# Comparing two groups: continuous data

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# What we are going to learn ...

- Some examples
- Estimation and test of hypothesis
- R analysis
- Interpretation

# **Difference between US and Viet women**

Table 1 Basic characteristics of participants			
Variable	US white ( <i>n</i> = 419)	Vietnamese (n = 210)	P value
Age (years)	71.5 (8.1)	61.7 (9.6)	<0.0001
Weight (kg)	66.7 (12.9)	53.3 (7.9)	<0.0001
Height (cm)	160.8 (6.1)	148.9 (5.7)	<0.0001
BMI (kg/m²)	25.8 (4.8)	24.1 (3.2)	<0.0001
Femoral neck BMD (g/cm²)	0.69 (0.12)	0.63 (0.11)	<0.0001
Lumbar spine BMD (g/cm²)	0.98 (0.19)	0.76 (0.14)	<0.0001
Whole body BMD (g/cm²)	1.05 (0.13)	0.89 (0.11)	<0.0001
Lean mass (kg)	38.6 (5.4)	32.3 (4.1)	<0.0001
Lean mass index (kg/m²)	14.8 (1.8)	14.6 (1.5)	0.0730
Fat mass (kg)	24.8 (8.1)	18.8 (4.9)	<0.0001
Percent body fat (%)	36.4 (6.5)	35.0 (6.2)	0.0122

#### Lan T Ho-Pham, et al obesity 2010

# Vitamin D in Vietnamese men and women

• Vitamin D (25-hydroxyvitamin D)

	Men	Women
Ν	222	336
Mean	28.57	23.79
SD (standard deviation)	8.94	7.86

• Is there real difference between men and women?

#### **Inference for 2-sample means**

• Estimation and test of hypothesis

**Assumptions:** 

- The two samples are *independent*
- The two sample sizes are *large*. That is,  $n_1 > 30$  and  $n_2 > 30$
- Both samples are *simple random samples*

# Estimation: *sample* and *population*

	Sample		Population	
	Men	Women	Men	Women
Ν	222 (n <sub>1</sub> )	336 (n <sub>2</sub> )	Infinite	Infinite
Mean	28.57 (x <sub>1</sub> )	23.79 (x <sub>2</sub> )	μ <sub>1</sub> = ?	μ2 <b>=?</b>
SD (standard deviation)	8.94 (s <sub>1</sub> )	7.86 (s <sub>2</sub> )	σ <sub>1</sub> = ?	σ2 <b>= ?</b>

# Estimation: *sample* and *population*

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Difference	$d = x_1 - x_1$		$\delta = \mu_1 - \mu_2$	
Status	Known		Unknown	

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Difference	$d = x_1 - x_1$		$\delta = \mu_1 - \mu_2$	
Status	Known		Unknown	

- "Is there real difference between men and women" means whether d = 0.
- We want to estimate the sampling variability around *d*

#### **Estimation**

 We need to estimate *d* and standard deviation of *d* (denoted by s)

$$S = \sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}$$

• 95% confidence interval of *d* is approximately:

*d*<u>+</u>1.96 s

# **Test of hypothesis**

#### **Null hypothesis**

$$H_{o}: \mu_{1} = \mu_{2}$$

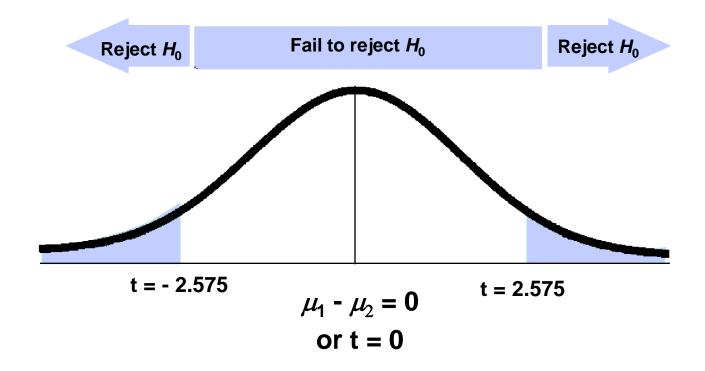
**Alternative hypothesis** 

 $\mathbf{H}_1: \mu_1 \neq \mu_2$ 

# Question: if *Ho is true*, what is the chance that we observed the data as reported? → P-value

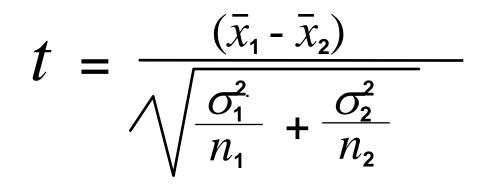
# **Test of hypothesis**

- Set alpha = 0.05 or 0.01
- Calculate a statistic
- Compare the statistic with the null distrribution



#### **Test statistic**





#### **Test statistic**

$$t = \frac{(\bar{x}_1 - \bar{x}_2)}{\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}}$$

 $\sigma_1$  and  $\sigma_2$ : If  $\sigma_1$  and  $\sigma_2$  are not known, use  $s_1$  and  $s_2$  in their places. provided that both samples are large.

