# **Data Mining**

CS57300 Purdue University

March 22, 2018

### Hypothesis Testing

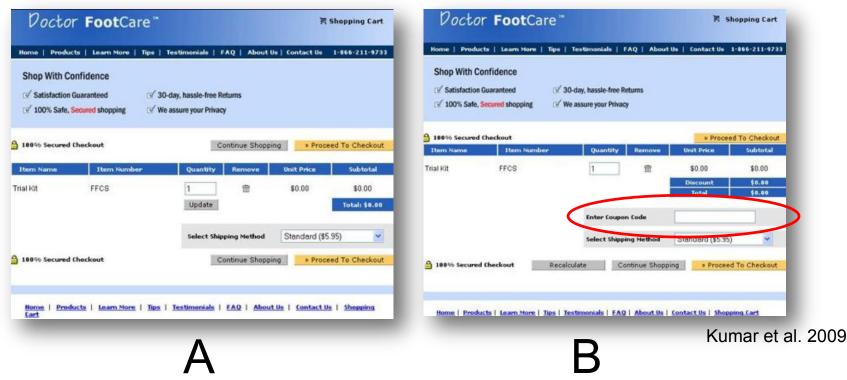
- Select 50% users to see headline A
  - Unlimited Clean Energy: Cold Fusion has Arrived
- Select 50% users to see headline B
  - Wedding War
- Do people click more on headline A or B?





#### Hypothesis Testing, Because Reality is not Easy

 Can you guess which page has a higher conversion rate (buying customers) and whether the difference is significant?

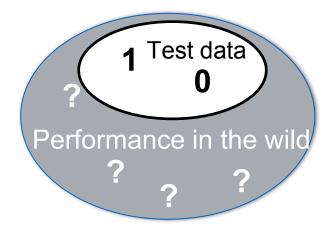


- When "upgraded" from the A to B the site lost 90% of their revenue
- Why? "There maybe discount coupons out there that I do not have. The price may be too high. I should try to find these coupons." [Kumar et al. 2009]

#### Testing Hypotheses over Two Populations

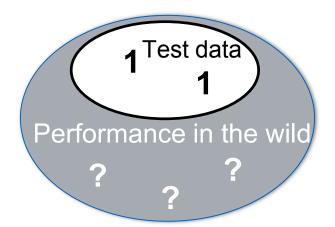
- "Is my classifier better than existing classifiers in the literature?"
- Why?
  - "I got higher accuracy and tested against all existing methods"
  - 0 correctly classified test example, 1 incorrectly classified test example

"My Classifier" Accuracy



True Average  $\mu_1$  error

"Competing Classifier" Accuracy



True Average  $\mu_2$ 

Student's Hypothesis:  $\mu_1 < \mu_2$ 

# Replication Crisis in Science (John Oliver)

#### Close to Home

- Machine Learning is somewhat going through a replication crisis
  - Depends on topic, some topics more prone to errors than others Examples:
  - Lucic et al.(2017) conducted a large-scale empirical comparison of generative adversarial networks methods and found that most of them reach similar scores with sufficient hyperparameter optimization.
    - Hyperparameters: Neural net number of layers, no. neurons, batch sizes, learning rates
  - Henderson et al. (2017) show they beat a host of sequence-to-sequence methods in the Penn Treebank dataset simply by doing better hyperparameter tuning on the baseline LSTM
  - Henderson et al. (2017) reviewed reproducibility in deep reinforcement learning and found significant variability between baseline implementations across recent work.

Peter Henderson, Riashat Islam, Philip Bachman, Joelle Pineau, Doina Precup, and David Meger. Deep reinforcement learning that matters. arXiv preprint arXiv:1709.06560, 2017.

Mario Lucic, Karol Kurach, Marcin Michalski, Sylvain Gelly, and Olivier Bousquet. Are gans created equal? a large-scale study. arXiv preprint arXiv:1711.10337, 2017.

