Basic statistical inference

Packages for this section

```r
library(tidyverse)
```

Inference for means (from STAB57)

Three kinds of inference for means of normally-distributed data:

- **One-sample** t: a single sample from a population, estimate that population's mean
- **Two-sample** t: one sample from each of 2 populations, estimate difference in population means
- **Matched pairs** t: two paired measurements on same (or matched) individuals, estimate population mean difference

Two forms of inference for a population parameter:

- **Confidence interval**: "what is the population parameter?"
- **Hypothesis test**: "could the population parameter be equal to this value?"

Examples:

- Blue jays attendances (one-sample)
- Kids learning to read (two-sample)
- Pain relief (matched pairs)

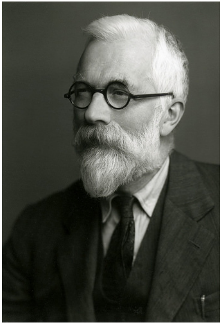
Confidence interval

- You have a sample from some population
- Imagine repeated sampling from that population
- Procedure that gives an interval containing the true parameter in 95% (or 90% or 99%) of all possible samples

Hypothesis test

- Null hypothesis gives value for population parameter
- Alternative hypothesis says how you are trying to prove the null hypothesis wrong (not equal, greater, less).
- Test statistic measures "distance" between data and null hypothesis
- P-value gives probability of observing test statistic *as extreme or more extreme*, **if the null hypothesis is true**.
- Reject null hypothesis if P-value small enough (eg smaller than 0.05).

Why 0.05? This man.



- analysis of variance
- Fisher information
- Linear discriminant analysis
- Fisher's z-transformation
- Fisher-Yates shuffle
- Behrens-Fisher problem

Sir Ronald A. Fisher, 1890–1962.

Why 0.05? (2)

- From The Arrangement of Field Experiments (1926):

the line at about the level at which we can say: "Either there is something in the treatment, or a coincidence has occurred such as does not occur more than once in twenty trials." This level, which we may call the 5 per cent. point, would be indicated, though very roughly, by the greatest chance deviation observed in twenty successive trials. To

- and

If one in twenty does not seem high enough odds, we may, if we prefer it, draw the line at one in fifty (the 2 per cent. point), or one in a hundred (the 1 per cent. point). Personally, the writer prefers to set a low standard of significance at the 5 per cent. point, and ignore entirely all results which fail to reach this level. A scientific fact should be regarded as experimentally established only if a properly designed experiment *rarely fails* to give this level of significance. The very high

α and errors

- Hypothesis test ends with decision:
  - reject null hypothesis
  - do not reject null hypothesis.
- but decision may be wrong:

	Decision	
Truth	**Do not reject**	**reject null**
Null true	Correct	Type I error
Null false	Type II error	Correct

- Either type of error is bad, but for now focus on controlling Type I error: write $\alpha =$ P(type I error), and devise test so that α small, typically 0.05.
- That is, **if null hypothesis true**, have only small chance to reject it (which would be a mistake).
- Worry about type II errors later (when we consider power of test).

One sample: the Blue Jays attendances

- The Toronto Blue Jays' average home attendance in part of 2015 season was 25,070 (up to May 27 2015, from baseball-reference.com).
- Does that mean the attendance at every game was exactly 25,070? Certainly not. Actual attendance depends on many things, eg.:
  - how well the Jays are playing
  - the opposition
  - day of week
  - weather
  - random chance

Reading the attendances

...as a `.csv` file:

```
my_url <- "http://ritsokiguess.site/datafiles/jays15-home.csv"
jays <- read_csv(my_url)
jays
```

```
# A tibble: 25 x 21
     row  game date   box    team  venue opp   result  runs Oppruns innings
   <dbl> <dbl> <chr>  <chr>  <chr> <lgl> <chr> <chr>  <dbl>   <dbl>   <dbl>
 1    82     7 Monda~ boxs~  TOR   NA    TBR   L          1       2      NA
 2    83     8 Tuesd~ boxs~  TOR   NA    TBR   L          2       3      NA
 3    84     9 Wedne~ boxs~  TOR   NA    TBR   W         12       7      NA
 4    85    10 Thurs~ boxs~  TOR   NA    TBR   L          2       4      NA
 5    86    11 Frida~ boxs~  TOR   NA    ATL   L          7       8      NA
 6    87    12 Satur~ boxs~  TOR   NA    ATL   W-wo       6       5      10
 7    88    13 Sunda~ boxs~  TOR   NA    ATL   L          2       5      NA
 8    89    14 Tuesd~ boxs~  TOR   NA    BAL   W         13       6      NA
 9    90    15 Wedne~ boxs~  TOR   NA    BAL   W          4       2      NA
10    91    16 Thurs~ boxs~  TOR   NA    BAL   W          7       6      NA
# i 15 more rows
# i 9 more variables: position <dbl>, gb <chr>, winner <chr>, loser <chr>,
#   save <chr>, `game time` <time>, Daynight <chr>, attendance <dbl>
```

