SAS for one-sample t-tests

- SAS automatically does a two-sided test
  
  \[ H_0 : \mu = \mu_0 \]
  \[ H_a : \mu \neq \mu_0 \]

Example: Using the "normtemp.dat" data on body temperatures measured on 130 healthy adults, we will test the hypotheses

\[ H_0 : \mu = 98.6 \]
\[ H_a : \mu \neq 98.6 \]

at the .05 significance level.

```
data normtemp ;
  infile 'normtemp.dat' ;
  input temp gender heart ;
run ;
```

```
proc means n mean std dev clm alpha = .05 ;
  var temp ;
run ;
```

<table>
<thead>
<tr>
<th>Variable</th>
<th>N</th>
<th>Mean</th>
<th>Std Dev</th>
<th>Lower 95.0%</th>
<th>Upper 95.0%</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>CLM</td>
<td>CLM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>temp</td>
<td>130</td>
<td>98.249</td>
<td>0.733</td>
<td>98.122</td>
<td>98.376</td>
</tr>
</tbody>
</table>

Note that:
- The 95% confidence interval for \( \mu \) does not contain 98.6.
- The p-value is less than .05, so we can reject the null hypothesis.

Example 2: We will use the same dataset to test a hypothesis regarding heart rates, namely:

\[ H_0 : \mu = 73 \]
\[ H_a : \mu \neq 73 \]

at the .05 significance level.

```
data normtemp ;
  infile 'normtemp.dat' ;
  input temp gender heart ;
run ;
```

```
proc means n mean std dev clm alpha = .05 ;
  var heart ;
run ;
```

<table>
<thead>
<tr>
<th>Analysis Variable : HEART</th>
</tr>
</thead>
<tbody>
<tr>
<td>N</td>
</tr>
<tr>
<td>-----</td>
</tr>
<tr>
<td>130</td>
</tr>
</tbody>
</table>

Note that:
- The 95% confidence interval for \( \mu \) does contain 73.
- The p-value is greater than .05, so we cannot reject the null hypothesis.
One-sample t-tests using proc univariate

```
data normtemp ;
infile '/group/ftp/pub/kcowles/datasets/normtemp.dat' ;
input temp gender heart ;
format gender sexfmt. ;
run ;
```

```
proc univariate mu0 = 98.6 data = normtemp ;
var temp ;
run ;
```

The UNIVARIATE Procedure

Variable: temp

Tests for Location: Mu0=98.6

<table>
<thead>
<tr>
<th>Test</th>
<th>-Statistic-</th>
<th>p Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Student’s t</td>
<td>-5.45482</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Sign</td>
<td>-21</td>
<td>0.0002</td>
</tr>
<tr>
<td>Signed Rank S</td>
<td>-1963</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>

Two-sample t-tests

So far we have talked about drawing inference about a single population mean $\mu$ based on data contained in one sample drawn from that population.

Now we will consider procedures for comparing two different population means.

There are different procedures depending on whether the samples are

- paired
- independent

Paired samples

- We are interested in the unknown population means $\mu_1$ and $\mu_2$ of two different populations.
- In our sample, each observation drawn from the first population is matched up with an observation drawn from the second population.

- self-pairing: two measurements are taken on each subject

Example:

- systolic blood pressure (sbp) upon entry into a clinical study
- sbp after 1 month on treatment

The population means of interest are

- $\mu_1 =$ mean sbp of untreated patients of this type
- $\mu_2 =$ mean sbp of patients of this type after 1 month of treatment with the study regimen

The question of interest is whether the treatment lowers blood pressure, i.e. is $\mu_2 < \mu_1$?
• matched pairs: investigator matches each subject in one treatment group with one subject in another treatment group so that members of a pair are as alike as possible

The population means of interest are

- $\mu_1$ = mean response (say sbp at 1 month) of patients receiving treatment 1
- $\mu_2$ = mean response of patients receiving treatment 2
- The question of interest is whether $\mu_1 = \mu_2$

Paired t-test

To carry out the hypothesis test of interest, we apply one-sample procedures to the differences between values measured on members of each pair.