**P-value:** Use the computed value of the test statistic *t*, and find the *P*-value

# **Using R**

```
setwd("C:/Documents and Settings/Tuan/My
   Documents/_Current Projects/_Vietnam/Huong/Vitamin D")
vd = read.csv("vitaminD.csv", header=T, na.strings=" ")
attach(vd)
library(psych)
describe.by(vitd, sex)
t = t.test(vitd ~ sex)
print(t)
```

# **R** outputs

<pre>&gt; describe.by(vitd, sex)</pre>	
group: 1	
var n mean sd median trimmed	mad min max range skew kurtosis se
1 1 222 28.57 8.94 28.29 28.45	8.46 4 59.87 55.87 0.17 0.66 0.6
group: 2	
var n mean sd median trimmed	mad min max range skew kurtosis se
1 1 336 23.79 7.86 24.26 23.93	7.1 4 59.6 55.6 0.07 1.22 0.43

### Routput – t-test

```
> t = t.test(vitd ~ sex)
> print(t)
```

```
t = 6.4768, df = 430.332, p-value = 2.562e-10
alternative hypothesis: true difference in means is not equal
to 0
```

```
95 percent confidence interval:
```

```
3.326365 6.224809
```

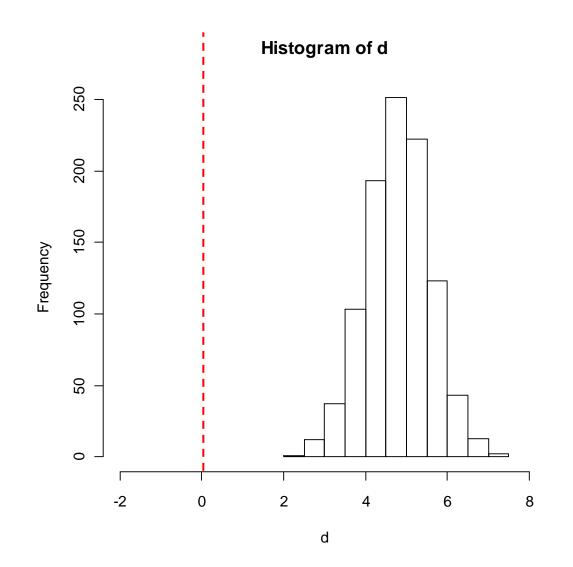
	Men	Women	Difference and 95% Cl	P-value
N	222	336	336	
Mean	28.6 (8.9)	23.8 (7.9)	4.8	<0.0001
			(3.3 – 6.2)	

# Interpretation

	Men	Women	Difference and 95% CI	P-value
N	222	336	336	
Mean	28.6 (8.9)	23.8 (7.9)	4.8	<0.0001
			(3.3 – 6.2)	

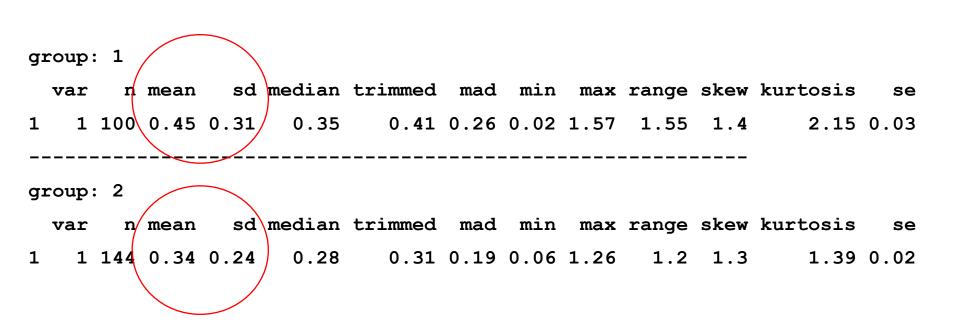
25(OH)D in men was higher than that in women, with average difference being 4.8 ng/mL (95% CI: 3.3 to 6.2 ng/mL; P < 0.0001).

