Displays for Statistics 5303

Lecture 3

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Class Web Page
http://www.stat.umn.edu/~kb/classes/5303

Example of Computer Randomization

Suppose you have N = 31 EU's you want to assign to 4 treatments, with $n_1 = n_2 = n_3 = 7$ and $n_4 = 10$.

You could put slips numbered 1, 2, ..., 31 into a box, shuffle well, and draw numbers sequentially, assigning treatment 1 to EU's whose numbers were the first 7 drawn, treatment 2 to the next 7, ...

This procedure provides you a random permutation (reordering) of {1, 2, 3, ..., 31} with all permutations equally likely. You use the permuted set of numbers in assigning treatments.

Any other way of producing a random permutation could be used instead of drawing numbers from a box. One such way uses random numbers (more accurately *pseudo-random* numbers) generated on a computer.

Here is one way to do this in MacAnova.

```
Cmd> n <- vector(7, 7, 7, 10) # sample sizes

Cmd> N <- sum(n); N # total number of EU's
(1)         31

Cmd> treatments <- rep(0,N) # empty vector to be filled

Cmd> u <- runi(N) # random sample of uniform random variables

Cmd> J <- rank(u); J # their ranks are a random permutation
 (1)       21         17         16         14         11
 (6)        3         29          6          1         26
(11)       27         25         13         28          2
(16)        4         18         23          9         31
(21)       10         30          7          5         24
(26)        8         19         20         22         12
(31)       15
                  underlining gives treatment groups

Cmd> treatments[J[run(n[1])]] <- 1 # Assign trt 1 to first 7

Cmd> treatments[J[n[1] + run(n[2])]] <- 2 # trt 2 to next 7

Cmd> treatments[J[n[1] + n[2] + run(n[3])]] <- 3 # 3 to next 7

Cmd> treatments[J[n[1] + n[2] + n[3] + run(n[4])]] <- 4

Cmd> print(paste(treatments)) # final assignment
2 3 1 3 4 2 4 4 3 3 1 4 2 1 4 1 1 3 4 4 1 4 3 4 2 2 2 2 1 4 3
```

With experience, you can use the looping facilities of MacAnova to do it more compactly.

```
Cmd> treatments <- rep(0,sum(n)); Ni <- 0

Cmd> for(i,1,nrows(n)){
        treatments[J[Ni + run(n[i])]] <- i
        Ni <- Ni + n[i];;
     }

Cmd> print(paste(treatments))
2 3 1 3 4 2 4 4 3 3 1 4 2 1 4 1 1 3 4 4 1 4 3 4 2 2 2 2 1 4 3
```

This works for any set of n's.

Randomization in Inference

Example from text.

Table 1 had data on the length of time it took each of 30 workers to runstitch a collar on a man's shirt, using a **standard** workplace and an **ergonomic** workplace, the tow "treatments".

The data are paired, because each worker stitched once at each workplace.

Here is how you might randomize the order:

```
Cmd> N <- 30 # numbers of pairs

Cmd> first <- rbin(N, 1, .5) + 1 #first treatment

Cmd> print(paste(first))
1 1 2 1 2 2 2 2 1 1 2 2 1 2 1 1 2 2 1 1 2 1 2 1 1 2 2 2 2 1
```

Here **rbin(N, 1, .5)** generates 30 independent Bernoulli (binomial with n = 1) random variables with p = .5 (computer generated coin flips). Adding 1 turns the 0's and 1's into 1's and 2's.

The standard "normal theory" test is the paired t-test, essentially a one sample t-test on the differences $x_1 - x_2$, where x_1 and x_2 are times using the standard and ergonomic workplaces, respectively.

You can use **tval()** in MacAnova to do it.

```
Cmd> readdata("",standard,ergonomic)
Read from file "TP1:Stat5303:Data:Ch02:emp2-1.dat"
Column 1 saved as REAL vector standard
Column 2 saved as REAL vector ergonomic

Cmd> list(standard,ergonomic)
ergonomic       REAL   30
standard        REAL   30

Cmd> d <- standard - ergonomic # differences

Cmd> d
 (1)       1.03      -0.04       0.26        0.3      -0.97
 (6)       0.04      -0.57       1.75       0.01       0.42
(11)       0.45       -0.8       0.39       0.25       0.18
(16)       0.95      -0.18       0.71       0.42       0.43
(21)      -0.48      -1.08      -0.57        1.1       0.27
(26)      -0.45       0.62       0.21      -0.21       0.82

Cmd> n <- nrows(d); n # number of pairs
(1)         30

Cmd> tstat <- tval(d); df <- n - 1

Cmd> vector(tstat,df,twotailt(tstat,df))
(1)       1.49         29     0.14701
        t-stat         DF     P-value
```


This paired t test assumes the d's are a random sample from $N(\mu_d,\sigma_d)$. It tests the null hypothesis H_0: $\mu_d = 0$ (no difference between workplace types), vs the alternative H_a: $\mu_d \neq 0$ (there is a difference).

