

# MTH 3210 Lab 4

Due Thu., May 2

## 1 Part A: Confidence Interval for $\mu$

### 1.1 Change in Blood Pressure Data Set

## 2 Part A: One-Sample $t$ Test for a Population Mean $\mu$

### 2.1 Change in Blood Pressure Data Set (Cont'd from Lab 3)

A study was designed to see if increased dietary calcium intake reduces blood pressure. Ten men were given a calcium supplement for 12 weeks. Blood pressure was measured before and after the twelve-week period. The changes in blood pressure for the ten subjects are below:

-7, -5, -5, -17, 8, 5, -1, -10, -11, 2

A **negative** value means the blood pressure **decreased**.

We want use the data to carry out a **hypothesis test** to decide if there's statistically significant evidence that calcium **lowers blood pressure**.

The **null** and **alternative hypotheses** are

$$\begin{aligned} H_0 : \mu &= 0 && \text{(calcium has no effect on blood pressure)} \\ H_a : \mu &< 0 && \text{(calcium decreases blood pressure)} \end{aligned}$$

where  $\mu$  is the true (unknown) mean change in blood pressure.

The *one-sample  $t$  test statistic* is

$$t = \frac{\bar{X} - 0}{S/\sqrt{n}}$$

and measures (approximately) how many standard errors  $\bar{X}$  is below zero. Thus, because  $\bar{X}$  estimates  $\mu$ , **negative  $t$  values provide evidence against  $H_0$  in favor of  $H_a$** .

Once we have the observed value of  $t$ , the  **$p$ -value** is the probability that just by chance we'd get a  $t$  value that far below zero *if calcium had no effect*. **A smaller  $p$ -value provides stronger evidence against  $H_0$  in favor of  $H_a$** .

Using a *level of significance*  $\alpha = 0.05$ , the *decision rule* is

Reject  $H_0$  if  $p\text{-value} < 0.05$   
Fail to reject  $H_0$  if  $p\text{-value} \geq 0.05$ .

1. Use `c()` create a vector that stores the data.
2. The function `t.test()` takes a vector argument `x` and carries out the *one-sample t test* for  $\mu$ . The option `alternative = "less"` is used to specify the direction " $<$ " for  $H_a$ .
3. The `t.test()` function takes a data vector `x` and carries out a *one-sample t test* for a population mean  $\mu$ . Among its arguments are:

<code>x</code>	a data vector.
<code>alternative</code>	the direction for the alternative hypothesis, one of "two.sided", "less", or "greater".
<code>mu</code>	the null hypothesized value for the unknown population mean, with default value 0.
<code>conf.level</code>	the confidence level for a confidence interval for the unknown population mean, with default value 0.95.

The optional argument, `alternative`, can be used to change the direction of  $H_a$ . For example, the **lower-tailed t test** based on data in a vector called `my.data`, would be carried out by typing:

```
t.test(x = my.data, alternative = "less")
```

Use `t.test()`, to carry out the hypothesis test. Be sure to note the value of the **test statistic t** and the **p-value**.