

Two group intervals

Statistical Inference

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Independent group t confidence intervals

- Suppose that we want to compare the mean blood pressure between two groups in a randomized trial; those who received the treatment to those who received a placebo
- · We cannot use the paired t test because the groups are independent and may have different sample sizes
- · We now present methods for comparing independent groups

Notation

- · Let X_1, \ldots, X_{n_x} be iid $N(\mu_x, \sigma^2)$
- · Let Y_1,\ldots,Y_{n_y} be iid $N(\mu_y,\sigma^2)$
- · Let \bar{X} , \bar{Y} , S_x , S_y be the means and standard deviations
- · Using the fact that linear combinations of normals are again normal, we know that $\bar{Y}-\bar{X}$ is also normal with mean $\mu_y-\mu_x$ and variance $\sigma^2(\frac{1}{n_x}+\frac{1}{n_y})$
- The pooled variance estimator

$$S_p^2 = \{(n_x-1)S_x^2 + (n_y-1)S_y^2\}/(n_x+n_y-2)$$

is a good estimator of σ^2

Note

- The pooled estimator is a mixture of the group variances, placing greater weight on whichever has a larger sample size
- · If the sample sizes are the same the pooled variance estimate is the average of the group variances
- The pooled estimator is unbiased

$$egin{split} E[S_p^2] &= rac{(n_x-1)E[S_x^2] + (n_y-1)E[S_y^2]}{n_x+n_y-2} \ &= rac{(n_x-1)\sigma^2 + (n_y-1)\sigma^2}{n_x+n_y-2} \end{split}$$

· The pooled variance estimate is independent of $\bar{Y}-\bar{X}$ since S_x is independent of \bar{X} and S_y is independent of \bar{Y} and the groups are independent

Result

- The sum of two independent Chi-squared random variables is Chi-squared with degrees of freedom equal to the sum of the degrees of freedom of the summands
- · Therefore

$$(n_x + n_y - 2)S_p^2/\sigma^2 = (n_x - 1)S_x^2/\sigma^2 + (n_y - 1)S_y^2/\sigma^2$$
 $= \chi_{n_x - 1}^2 + \chi_{n_y - 1}^2$
 $= \chi_{n_x + n_y - 2}^2$

Putting this all together

· The statistic

To test differences in means:

$$\frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{\sigma \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} \sqrt{\frac{(n_x + n_y - 2)S_p^2}{(n_x + n_y - 2)\sigma^2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)}{S_p \left(\frac{1}{n_x} + \frac{1}{n_y}\right)^{1/2}} = \frac{\bar{Y} - \bar{X} - (\mu_y - \mu_x)$$

is a standard normal divided by the square root of an independent Chi-squared divided by its degrees of freedom

- · Therefore this statistic follows Gosset's t distribution with $n_x + n_y 2$ degrees of freedom
- Notice the form is (estimator true value) / SE

Confidence interval

- Therefore a (1-lpha) imes 100% confidence interval for $\mu_y-\mu_x$ is

$$ar{Y} - ar{X} \pm t_{n_x + n_y - 2, 1 - lpha/2} \, S_p \Bigg(rac{1}{n_x} + rac{1}{n_y} \Bigg)^{1/2}$$

- · Remember this interval is assuming a constant variance across the two groups
- · If there is some doubt, assume a different variance per group, which we will discuss later