# Statistical Analysis: Hypothesis testing

## t-Test (Independent Samples)

The goal is to evaluate if the average difference between two populations is zero

$$m{X}^{(1)} = ext{random variable of population 1 values}$$
  
vectors  $m{X}^{(2)} = ext{random variable of population 2 values}$ 

Two hypotheses:

population 1 average 
$$H_0$$
:  $\mu_1$   $\mu_2 = 0$   $\mu_1$ :  $\mu_1 - \mu_2 \neq 0$ 

$$H_1$$
:  $\mu_1 - \mu_2 \neq 0$ 

In the t-test we make the following assumptions

- The averages  $\bar{\boldsymbol{X}}^{(1)}$  and  $\bar{\boldsymbol{X}}^{(2)}$  follow a normal distribution (we will see why)
- Observations are independent

#### t-Test Calculation

#### General t formula

t = sample statistic - hypothesized population difference estimated standard error

#### Independent samples t

**Empirical averages** 

$$t = \frac{(\bar{x}^{(1)} - \bar{x}^{(2)}) - (\mu_1 - \mu_2)}{\text{SE}}$$

Empirical standard deviation (formula later)

### t-Statistics p-value

$$H_0$$
:  $\mu_1 - \mu_2 = 0$ 

$$H_1: \mu_1 - \mu_2 > 0$$

What is the p-value?

 $\bar{x}^{(i)} = \text{empirical average of population } i$ 

Random variables

$$P[\bar{X}^{(1,n_1)} - \bar{X}^{(2,n_2)} > \bar{x}^{(1,n_1)} - \bar{x}^{(2)} | \underline{H_0}] = p$$

$$= \text{test } \mathbf{H_1?}$$

$$= \mathbf{T}(1,n_1) - \bar{x}^{(2,n_2)} > (1,n_1) - \bar{x}^{(2)} | \underline{H_0}] = p$$

$$= \frac{\ln(1,n_1)}{\ln(1,n_1)} - \frac{1}{2} \mathbf{T}^{(2,n_2)} > (1,n_1) - \frac{1}{2} \mathbf{T}^{(2)} | \underline{H_0}] = p$$

$$= \frac{\ln(1,n_1)}{\ln(1,n_1)} - \frac{1}{2} \mathbf{T}^{(2,n_2)} > (1,n_1) - \frac{1}{2} \mathbf{T}^{(2)} | \underline{H_0}] = p$$

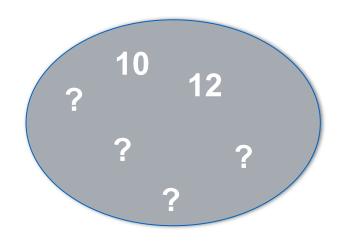
$$= \frac{\ln(1,n_1)}{\ln(1,n_1)} - \frac{1}{2} \mathbf{T}^{(2,n_2)} = \frac{1}{2} \mathbf{T}^{(2,n_2)} - \frac{1}{$$

Can we test H<sub>1</sub>?

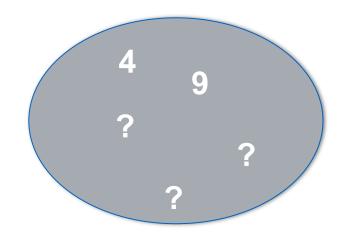
$$P[\bar{X}^{(1,n_1)} - \bar{X}^{(2,n_2)} > \bar{x}^{(1,n_1)} - \bar{x}^{(2)}|H_1] = 1 - p?$$
 Interpretation: an we ever directly accept hypothesis  $H_1$ ? Interpretation: averages are different  $H_1$ ? Averages are different  $H_1$ ?

- Can we ever directly accept hypothesis H<sub>1</sub>?
  - No, we can't test H<sub>1</sub>, we can only reject H<sub>0</sub> in favor of H<sub>1</sub>
  - Why? Because if H₁ does not tell us how different the averages are, how can we compute the probability?