Example:

• We are interested in whether the use of oral contraceptive (OC) drugs affects the level of systolic blood pressure (sbp) in women.
• We identify a group of nonpregnant, premenopausal women aged 16-49 from a prepaid health plan who are not currently OC users and measure their sbp, which we will refer to as baseline sbp.
• We rescreen these women 1 year later to ascertain a subgroup who have remained non-pregnant throughout the year and have be-

come OC users. This subgroup will be the study sample.

• Measure the sbp of the study sample at the follow-up visit.
• We will compare the baseline and follow-up sbps of the women in the study sample.

We will do a two-sided test, because we do not know in advance whether to expect $\mu_1$ (mean sbp in OC users) to be higher or lower than $\mu_2$ (mean sbp in non-users).

$$H_0 : \mu_1 = \mu_2$$
$$H_a : \mu_1 \neq \mu_2$$

or equivalently:

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

or equivalently:

$$H_0 : \delta = 0$$
$$H_a : \delta \neq 0$$

where $\delta$ denotes $\mu_1 - \mu_2$. 
We will use the observed differences between the before and after values observed on each woman as our data to carry out the hypothesis test regarding $\delta$ at the .05 significance level.

```
data sbpoc;
  infile '/group/ftp/pub/kcowles/datasets/sbpoc.dat';
  input sbpnooc sbpoc;
diff = sbpoc - sbpnooc;
run;

proc print;
run;
```

```
OBS SBPNOOC SBPOC DIFF
1 115 128 13
2 112 115 3
3 107 106 -1
4 119 128 9
5 115 122 7
6 138 145 7
7 126 132 6
8 105 109 4
9 104 102 -2
10 115 117 2
```

We will compute the sample mean of the $d_i$s

$$\bar{d} = \frac{\sum d_i}{n}$$

and the sample standard deviation of the $d_i$s

$$s_d = \sqrt{\frac{\sum (d_i - \bar{d})^2}{n - 1}}$$

```
proc means data = sbpoc;
  var diff;
run;
```

```
Analysis Variable : DIFF

<table>
<thead>
<tr>
<th>N</th>
<th>Mean</th>
<th>Std Dev</th>
<th>Minimum</th>
<th>Maximum</th>
</tr>
</thead>
<tbody>
<tr>
<td>10</td>
<td>4.800</td>
<td>4.5655716</td>
<td>-2.0000</td>
<td>13.0000</td>
</tr>
</tbody>
</table>
```

Then the $t$ statistic is

$$t = \frac{\bar{d} - \delta_0}{s_d/\sqrt{n}}$$

From our data,

$$\bar{d} = 4.80$$
$$s_d = 4.566$$
$$t = \frac{4.80}{4.566/\sqrt{10}}$$
$$= 3.32$$

Using Table A, we see that the value that cuts off the upper .025 area under a $t$ distribution with 9 degrees of freedom is 2.262.

Because $3.32 > 2.262$ (our result is more extreme than the required cutoff), we can reject the null hypothesis at the .05 level.
We could use SAS to find the exact p-value, which is 0.0089.

Note that the one-sample t-test in `proc univariate` by default tests the null hypothesis that $\mu = 0$.

```sas
proc univariate data = sbpoc ;
var diff ;
run ;
```

The UNIVARIATE Procedure
Variable: temp

Tests for Location: Mu0=0

<table>
<thead>
<tr>
<th>Test</th>
<th>-Statistic-</th>
<th>-----p Value-----</th>
</tr>
</thead>
<tbody>
<tr>
<td>Student’s t</td>
<td>t 3.324651</td>
<td>Pr &gt;</td>
</tr>
<tr>
<td>Sign</td>
<td>M 3</td>
<td>Pr &gt;=</td>
</tr>
<tr>
<td>Signed Rank</td>
<td>S 24</td>
<td>Pr &gt;=</td>
</tr>
</tbody>
</table>