Another way

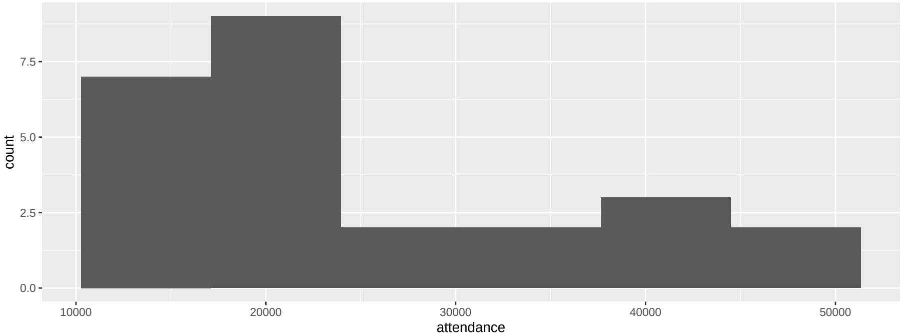
- This is a "big" data set: only 25 observations, but a lot of *variables*.
- To see the first few values in all the variables, can also use `glimpse`:

```
glimpse(jays)
```

```
Rows: 25
Columns: 21
$ row        <dbl> 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96~
$ game       <dbl> 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 27, 28, 29, 30, 31, 3~
$ date       <chr> "Monday, Apr 13", "Tuesday, Apr 14", "Wednesday, Apr 15", ~
$ box        <chr> "boxscore", "boxscore", "boxscore", "boxscore", "boxscore"~
$ team       <chr> "TOR", "TOR", "TOR", "TOR", "TOR", "TOR", "TOR", "TOR", "T~
$ venue      <lgl> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA~
$ opp        <chr> "TBR", "TBR", "TBR", "TBR", "ATL", "ATL", "ATL", "BAL", "B~
$ result     <chr> "L", "L", "W", "L", "L", "W-wo", "L", "W", "W", "W", "W", ~
$ runs       <dbl> 1, 2, 12, 2, 7, 6, 2, 13, 4, 7, 3, 3, 5, 7, 7, 3, 10, 2, 3~
$ Oppruns    <dbl> 2, 3, 7, 4, 8, 5, 5, 6, 2, 6, 1, 6, 1, 0, 1, 6, 6, 3, 4, 4~
$ innings    <dbl> NA, NA, NA, NA, NA, 10, NA, NA, NA, NA, NA, NA, NA, NA, NA~
$ wl         <chr> "4-3", "4-4", "5-4", "5-5", "5-6", "6-6", "6-7", "7-7", "8~
$ position   <dbl> 2, 3, 2, 4, 4, 3, 4, 2, 2, 1, 4, 5, 3, 3, 3, 3, 5, 5, 5, 5~
$ gb         <chr> "1", "2", "1", "1.5", "2.5", "1.5", "1.5", "2", "1", "Tied~
$ winner     <chr> "Odorizzi", "Geltz", "Buehrle", "Archer", "Martin", "Cecil~
$ loser      <chr> "Dickey", "Castro", "Ramirez", "Sanchez", "Cecil", "Marimo~
$ save       <chr> "Boxberger", "Jepsen", NA, "Boxberger", "Grilli", NA, "Gri~
```

Attendance histogram

```
ggplot(jays, aes(x = attendance)) + geom_histogram(bins = 6)
```



Comments

- Attendances have substantial variability, ranging from just over 10,000 to around 50,000.
- Distribution somewhat skewed to right (but no outliers).
- These are a sample of "all possible games" (or maybe "all possible games played in April and May"). What can we say about mean attendance in all possible games based on this evidence?

CI for mean attendance

- t.test function does CI and test. Look at CI first:

```
t.test(jays$attendance)
```

```

	One Sample t-test

data:  jays$attendance
t = 11.389, df = 24, p-value = 3.661e-11
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 20526.82 29613.50
sample estimates:
mean of x 
 25070.16 
```

- From 20,500 to 29,600.