### Two Sample Tests (Fisher)



True Population Average:  $\mu_1$ Empirical Average over Test Data:  $\overline{x}_1$ 



True Population Average:  $\mu_2$  Empirical Average over Test Data:  $\overline{x}_2$ 

Null hypothesis H <sub>0</sub>	Alternative hypothesis H <sub>1</sub>	No. Tails
$\mu_1 - \mu_2 = d$	$\mu_1$ - $\mu_2 \neq d$	2
$\mu_1 - \mu_2 = d$	$\mu_1 - \mu_2 > d  (\overline{x}_1 - \overline{x}_2 > d)$	1
$\mu_1 - \mu_2 = d$	$\mu_1 - \mu_2 < d  (\overline{x}_1 - \overline{x}_2 < d)$	1

#### Types of Hypothesis Tests

- Fisher's test
  - Test can only reject H<sub>0</sub> (we never accept a hypothesis)
  - H<sub>0</sub> is unlikelyin real-life, so rejection depends on the amount of data
    - More data, more likely we will reject H<sub>0</sub>
- Neyman-Pearson's test
  - Compare H<sub>0</sub> to alternative H<sub>1</sub>
  - E.g.:  $H_0$ :  $\mu = \mu_0$  and  $H_1$ :  $\mu = \mu_1$
  - P[Data | H<sub>0</sub>] / P[Data | H<sub>1</sub>]
- Bayesian test
  - Compute probability P[H<sub>0</sub> | Data] and compare against P[H<sub>1</sub> | Data]
  - More precisely, test P[H<sub>0</sub> | Data] / P[H<sub>1</sub> | Data]
    - >1 implies H<sub>0</sub> is more likely
    - <1 implies H₁ is more likely</li>
  - Neyman-Pearson's test = Bayes factor when  $H_0$  and  $H_1$  have same priors

# Back to Fisher's test (no priors)

## How to Compute Two-sample t-test (1)

1) Compute the pooled empirical standard error

$$SE = \sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$$

where,

Sample variance of 
$$\mathbf{x^{(i)}}$$
 
$$\underbrace{s_i^2}_{n_i} \underbrace{\sum_{k=1}^{n_i} (x_k^{(i)} - \bar{x}^{(i)})^2}_{}$$
 and

Number of observations in x<sup>(i)</sup>

$$\bar{x}_i = \frac{1}{n_i} \sum_{m=1}^{n_i} x_m^{(i)}$$

(assumes both populations have equal variance)

## How to Compute Two-sample t-test (2)

2) Compute the degrees of freedom

DF = 
$$\left[ \frac{\left(\sigma_1^2/n_1 + \sigma_2^2/n_2\right)^2}{(\sigma_1^2/n_1)^2/(n_1 - 1) + (\sigma_2^2/n_2)^2/(n_2 - 1)} \right]$$

3) Compute test statistic (t-score, also known as Welsh's t)

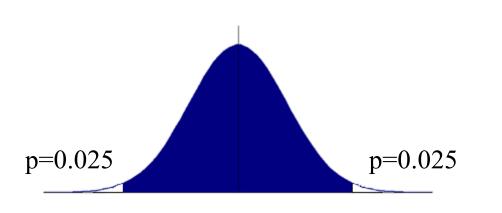
$$t_d = \frac{(\bar{x}_1 - \bar{x}_2) - d}{SE}$$

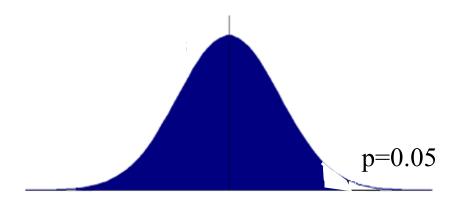
where d is the Null hypothesis difference.

- 4) Compute p-value (depends on  $H_1$ )
  - $p = P[T_{DF} < -|t_d|] + P[T_{DF} > |t_d|]$  (Two-Tailed Test  $H_1$ :  $\mu_1 \mu_2 \neq d$ )
  - $p = P[T_{DF} > t_d]$  (One-Tailed Test for  $H_1 : \mu_1 \mu_2 > d$  (&  $\overline{x}_1 \overline{x}_2 > d$ ))
  - Important:  $H_0$  is always  $\mu_1 \mu_2 = d$  even when  $H_1 : \mu_1 \mu_2 > d$ !! Testing  $H_0$ :  $\mu_1 - \mu_2 \le d$  is harder and "has same power" as  $H_0$ :  $\mu_1 - \mu_2 = d$

# Rejecting H<sub>0</sub> in favor of H<sub>1</sub>

Back to step 4 of slide 16:





