

## Tests for Mixed Paired and Two-Sample Designs/Classification

# My Research I: New Statistics

- ▶ Develop new and improved statistical methodology
  - ▶ Nonparametric and Robust Methods

# Nonparametric and Robust Methods

- ▶ e.g., t-test
  - ▶ Mathematically exact if data come from normal distribution
  - ▶ Otherwise, other methods can work better
    - ▶ I try to develop such methods

## My Research II: Interdisciplinary Research

- ▶ Develop new statistical methodology
- ▶ Novel application of existing methodology

# Two Topics Today

- ▶ New Statistics: *Tests for Mixed Paired and Two-Sample Designs*
- ▶ Interdisciplinary: *Classification for zooarchaeology*

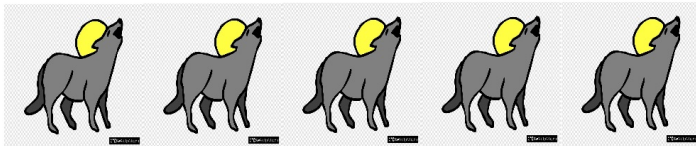
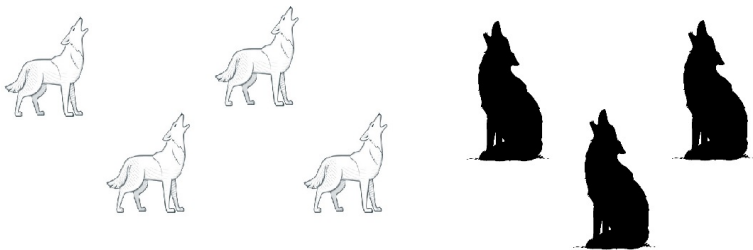
# Mixed Paired and Two-Sample Designs

## **Coyotes.**

- ▶ It was desired to compare two methods (QIAGEN DNeasy Kit, traditional chloroform isoamyl alcohol method) for extracting DNA from coyote blood samples.
- ▶ The response variable ( $Y$ ) was mean concentration of DNA.
- ▶ A total of 30 coyotes were available for the study.
- ▶ Ideally, both methods would be used on each coyote
  - ▶ Reduced variability, as differences between treatments would be on the same subject
  - ▶ Fewer subject (coyotes) required

## Mixed Paired and Two-Sample Designs-Coyotes

Due to constraints, however, both methods were used on only 6 coyotes (randomly selected). The kit was randomly assigned to be used for 8 of the remaining coyotes and the traditional method for the remaining 16 coyotes.



# Mixed Paired and Two-Sample Designs-Laser Eye Surgery

Clinical trial to compare two methods of laser eye surgery.

- ▶ Patients with both eyes eligible have one eye randomly assigned to each treatment (dependent samples)
- ▶ Patients with only one eye eligible will each have one eye randomly assigned to one treatment (independent samples)



# Analysis of Paired Data: Paired $t$ -test

Under the assumptions

- ▶ The treatment response differences for the 6 coyotes receiving both treatments are independent
- ▶ The response differences for the population of all coyotes are normally distributed

The statistic

$$t_{paired} = \frac{\bar{d}}{s/\sqrt{n}} \sim t(n-1)$$

where

- ▶  $n = 6$  is the number of paired data points
- ▶  $\bar{d} = \bar{x} - \bar{y}$  is the mean of the paired differences
- ▶  $s$  is the standard deviation of the paired differences
- ▶  $t(n-1)$  is the Student's  $t$ -distribution with  $n-1$  degrees of freedom

# Analysis of Unpaired Data: Pooled $t$ -test

Under the assumptions

- ▶ The responses for the 24 “unpaired” coyotes are independent
- ▶ The populations of responses are both normally distributed
- ▶ The populations of treated and untreated responses have the same variance

The statistic

$$t_{unpaired} = \frac{(\bar{X} - \bar{Y}) - (\mu_1 - \mu_2)}{\sqrt{\frac{s_p^2}{n_1} + \frac{s_p^2}{n_2}}} \sim t(n_1 + n_2 - 2)$$

where

- ▶  $n_1 = 8, n_2 = 16$  are the sizes of the unpaired samples
- ▶  $\bar{X} - \bar{Y}$  is the treatment mean difference for the unpaired data
- ▶  $s_1, s_2$  are the standard deviations of the unpaired samples
- ▶  $s_p^2 = \frac{(n_1-1)s_1^2 + (n_2-1)s_2^2}{n_1 + n_2 - 2}$  is the pooled variance
- ▶  $t(n_1 + n_2 - 2)$  is the **Student's  $t$ -distribution** with  $n_1 + n_2 - 2$  degrees of freedom

