

# 140.615.HW.Number.Jin.Vincent

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2023-03-10

## Homework 05

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### Question 01

In a trial to compare a stannous fluoride dentifrice A, with a commercially available fluoride free dentifrice D, 260 children received A and 289 received D for a 3-year period. The mean DMFS increments (the number of new Decayed Missing and Filled tooth Surfaces) were 9.78 with standard deviation 7.51 for A, and 12.83 with standard deviation 8.31 for D. Is this good evidence that, in general, one of these dentifrices is better than the other at reducing tooth decay?

#### *Answer*

To determine if one of these dentifrices is better than the other one, we can perform a two sample t test with the following hypothesis:

$H_0$ : The mean DMFS increments of the children received fluoride dentifrice A is equal to the mean of the children who received dentifrice D.  $H_a$ : The mean DMFS increments of the children received fluoride dentifrice A does not equal to the mean of the children who received dentifrice D.

```
mean_A <- 9.78
mean_D <- 12.83
sd_A <- 7.51
sd_D <- 8.31
n_A <- 260
n_D <- 289

sd_pool <- sqrt(((sd_A ^ 2 * (n_A - 1)) + (sd_D ^ 2 * (n_D - 1))) / (n_A + n_D - 2))
t <- (mean_A - mean_D) / (sd_pool * sqrt((1 / n_A) + (1 / n_D)))

p <- 2 * pt(t, n_A + n_D - 2)

print(p < 0.05)
```

```
## [1] TRUE
```

```
print(t)
```

```
## [1] -4.493243
```

```
print(p)
```

```
## [1] 8.564533e-06
```

Therefore, the two sample t-test suggested a t-statistic of -4.49 under 547 degree of freedom with associated p-value of  $8.56 \times 10^{-4}$ , which is less than 0.05, so that we can reject the null hypothesis and conclude that the mean DMFS increments of children received fluoride dentifrice A does not equal to children who received dentifrice D. This means that one of these dentifrices is better than the other at reducing tooth decay.

## Question 02

You want to detect differences in protein abundances between affected probands and normal controls, measured by ELISA. Since you are interested in fold changes, you record your measurements as  $\log_2(abundance)$ . Thus, a two-fold change in abundance corresponds to a difference  $\Delta$  of 1 on the  $\log_2$  scale, a four-fold change corresponds to  $\Delta$  of 2, etc. Also assume that in each group the  $\log_2(abundance)$  are independent measurements from a Normal distribution.

(a)

Assuming you plan on running ELISAs for the same number of cases and controls, how many subjects do you need to have 80% power to detect a two-fold change in abundance between cases and controls, i. e.  $\Delta = 1$ , if the within-group standard deviation of the  $\log_2(abundance)$  is the same as the differences in means of the  $\log_2(abundance)$ , i. e.  $\sigma = \Delta$ ?

*Answer*

```
power.t.test(delta = 1, sd = 1, sig.level = 0.05, power = 0.8, type = "two.sample")
```

```
##
##      Two-sample t test power calculation
##
##              n = 16.71477
##              delta = 1
##              sd = 1
##      sig.level = 0.05
##              power = 0.8
##      alternative = two.sided
##
## NOTE: n is number in *each* group
```

Therefore, we would need 17 affected probands and 17 normal controls to have 80% power to detect a two-fold change in abundance between cases and controls.

(b)

How much power would you have if you only ran ten ELISAs per group?

*Answer*

```
power.t.test(n = 10, delta = 1, sd = 1, sig.level = 0.05, type = "two.sample")
```

```
##
##      Two-sample t test power calculation
##
##              n = 10
##            delta = 1
##              sd = 1
##      sig.level = 0.05
##            power = 0.5619846
##      alternative = two.sided
##
## NOTE: n is number in *each* group
```

Therefore, if we only have 10 ELISAs per group, we will have 56.20% power to detect a two-fold change in abundance between cases and controls.

(c)

How much power would you have if you only ran ten ELISAs per group, but knew that in truth the protein you are interested could not be down-regulated in the affected probands?

**Answer**

If we know that the protein interested in could not be down-regulated in the affected probands, we can assume a one-sample t-test.

```
power.t.test(n = 10, delta = 1, sd = 1, sig.level = 0.05, type = "one.sample")
```

```
##
##      One-sample t test power calculation
##
##              n = 10
##            delta = 1
##              sd = 1
##      sig.level = 0.05
##            power = 0.8030962
##      alternative = two.sided
```

Therefore, if we know the protein will not be down-regulated, the power will be 80.31% to detect two-fold change if we perform 10 ELISAs per group.