Assuming the order was in fact randomized, you can do a randomization-based test whose only assumption is that the randomization was done properly.

Randomization inference is conditional on the actual data observed.

The null hypothesis tested is stated somewhat differently, but has the same interpretation as stating there was no treatment effect.

> H_0: the type of workplace is irrelevant so which number in each pair is labeled standard and which ergonomic is arbitrary.

The numbers observed are considered as if they were fixed. Inferences considers all possible results that might have occurred for the possible outcomes of the randomization.

To simplify, suppose we had only the first n = 5 pairs.

Then there are 32 different possible assignments of treatments to the first and second elements of the pairs.

Each possible assignment is essentially a specification of the signs for all the differences.

```
Cmd> d1 <- d[run(5)] # d1 is first 5 differences

Cmd> tvalobs <- tval(d1); tvalobs # paired t
(1)     0.35852

Cmd> twotailt(tvalobs,4) # two tail P-value
(1)     0.73808
```

Omitting some steps, I created a 32 by matrix **Signs**, each row of which contains a different ordered set of -1's and +1's.

```
 Wkr1  Wkr2  Wkr3  Wkr4  Wkr5
   -1    -1    -1    -1    -1 All workers ergon 2nd
   -1    -1    -1    -1     1 All but 5th workers ergon 2nd
   -1    -1    -1     1    -1 All but 4th workers ergon 2nd
   -1    -1    -1     1     1
   -1    -1     1    -1    -1
   -1    -1     1    -1     1
   -1    -1     1     1    -1
   -1    -1     1     1     1
   -1     1    -1    -1    -1
   -1     1    -1    -1     1
   -1     1    -1     1    -1
   -1     1    -1     1     1
   -1     1     1    -1    -1
   -1     1     1    -1     1
   -1     1     1     1    -1
   -1     1     1     1     1
    1    -1    -1    -1    -1
    1    -1    -1    -1     1
    1    -1    -1     1    -1
    1    -1    -1     1     1
    1    -1     1    -1    -1
    1    -1     1    -1     1
    1    -1     1     1    -1
    1    -1     1     1     1
    1     1    -1    -1    -1
    1     1    -1    -1     1
    1     1    -1     1    -1
    1     1    -1     1     1
    1     1     1    -1    -1
    1     1     1    -1     1
    1     1     1     1    -1
    1     1     1     1     1
```

```
Cmd> tstats <- rep(0,32) # place to put t-statistics

Cmd> for(i,1,32){tstats[i] <- tval(d1*vector(Signs[i,]));;}
```

`Signs[i,]` is row i of `Signs` and contains one possible outcome of the randomization. `d1*vector(Signs[i,])` applies the signs to the differences.

This last computed paired t-statistics for each of the possible sets of data that might have been observed for the 32 outcomes of the randomization. One of the values must be the actual t-statistic we observed.

```
Cmd> stemleaf(tstats) # glimpse of the distribution
    1   -2.|5
    2   -2*|3
    5   -1.|655
    7   -1*|40
    8   -0.|9
   16   -0*|43320000
   16   +0*|00002334
    8   +0.|9
    7    1*|04
    5    1.|556
    2    2*|3
    1    2.|5

         1*|1 represents 1.1  Leaf digit unit = 0.1

Cmd> tvalobs <- tval(d1); tvalobs # observed value
(1)     0.35852

Cmd> tstats >= tvalobs # comparison with observed
 (1) F       F       F       F       F       F       F
 (8) F       F       F       F       F       F       F
(15) F       F       T       F       T       F       T
(22) F       T       T       T       F       T       F
(29) T       F       T       T
```

T means **tstat** $\geq$ observed t; **F** means **tstat** < observed t.


```
Cmd> twotailt(tvalobs,4) # normal theory P-value
(1)     0.73808

Cmd> sum(tstats >= tvalobs) # counts number ≥ observed
(1)          10

Cmd> 2*sum(tstats >= tvalobs)/32 # randomization P-value
(1)       0.625
```

It's not the same as the normal theory but gives the same conclusion. For larger samples it is usually quite close.