Example

Based on Rosner, Fundamentals of Biostatistics

- · Comparing SBP for 8 oral contraceptive users versus 21 controls
- \cdot $ar{X}_{OC}=132.86$ mmHg with $s_{OC}=15.34$ mmHg
- $\cdot \; ar{X}_C = 127.44 \; ext{mmHg} \; ext{with} \; s_C = 18.23 \; ext{mmHg}$
- · Pooled variance estimate

```
sp <- sqrt((7 * 15.34^2 + 20 * 18.23^2) / (8 + 21 - 2))
132.86 - 127.44 + c(-1, 1) * qt(.975, 27) * sp * (1 / 8 + 1 / 21)^.5
```

```
[1] -9.521 20.361 contains 0 >> difference can be attributed to chance
```

```
data(sleep)
x1 <- sleep$extra[sleep$group == 1]
x2 <- sleep$extra[sleep$group == 2]
n1 <- length(x1)
n2 <- length(x2)
sp <- sqrt( ((n1 - 1) * sd(x1)^2 + (n2-1) * sd(x2)^2) / (n1 + n2-2))
md <- mean(x1) - mean(x2)
semd <- sp * sqrt(1 / n1 + 1/n2)
md + c(-1, 1) * qt(.975, n1 + n2 - 2) * semd</pre>
```

```
[1] -3.3639 0.2039 0 included >> no differences
```

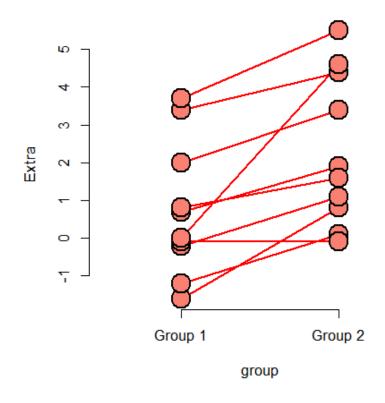
```
t.test(x1, x2, paired = FALSE, var.equal = TRUE)$conf
```

```
[1] -3.3639 0.2039
attr(,"conf.level")
[1] 0.95
```

```
t.test(x1, x2, paired = TRUE)$conf
```

[1] -2.4599 -0.7001

Ignoring pairing



Wenn man die Paare nicht beruecksichtigt, scheinen die beiden Gruppen gleich zu sein.

Aber wenn man das Repeated measurement beachtet, wird die Varianz viel kleiner (visuell: Parallelitaet der Linien)

Unequal variances

Under unequal variances

$$ar{Y} - ar{X} \sim N \Bigg(\mu_y - \mu_x, rac{s_x^2}{n_x} + rac{\sigma_y^2}{n_y} \Bigg)$$

· The statistic

$$rac{ar{Y}-ar{X}-\left(\mu_y-\mu_x
ight)}{\left(rac{s_x^2}{n_x}+rac{\sigma_y^2}{n_y}
ight)^{1/2}}$$

approximately follows Gosset's t distribution with degrees of freedom equal to

$$rac{\left(S_{x}^{2}/n_{x}+S_{y}^{2}/n_{y}
ight)^{2}}{\left(rac{S_{x}^{2}}{n_{x}}
ight)^{2}/(n_{x}-1)+\left(rac{S_{y}^{2}}{n_{y}}
ight)^{2}/(n_{y}-1)}$$

just a number,
plug it in (not much
intuition in this
formula)

Example

- · Comparing SBP for 8 oral contraceptive users versus 21 controls
- $\cdot \; ar{X}_{OC} = 132.86 \; ext{mmHg} \; ext{with} \; s_{OC} = 15.34 \; ext{mmHg}$
- $\cdot \; ar{X}_C = 127.44 \; ext{mmHg} \; ext{with} \; s_C = 18.23 \; ext{mmHg}$
- $\cdot \ df = 15.04$, $t_{15.04,.975} = 2.13$
- Interval

$$132.86 - 127.44 \pm 2.13 \left(rac{15.34^2}{8} + rac{18.23^2}{21}
ight)^{1/2} = [-8.91, 19.75]$$

• In R, t.test(..., var.equal = FALSE)

Comparing other kinds of data

- For binomial data, there's lots of ways to compare two groups
 - Relative risk, risk difference, odds ratio.
 - Chi-squared tests, normal approximations, exact tests.
- For count data, there's also Chi-squared tests and exact tests.
- We'll leave the discussions for comparing groups of data for binary and count data until covering glms in the regression class.
- In addition, Mathematical Biostatistics Boot Camp 2 covers many special cases relevant to biostatistics.