4) Compute p-value (depends on H<sub>1</sub>)

$$p = P[T_{DF} < -|t_d|] + P[T_{DF} > |t_d|] \text{ (Two-Tailed Test } H_1: \mu_1 - \mu_2 \neq d)$$

$$p = P[T_{DF} > t_d]$$
 (One-Tailed Test for  $H_1 : \mu_1 - \mu_2 > d$ )

Reject  $H_0$  with 95% confidence if p < 0.05

## Some assumptions about $X_1$ and $X_2$

- $m{X}^{(1)} = [m{X}_1^{(1)}, m{X}_2^{(1)}, \dots, m{X}_{n_1}^{(1)}]$
- $m{X}^{(2)} = [m{X}_1^{(2)}, m{X}_2^{(2)}, \dots, m{X}_{n_2}^{(2)}]$
- Observations of X<sub>1</sub> and X<sub>2</sub> are independent and identically distributed (i.i.d.)
- Central Limit Theorem (Classical CLT)
  - If:  $E[X_k^{(i)}] = \mu_i$  and  $Var[X_k^{(i)}] = \sigma_i^2 < \infty$

$$\sqrt{n_i} \left( \left( \frac{1}{n_i} \sum_{k=1}^n x_k^{(i)} \right) - \mu_i \right) \xrightarrow{d} N(0, \sigma_i^2)$$
 (here  $\infty$  is with respect to  $\mathbf{n_i}$ )

 CLT: If we have enough independent observations with relative small variance (wrt number of observations) we can approximate the distribution of their average with a normal distribution

#### But we don't know the variance of $X^{(1)}$ or $X^{(2)}$

- $N(0,\sigma_i^2)$  approximation not too useful if we don't know  $\sigma_i^2$
- We can estimate  $\sigma_i^2$  with  $\emph{n}_\emph{i}$  observations of  $N(0,\sigma_i^2)$
- But we cannot just plug-in estimate  $\hat{\sigma}_i^2$  on the normal
  - It has some variability if  $n_i < \infty$
  - $\hat{\sigma}_i^2$  is Chi-Squared distributed
  - The t-distribution is a convolution of the standard normal with a Chi-Square distribution to compute

$$t = \frac{\mu_i}{\sqrt{\hat{\sigma}_i^2/\mathrm{DF}}}$$

#### For small samples we can use the Binomial distribution

- If results are 0 or 1 (wrong class / correct class) we can use exact Bernoulli random variables rather than the Normal approximation
- Normal approximation generally OK for large enough number of examples (> 30)

What about false positives and false negatives of a test?

#### Hypothesis Test Possible Outcomes

Errors:

Variable:  $R = 1 - H_0$  hypothesis rejected,  $R = 0 - H_0$  hypothesis not rejected

 $P[R = 1 | H_0]$  - Reject  $H_0$  given  $H_0$  is true

 $P[R = 1 \mid not H_0]$  - - Accept  $H_0$  given  $H_0$  is false

In medicine our "goal" is to reject  ${\rm H}_0$  (drug, food has no effect / not sick), thus a "positive" result rejects  ${\rm H}_0$ 

$$P[R = 0 | H_0]$$

Type I error (false positive)

$$P[R = 1 | H_0]$$

Type II error (false negative)