In fact, with many randomization tests, you don't need to compute the t-statistics, since there is a simpler statistic that is monotonically related.

Paired t statistic is $t = \sqrt{n}\,\bar{d}/s_d$,
$\bar{d} = \sum d/n$, $s_d = \sqrt{\{\sum(d-\bar{d})^2/(n-1)\}}$

A little algebra shows that

$$t = \sqrt{\{n-1\}}\,\tau/\sqrt{\{1 - \tau^2\}}$$
$$\tau = \sqrt{n}\,\bar{d}/\sqrt{\{\sum d^2\}} = \sum d/\sqrt{\{n\sum d^2\}}$$

$n\sum d^2$ is is the same for all sets of signs, so t depends only on $\sum d$


```
Cmd> sums <- rep(0,32) # place to put sums

Cmd> for(i,1,32){sums[i] <- sum(d1*vector(Signs[i,]));;}

Cmd> stemleaf(sums) #distribution of sums
    2   -2.|65
    5   -2*|000
    6   -1.|9
    8   -1*|44
   11   -0.|655
   16   -0*|41000
   16   +0*|00014
   11   +0.|556
    8    1*|44
    6    1.|9
    5    2*|000
    2    2.|56

         1*|1 represents 1.1  Leaf digit unit = 0.1

Cmd> sumobs <- sum(d1); sumobs # observed value of sum
(1)        0.58

Cmd> sums >= sumobs # compare with observed
 (1) F       F       F       F       F       F       F
 (8) F       F       F       F       F       F       F
(15) F       F       T       F       T       F       T
(22) F       T       T       T       F       T       F
(29) T       F       T       T
```

This is the same pattern of **T**'s and **F**'s as for the t-statistics.

```
Cmd> 2*sum(sums >= sumobs)/32 # same P-value, too
(1)       0.625
```

There is a macro **randsign()** that does this for you automatically.

```
Cmd> stuff <- randsign(d1)
WARNING: searching for unrecognized macro randsign near
stuff <- randsign(

Cmd> list(stuff)
stuff           REAL   32

Cmd> stemleaf(stuff) # exactly the same as before
    2   -2.|65
    5   -2*|000
    6   -1.|9
    8   -1*|44
   11   -0.|655
   16   -0*|41000
   16   +0*|00014
   11   +0.|556
    8    1*|44
    6    1.|9
    5    2*|000
    2    2.|56

         1*|1 represents 1.1  Leaf digit unit = 0.1

Cmd> 2*sum(stuff >= abs(sum(d1)))/32
(1)       0.625
```

Unfortunately, you can't do this for the complete data set, since with n = 30 there are $2^{30} = 1073741824 = 1.07\times10^9$ different assignments of signs. You can, however, randomly select a large number of these. You use keyword **trials**.


```
Cmd> stuff <- randsign(d,trials:5000); list(stuff)
stuff           REAL   5000

Cmd> 2*sum(stuff >= abs(sum(d)))/5000 # approximate P-value
(1)      0.1508

Cmd> twotailt(tval(d),n-1) # normal theory P-value
(1)      0.1868
```

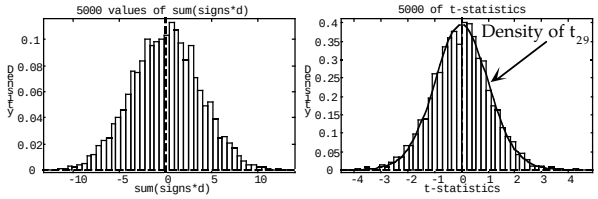
randsign() generated 5000 sums of signed differences.

Here are histograms of the $\sum \pm d_i$ as well as the equivalent t statistics computed as $t = \sqrt{(n-1)}\tau/\sqrt{(1 - \tau^2)}$.

```
Cmd> tau <- stuff/sqrt(30*sum(d^2))

Cmd> hist(stuff,50,xlab:"sum(signs*d)",\
     title:"5000 values of sum(signs*d)")

Cmd> hist(sqrt(n-1)*tau/sqrt(1 - tau^2),50,\
         title:"5000 of t-statistics",\
         xlab:"t-statistics")
```



On the right, I added the density for t_{29}, You see it is a good approximation to the histogram.