Or, 90% CI

- by including a value for conf.level:

```
t.test(jays$attendance, conf.level = 0.90)
```

```

	One Sample t-test

data:  jays$attendance
t = 11.389, df = 24, p-value = 3.661e-11
alternative hypothesis: true mean is not equal to 0
90 percent confidence interval:
 21303.93 28836.39
sample estimates:
mean of x 
 25070.16 
```

- From 21,300 to 28,800. (Shorter, as it should be.)

Comments

- Need to say "column attendance within data frame `jays`" using `$`.
- 95% CI from about 20,000 to about 30,000.
- Not estimating mean attendance well at all!
- Generally want confidence interval to be shorter, which happens if:
  - SD smaller
  - sample size bigger
  - confidence level smaller
- Last one is a cheat, really, since reducing confidence level increases chance that interval won't contain pop. mean at all!

Another way to access data frame columns

```
with(jays, t.test(attendance))
```

```

	One Sample t-test

data:  attendance
t = 11.389, df = 24, p-value = 3.661e-11
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 20526.82 29613.50
sample estimates:
mean of x 
 25070.16 
```

Hypothesis testing for Blue Jays attendances

- Previous year's mean attendance was 29,327, so test to see whether the mean is different from that in any way (two-sided test):

```
t.test(jays$attendance, mu = 29327)
```

```

    One Sample t-test

data:  jays$attendance
t = -1.9338, df = 24, p-value = 0.06502
alternative hypothesis: true mean is not equal to 29327
95 percent confidence interval:
 20526.82 29613.50
sample estimates:
mean of x
 25070.16
```

- See test statistic -1.93, P-value 0.065.

Another example: learning to read

- You devised new method for teaching children to read.
- Guess it will be more effective than current methods.
- To support this guess, collect data.
- Want to generalize to "all children in Canada".
- So take random sample of all children in Canada.
- Or, argue that sample you actually have is "typical" of all children in Canada.
- Randomization (1): whether or not a child in sample or not has nothing to do with anything else about that child.
- Randomization (2): randomly choose whether each child gets new reading method (t) or standard one (c).

Reading in data

- File at http://ritsokiguess.site/datafiles/drp.txt.
- Proper reading-in function is `read_delim` (check file to see)
- Read in thus:

```
my_url <- "http://ritsokiguess.site/datafiles/drp.txt"
kids <- read_delim(my_url," ")
```

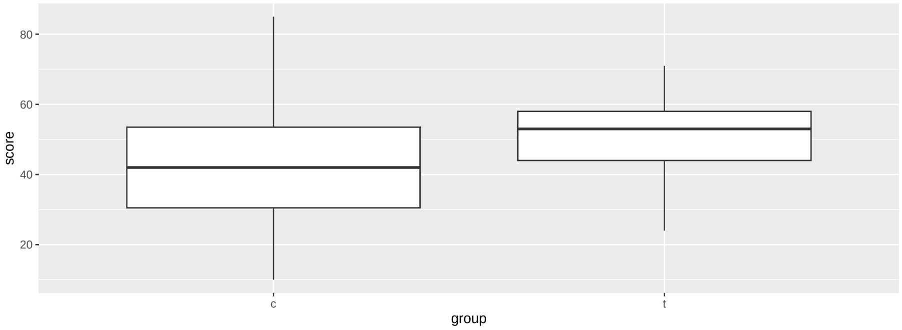
The data (some)

```
kids
```

```
# A tibble: 44 x 2
   group score
   <chr> <dbl>
 1 t        24
 2 t        61
 3 t        59
 4 t        46
 5 t        43
 6 t        44
 7 t        52
 8 t        43
 9 t        58
10 t        67
# i 34 more rows
```

Boxplots

```
ggplot(kids, aes(x = group, y = score)) + geom_boxplot()
```



Two kinds of two-sample t-test

- Do the two groups have same spread (SD, variance)?
  - If yes (shaky assumption here), can use pooled t-test.
  - If not, use Welch-Satterthwaite t-test (safe).
- Pooled test derived in STAB57 (easier to derive, but assumes equal variances).
- Welch-Satterthwaite does not assume equality of variances.
- Assess (approx) equality of spreads using boxplot.

The (Welch-Satterthwaite) t-test

- `c` (control) before `t` (treatment) alphabetically, so proper alternative is "less".
- R does Welch-Satterthwaite test by default
- Answer to "does the new reading program really help?"
- (in a moment) how to get R to do pooled test?