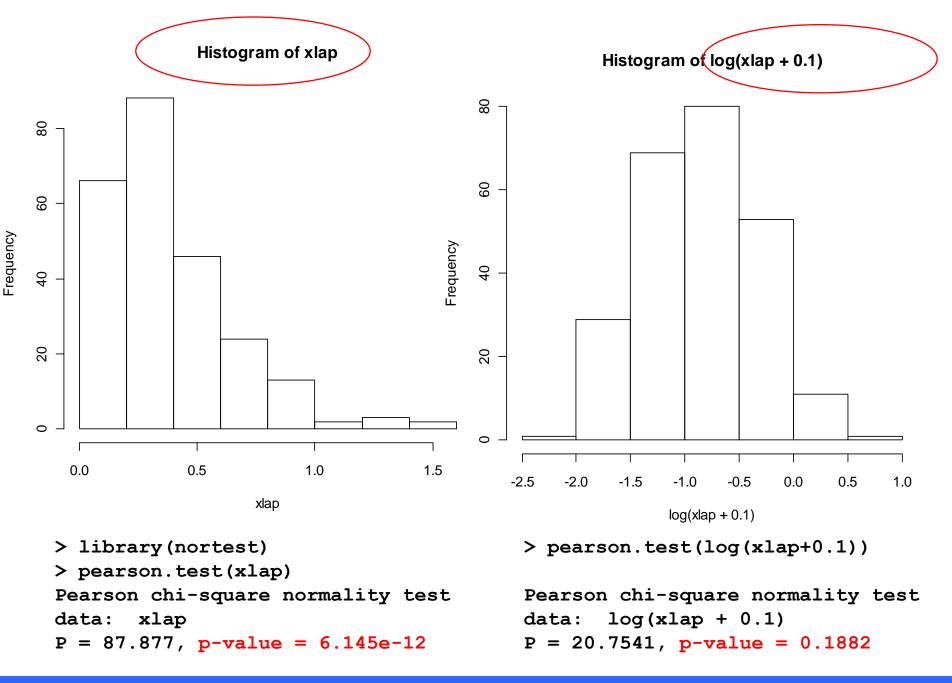
```
se = (6.2-3.3)/(2*1.96)
d = rnorm(1000, mean=4.8, sd=se)
> hist(d, xlim=c(-2, 8))
```



#### **Transformation of data**

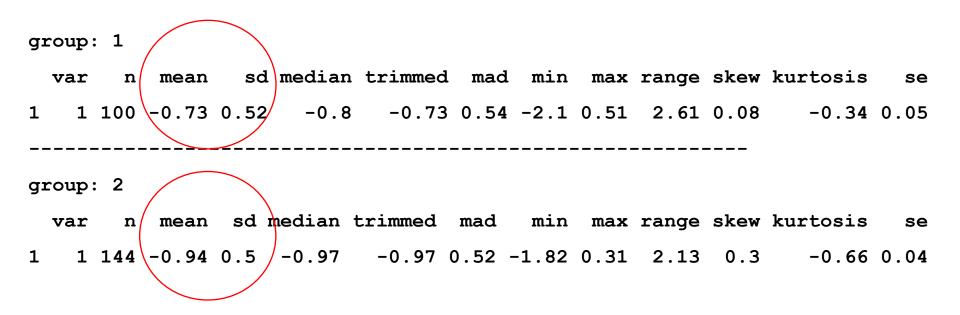
> describe.by(xlap, sex)





### Analysis of transformed data

> describe.by(log(xlap+0.1), sex)



#### **T-test on transformed data**

```
> t.test(log(xlap+0.1) ~ sex)
data: log(xlap + 0.1) by sex
t = 3.216, df = 206.284, p-value = 0.001509
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
    0.08306888 0.34626674
sample estimates:
mean in group 1 mean in group 2
    -0.7300382 -0.9447060
```

Exp(-0.73+0.9447) = 1.234Exp(0.083) = 1.086Exp(0.346) = 1.413

# Interpretation

	Men	Women	Percentage difference and 95% CI	P-value
Ν	100	144		
Mean	0.45 (0.31)	0.34 (0.24)	23% (8.6, 41.3)	0.0015

**Compared with women, beta crosslap was 23%** (95% CI: 8.6 to 41.3%) **higher in men , and the difference was statistically significant (***P***= 0.001)** 

#### **Non-parametric analysis**

• Wilcoxon's rank sum test

```
> wilcox.test(xlap ~ sex)
```

Wilcoxon rank sum test with continuity correction

```
data: xlap by sex
W = 8890, p-value = 0.001834
alternative hypothesis: true location shift is not equal to 0
```

#### **Non-parametric analysis**

Permutation and median test

```
> library(coin)
> oneway test(xlap ~ as.factor(sex))
        Asymptotic 2-Sample Permutation Test
data: xlap by as.factor(sex) (1, 2)
Z = 3.1073, p-value = 0.001888
alternative hypothesis: true mu is not equal to 0
> median test(xlap ~ as.factor(sex))
        Asymptotic Median Test
data: xlap by as.factor(sex) (1, 2)
Z = -2.8579, p-value = 0.004265
```

```
alternative hypothesis: true mu is not equal to 0
```

# Summary

- Statistical tests:
  - T-test: comparing two groups, for continuous outcomes
  - Non-parametric tests: Wilcoxon, median, and permutation tests
- Assumptions: normal distribution, similar variance, independence
- Trasnformation of data if necessary