  - Alternative hyphothesis: a hyphothesis contradicts the null hyphothesis



#### **Hyphothesis Testing: Test Statistic**

- Our goal is to test
  - If null hyphothesis is rejected, or
  - If alternative hyphothesis is accepted
- Compute p-value under assumption that H<sub>0</sub> is true.
   (i.e., we give the benefit of the doubt to the null hyphothesis)
  - Analyze how likely the observed data would be if that hyphothesis were true Ho: APP B≥ 2001

H,: A와B는 같지않아

- Example: t-test
  - Measures difference of means when comparing two distributions



#### **Hyphothesis Testing: p-value**

- The probability when  $H_0$  is true, of a test statistic value at least as contradictory to  $H_0$  as the value actually observed.

  The smaller the p-value, the more strongly contradict  $H_0$  (Agresti & Finlay, 1997)

  P-value gracue  $\mathcal{F}$  ?  $\mathcal{F}$
- p-value is often defined with respect to a chosen confidence level (95%, 99%, ... ←→ 0.1, 0.05, 0.01, ...)

  P-value リ → H. ツは東東介 またので 以다
- The t-test has important assumptions that must be satisfied in order for the associated p-value to be valid
  - The samples are independent
  - Each sample is from a normally distributed population



#### **Example of T-test**

Calculating t-test for the means of TWO INDEPENDENT samples of scores

```
>>> from scipy import stats

>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)

>>> rvs2 = stats.norm.rvs(loc=5,scale=10,size=500)

>>> stats.ttest_ind(rvs1,rvs2)

Alter. hyphothesis is NOT reliable

(0.26833823296239279, 0.78849443369564776)

>>> rvs4 = stats.norm.rvs(loc=5, scale=20, size=100)

>>> stats.ttest_ind(rvs1, rvs4, equal_var = False)

(-0.69712570584654099, 0.48716927725402048)
```

i.e., mean is statistically same



#### **U-test as an alternative way**

- Limitation of t-test
  - Should be **normal** distribution
  - Not work when n is small
  - Not work when the values are order (or rank)

Not considering population

- The Mann-Whitney U test is a nonparametic test of the null hyphothesis that two populations are the same against an alternative hyphothesis ਪਰੀ ਫੋਰ ਫੋਟੋਕੋਂ ਫੋਟੋਕੋਂ ਫੋਟੋਕੋਂ ਨੇ ਮਹਾਂ ਅਤੇ ਰੈਫੋਰਿਕੋਰਿਕ ਫੋਟੋਕੋਂ ਫ
  - Good when a particular population tends to have larger values than the other

```
>>> from scipy import stats
>>> rvs2 = stats.norm.rvs(loc=5) scale=10, size=500)
>>> rvs5 = stats.norm.rvs(loc=50) scale=10, size=200)
>>> stats.ranksums(rvs2,rvs5)
(-17.268624879732251, 8.1050738020911939e-67) = $10171 0.151.
```



#### **NOTE: Type error**

Type Error: "INCORRECTLY" determining Null hyphothesis

- **Type Error 1**: Determines as "rejects" even though  $H_0$  is true = H 집 이지만 통령하고 예상
  - When two "same" distribution is different sampled

 Type Error 2: Determines as "accepts" even though H<sub>0</sub> is false



#### **ANOVA** as a Generalization of T-test

- Doing multiple two-sample t-tests would result in an increased chance of committing a statistical type I error
- ANOVA provides a statistical test of whether or not the means of several <u>groups</u> are equal
  - Generalizes the t-test to more than two
- Note: Similar to t-test, ANOVA assumes three key items
  - The samples are independent
  - Each sample is from a normally distributed population
  - Homoscedasticity: the standard deviations of the groups are all equal
    - How we can measure this? → F-test!

$$F = \frac{\text{variance between treatments}}{\text{variance within treatments}}$$



#### **ANOVA Testing**

1-way ANOVA for three independent samples:



#### Kruskal Wallis H test

 If any of three assumptions of ANOVA are not true, it is recommended to use the **Kruskal Wallis H test** which is a non-parametic version of ANOVA

```
- Rank or 714 Et
```

- The Kruskal-Wallis H-test tests the null hyphothesis that the population median of all of the groups are equal
- The test works on 2 or more independent samples, which may have different sizes

```
>>> from scipy import stats
>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> rvs2 = stats.norm.rvs(loc=5,scale=10,size=200)
>>> rvs4 = stats.norm.rvs(loc=5 scale=20 size=240)
>>> stats.kruskal(rvs1,rvs2,rvs4)
(2.9637587853571858, 0.22721026954861492)
```



#### **Kolmogorov-Smirnov Statistic**

 A two-sided test for the null hypthothesis that 2 independent samples are drawn from the same continuous distribution

```
>>> from scipy import stats
>>> rvs1 = stats.norm.rvs(size=200, loc=0., scale=1)
>>> rvs2 = stats.norm.rvs(size=200, loc=0.5, scale=1.5)
>>> stats.ks_2samp(rvs1, rvs2)
(0.20833333333333337, 4.6674975515806989e-005)
```



## Thank you!

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