# Nonparametric Alternative: Randomization/Permutation tests

Idea: Compute  $p$ -value based on the results of all hypothetical experiments

- ▶ **Assume there is no treatment effect**
- ▶ “Rerandomize (permute)” the observed data and compute the resulting test statistic
- ▶ Repeat for all possible rerandomizations
- ▶ Compare the test statistic of the actual randomization to the set all possible results
  - ▶ If the result looks “unusual”, it is likely because the initial assumption is wrong, and there is a treatment effect

# Nonparametric Alternative: Rank-based tests

Rank-based analogues to  $t_{paired}$  and  $t_{unpaired}$  tests:

- ▶ Wilcoxon signed-ranks test ( $W_{paired}$ )
- ▶ Wilcoxon rank-sum/Mann-Whitney test ( $W_{unpaired}$ )
- ▶
- ▶ Rank-based methods are resistant to outliers

Can the separate tests be combined to use all of the data in a single test?

Consider the statistic

$$t_{combined} = \lambda t_{paired} + (1 - \lambda) t_{unpaired}$$

Note that  $t_{combined} = t_{paired}$  when  $\lambda = 1$  and  $t_{combined} = t_{unpaired}$  when  $\lambda = 0$ .

- Much of the previous research has been focused on trying to approximate the distribution of  $t_{combined}$ .

## Previous Research: Combined t-tests

- ▶ Lin & Stivers (1974)
- ▶ Bhoj (1978)
- ▶ Bhoj (1989)

All of these assumed normally distributed data and derived approximate t-distributions.

## Previous Research: Randomization tests

- ▶ Einsporn & Habtzghi (2013).
- ▶ Investigated randomization/permutation version of Bhoj (1978) test.

## Previous Research: Nonparametric tests

- ▶ Dubnicka, et. al. (2002); Magel & Fu (2014).
- ▶ Proposed combined test based on Wilcoxon statistics.
- ▶ Johnson (2018). Proposed permutation versions of Dubnicka and Magel & Fu tests; performed extensive simulation study to compare various tests.
- ▶ Wang (2020(REU)). Investigated confidence intervals based on combined statistics.



# Comparison of Approaches

- ▶ **None of the tests has been shown to be superior under all conditions**
- ▶ Bhoj (1989) method best for normally distributed data
- ▶ Einsporn & Habtzghi (2013) method best for nonnormal, “light-tailed” data
- ▶ Rank methods best for nonnormal “heavy-tailed” data
  - ▶ **Neither of the rank tests was best in all situations**

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AND NOW FOR  
SOMETHING  
COMPLETELY  
DIFFERENT

# Zooarchaeology

- ▶ Zooarchaeology: studies the remains of animals from archaeological sites

# Problem

Predict the percent of human vs. carnivore presence based on bone samples from a site

## Solution?

- ▶ Compiled database of bone characteristics from experiments
  - ▶ Human only
  - ▶ Carnivore only
- ▶ Create a classification algorithm from these data to predict percent of human vs. carnivore presence for a sample from a site with unknown percents

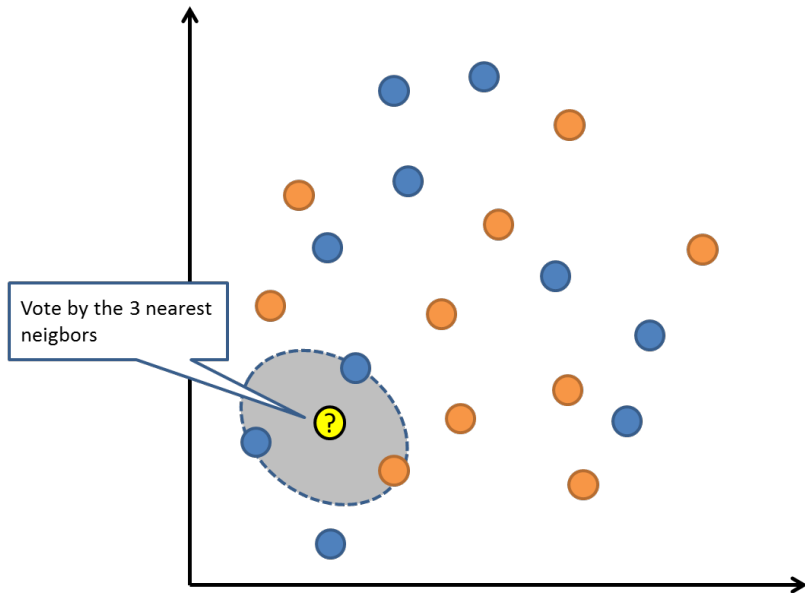
# The Classification Problem

- ▶ Outcome: Known group label (e.g., human/carnivore)
- ▶ Features/Predictors: Characteristics of individuals in groups
- ▶
- ▶ Want to be able to “predict” Group membership based on Features

## Example: Spam emails

- ▶ Email service compiles data on emails reported as spam vs. OK
- ▶ Uses these data to “predict” whether an email is spam

## Example algorithm: k-Nearest Neighbor Classifier





## References

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