$$P[R = 0 \mid not H_0]$$

 $P[R = 1 | not H_0]$ 

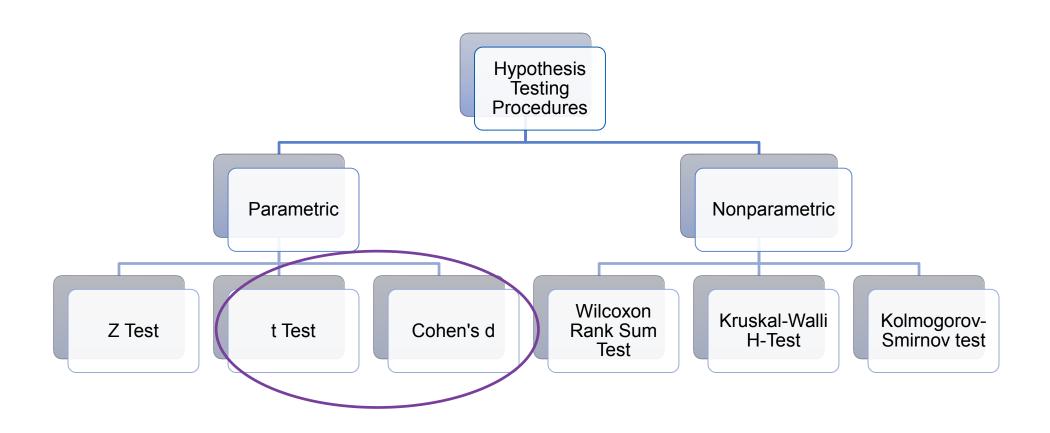
#### **Statistical Power**

Power = P[R = 1 | not 
$$H_0$$
]

- Statistical power is probability of rejecting H<sub>0</sub>
   when H<sub>0</sub> is indeed false
- Statistical Power ⇒ Number of Observations Needed
- Standard value is 0.80 but can go up to 0.95
- E.g.:  $H_0$  is  $\mu_1 \mu_2 = 0$ , where  $\mu_i$  = true average of population i
  - Define  $n = n_1 = n_2$  such that statistical power is 0.8 under assumption  $|\mu_1 \mu_2| = \Delta$ :
  - $P[R = 1 \mid |\mu_1 \mu_2| = \Delta] = 0.8$  where  $R = \mathbf{1}\{P[x^{(1)}, x^{(2)} \mid \mu_1 \mu_2 = 0] < 0.05\}$  which gives

$$n = \frac{16\sigma^2}{\Delta^2}$$

#### More Broadly: Hypothesis Testing Procedures



# Multiple Hypothesis Testing

## Paul the Octopus (2008-2010)

- Paul was an animal oracle
- Paul's keepers would present him with two boxes containing food
- Whichever teams is in the box Paul chooses first is the predicted winner



#### **Results involving Germany**

Opponent +	Tournament +	Outcome \$
Poland	Euro 2008	Correct
<b>Croatia</b>	Euro 2008	Incorrect
<b>Austria</b>	Euro 2008	Correct
<b>Portugal</b>	Euro 2008	Correct
<b>C</b> Turkey	Euro 2008	Correct
<b>Spain</b>	Euro 2008	Incorrect
Australia	World Cup 2010	Correct
Serbia	World Cup 2010	Correct
<b></b> Ghana	World Cup 2010	Correct
<b>England</b>	World Cup 2010	Correct
<b>Argentina</b>	World Cup 2010	Correct
<b>Spain</b>	World Cup 2010	Correct
Uruguay	World Cup 2010	Correct

## Hypothesis Testing Paul the Octopus as an Oracle

Random variable (i.i.d.)

$$X_i = \begin{cases} 1 & \text{, if Paul predicts correct outcome} \\ 0 & \text{, otherwise} \end{cases}$$

Variable of interest:

$$Y_{13} = \sum_{i=1}^{13} X_i$$

- What is the Null Hypothesis?
  - Paul is not an animal oracle
  - Mathematical definition?

• 
$$H_0 := P[X_i = 1] = p = 0.5$$

Should we reject H<sub>0</sub> with significance level 0.05? (one-sided test)

$$\Rightarrow P[Y_{13} = k | H_0] = {13 \choose k} 0.5^k (1 - 0.5)^{n-k}$$

$$P[Y_{13} \ge 11|H_0] = \sum_{k=11}^{13} {13 \choose k} 0.5^k (1-0.5)^{n-k} = 0.0112 < 0.05$$

Anything Wrong in our Hypothesis Test?

## Hypothesis Test as Random Variable

$$X_i = \begin{cases} 1 & \text{, if Paul predicts correct outcome} \\ 0 & \text{, otherwise} \end{cases}$$