### Question 03

Consider data on the treatment response of 12 mice from strain A and 9 mice from strain B. Assume that the true within-group standard deviations are the same.

Strain A 55.2 58.1 41.7 44.9 44.8 48.9 47.5 48.1 48.4 51.6 40.6 48.0

Strain B 48.7 52.6 65.2 70.4 44.2 54.7 44.0 66.5 56.8

(a)

Test the hypothesis  $H_0 : \mu_A = \mu_B$  versus the alternative  $H_a : \mu_A \neq \mu_B$  using the function `t.test()`.

*Answer*

```
A <- c(55.2, 58.1, 41.7, 44.9, 44.8, 48.9, 47.5, 48.1, 48.4, 51.6, 40.6, 48.0)
B <- c(48.7, 52.6, 65.2, 70.4, 44.2, 54.7, 44.0, 66.5, 56.8)
t.test(A, B, var.equal = TRUE)
```

```
##
## Two Sample t-test
##
## data: A and B
## t = -2.3817, df = 19, p-value = 0.02784
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -14.5607027 -0.9392973
## sample estimates:
## mean of x mean of y
## 48.15 55.90
```

The `t.test` function suggested a t-statistic of -2.38 under 19 degree of freedom with associated p-value of 0.028, which is less than 0.05, so we reject the null hypothesis of  $\mu_A = \mu_B$  and conclude that the mean of strain A mice is significantly different from strain B mice.

(b)

Use the `wilcox.test()` function to perform a rank-sum test on these data.

*Answer*

```
wilcox.test(A, B)

##
## Wilcoxon rank sum exact test
##
## data: A and B
## W = 29, p-value = 0.08154
## alternative hypothesis: true location shift is not equal to 0
```

(c)

Give an interpretation of your results.

*Answer*

Based on the results of two tests, for `t.test` in which a p-value of 0.028 was suggested, we rejected the null hypothesis and conclude that the mean of treatment response for strain A group is different from strain B group. However, for Wilcoxon rank sum test in which a p-value of 0.08 ( $> 0.05$ ) was suggested, we failed to reject the null hypothesis and could not conclude that the mean of treatment response for strain A group is different from strain B group.

## Question 04

(a)

Test  $H_0 : p = \frac{1}{2}$  vs.  $H_a : p \neq \frac{1}{2}$  for  $X \sim \text{Binomial}(n=45, p)$ , when we observe 16 successes.

*Answer*

```
binom.test(16, 45, p = 0.5)
```

```
##
## Exact binomial test
##
## data: 16 and 45
## number of successes = 16, number of trials = 45, p-value = 0.07245
## alternative hypothesis: true probability of success is not equal to 0.5
## 95 percent confidence interval:
##  0.218684 0.512199
## sample estimates:
## probability of success
##           0.3555556
```

The binomial test suggested a p-value of 0.072 which is greater than 0.05. Therefore, we failed to reject null hypothesis and conclude that the p value is not statistically different from  $\frac{1}{2}$ .

(b)

Calculate a 95% confidence interval for p for the data above.

*Answer*

```
binom.test(16, 45, conf.level = 0.95)
```

```
##
## Exact binomial test
##
## data: 16 and 45
## number of successes = 16, number of trials = 45, p-value = 0.07245
## alternative hypothesis: true probability of success is not equal to 0.5
## 95 percent confidence interval:
##  0.218684 0.512199
## sample estimates:
## probability of success
##           0.3555556
```

The confidence interval for p for the data above is (0.22, 0.51).

(c)

Calculate a 95% confidence interval for p when  $X \sim \text{Binomial}(15, p)$  and we observe only successes.

*Answer*

```
binom.test(15, 15, conf.level = 0.95)
```

```
##  
## Exact binomial test  
##  
## data: 15 and 15  
## number of successes = 15, number of trials = 15, p-value = 6.104e-05  
## alternative hypothesis: true probability of success is not equal to 0.5  
## 95 percent confidence interval:  
## 0.7819806 1.0000000  
## sample estimates:  
## probability of success  
## 1
```

The 95% confidence interval for  $p$  when  $X \sim \text{Binomial}(15, p)$  and we only observe successes is  $(0.78, 1.00)$ .