Welch-Satterthwaite

```r
t.test(score ~ group, data = kids, alternative = "less")
```

```
    Welch Two Sample t-test

data:  score by group
t = -2.3109, df = 37.855, p-value = 0.01319
alternative hypothesis: true difference in means between group
95 percent confidence interval:
      -Inf -2.691293
sample estimates:
mean in group c mean in group t
       41.52174        51.47619
```

The pooled t-test

```
t.test(score ~ group, data = kids,
       alternative = "less", var.equal = TRUE)
```

```

    Two Sample t-test

data:  score by group
t = -2.2666, df = 42, p-value = 0.01431
alternative hypothesis: true difference in means between grou
95 percent confidence interval:
      -Inf -2.567497
sample estimates:
mean in group c mean in group t
       41.52174        51.47619
```

Two-sided test; CI

- To do 2-sided test, leave out `alternative`:

```
t.test(score ~ group, data = kids)
```

```

	Welch Two Sample t-test

data:  score by group
t = -2.3109, df = 37.855, p-value = 0.02638
alternative hypothesis: true difference in means between grou
95 percent confidence interval:
 -18.67588  -1.23302
sample estimates:
mean in group c mean in group t 
       41.52174        51.47619 
```

Comments:

- P-values for pooled and Welch-Satterthwaite tests very similar (even though the pooled test seemed inferior): 0.013 vs. 0.014.
- Two-sided test also gives CI: new reading program increases average scores by somewhere between about 1 and 19 points.
- Confidence intervals inherently two-sided, so do 2-sided test to get them.

Pain relief

Some data:

subject	druga	drugb
1	2.0	3.5
2	3.6	5.7
3	2.6	2.9
4	2.6	2.4
5	7.3	9.9
6	3.4	3.3
7	14.9	16.7
8	6.6	6.0
9	2.3	3.8
10	2.0	4.0
11	6.8	9.1
12	8.5	20.9

Matched pairs data

- Data are comparison of 2 drugs for effectiveness at reducing pain.
  - 12 subjects (cases) were arthritis sufferers
  - Response is #hours of pain relief from each drug.
- In reading example, each child tried only one reading method.
- But here, each subject tried out both drugs, giving us two measurements.
  - Possible because, if you wait long enough, one drug has no influence over effect of other.
  - Advantage: focused comparison of drugs. Compare one drug with another on same person, removes a lot of variability due to differences between people.
  - Matched pairs, requires different analysis.
- Design: randomly choose 6 of 12 subjects to get drug A first, other 6 get drug B first.

Paired t test: reading the data

Values aligned in columns:

```
my_url <- "http://ritsokiguess.site/datafiles/analgesic.txt"
pain <- read_table(my_url)
```

The data

```
pain
```

```
# A tibble: 12 x 3
   subject druga drugb
     <dbl> <dbl> <dbl>
 1       1   2     3.5
 2       2   3.6   5.7
 3       3   2.6   2.9
 4       4   2.6   2.4
 5       5   7.3   9.9
 6       6   3.4   3.3
 7       7  14.9  16.7
 8       8   6.6   6  
 9       9   2.3   3.8
10      10   2     4  
11      11   6.8   9.1
12      12   8.5  20.9
```

Paired *t*-test

```
with(pain, t.test(druga, drugb, paired = T))
```

```
    Paired t-test

data:  druga and drugb
t = -2.1677, df = 11, p-value = 0.05299
alternative hypothesis: true mean difference is not equal to 0
95 percent confidence interval:
 -4.29941513  0.03274847
sample estimates:
mean difference
      -2.133333
```

- P-value is 0.053.
- Not quite evidence of difference between drugs.

t-testing the differences

- Likewise, you can calculate the differences yourself and do a 1-sample t-test on them.
- First calculate a column of differences:

```
(pain %>% mutate(diff=druga-drugb) -> pain)
```

```
# A tibble: 12 x 4
   subject druga drugb    diff
     <dbl> <dbl> <dbl>   <dbl>
 1       1   2     3.5  -1.5
 2       2   3.6   5.7  -2.1
 3       3   2.6   2.9  -0.300
 4       4   2.6   2.4   0.200
 5       5   7.3   9.9  -2.6
 6       6   3.4   3.3   0.100
 7       7  14.9  16.7  -1.80
 8       8   6.6   6     0.600
 9       9   2.3   3.8  -1.5
10      10   2     4    -2
11      11   6.8   9.1  -2.3
12      12   8.5  20.9 -12.4
```

t-test on the differences

- then throw them into t.test, testing that the mean is zero, with same result as before:

```
with(pain, t.test(diff, mu=0))
```

```

	One Sample t-test

data:  diff
t = -2.1677, df = 11, p-value = 0.05299
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -4.29941513  0.03274847
sample estimates:
mean of x 
-2.133333 
```