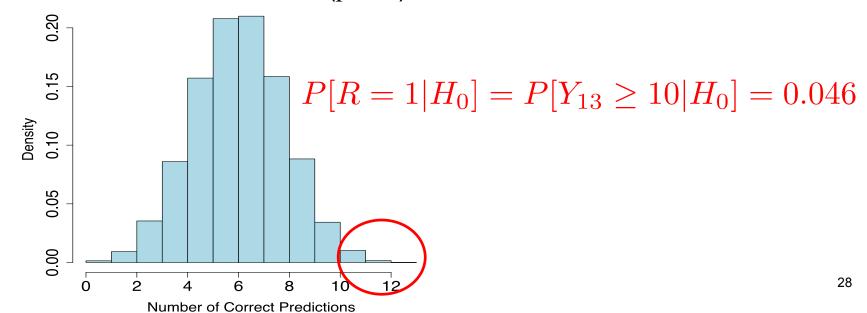


R is random variable that defines if hypothesis is rejected

if 
$$P[Y_{13} \ge k | H_0] < 0.05 \text{ then } R = 1; \text{ otherwise } R = 0$$

#### *k* correct predictions by animal

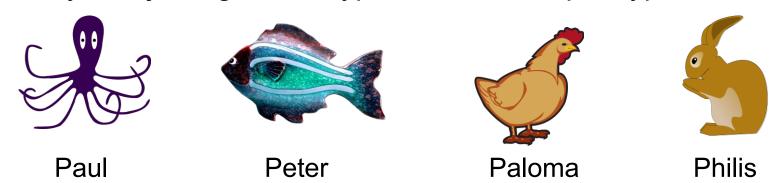
Binomial Distribution (p=0.5)



**Testing Multiple Hypotheses** 

## Familywise Error

(probability of rejecting a true hypothesis in multiple hypotheses tests)



 Probability we reject "not an oracle" hypothesis of Paul based on chance alone?

$$P[R = 1|H_0] = 0.046$$

 Probability we reject "not an oracle" hypothesis of one or more animals (Paul, Peter, Paloma, Philis)

$$1 - (1 - P[R = 1|H_0])^4 = 0.17$$

 $P[R=0|H_0]^4$  = Probability we correctly reject all 4 hypotheses

#### Example

Bob is developing a new caching policy for high-performance databases. For this research Bob secured a real-world dataset containing *N* user query requests to a large real-world database. Bob tells Alice he is now ready to publish his research. His method incurs a 10% less cache misses than the competing state-of-the-art method, a very good result that will change the industry. Bob complains to Alice that this has been very hard work, he has tried over 100 different caching algorithms for his research. Alice took CS57300 and is skeptical about Bob's results.

What is the problem with Bob's claim?

#### Bonferoni's correction

- Used when there aren't too many hypotheses
- Tends to be too conservative for large number of hypotheses









Paul

Peter

Paloma

**Philis** 

- Per-hypothesis significance level of m hypotheses:  $\alpha/m$
- In our animal oracle example:
  - Old significance level  $\alpha$ =0.05
  - Bonferoni's corrected significance level  $\alpha'=0.05/4=0.0125$
  - Hypothesis test: "Paul is not an animal oracle"

$$P[Y_{13} \ge 11|H_0] = \sum_{k=11}^{13} {13 \choose k} 0.5^k (1 - 0.5)^{n-k} = 0.0112 < 0.0125$$

#### False Discovery Rate

- Often used for large number of tests
- Bonferoni's correction seeks to ensure that no true hypotheses are rejected
  - Low statistical power for large number of hypotheses (rejects no hypotheses m >> 1)
- False Discovery Rate:
  - Controls:
  - Greater statistical power at expense of more false positives
  - Order p-values of all m tests: recall p-value is related to P[R=1 | H<sub>0</sub>]
  - Holm's Method:

• 
$$\tilde{p}_i = \min((m-i+1)p_i, 1)$$
  $p_1 \le p_2 \le \dots \le p_m$ 

- Reject if adjusted p-value < α</li>
- Benjamini-Hochberg method:
  - · Reject j null hypothesis if

$$p_j \le \alpha \frac{j}{m}$$

# **Important Warning**

# American Statistical Association Statement On Statistical Significance And p-values

- 1. p-values can indicate how incompatible the data are with a specified statistical model.
- 2. p-values do not measure the probability that the studied hypothesis is true, or the probability that the data were produced by random chance alone.
- 3. Scientific conclusions and business or policy decisions should not be based only on whether a p-value passes a specific threshold.
- 4. Proper inference requires full reporting and transparency.
- 5. A p-value, or statistical significance, does not measure the size of an effect or the importance of a result.
- 6. By itself, a p-value does not provide a good measure of evidence regarding a model or hypothesis.