

# STAT234: Lecture 6 - Confidence Intervals

Kushal K. Dey

## A Romantic Experiment !

Most people are right-handed and even the right eye is dominant for most people. Molecular biologists have suggested that late-stage human embryos tend to turn their heads to the right. German bio-psychologist Onur Güntürkün conjectured that this tendency to turn to the right manifests itself in other ways as well, so he studied kissing couples to see if both people tended to lean to their right more often than to their left (and if so, how strong the tendency is). He and his researchers observed couples from age 13 to 70 in public places such as airports, train stations, beaches, and parks in the United States, Germany, and Turkey. They were careful not to include couples who were holding objects such as luggage that might have affected which direction they turned. In total, 124 kissing pairs were observed with 80 couples leaning right (*Nature*, 2003).

You and your boss !



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Then I cheat again

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$$Pr [-1.414214 < Z < 0.942809] \approx 0.7484612$$

So, I am 75% confident that the actual  $p$  lies in the interval

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- ▶ **Boss:** What do you mean kind of?
- ▶ **You:** Well I cheated in the middle and used replace  $p$  by  $\hat{p}$  and said essentially

$$\sqrt{n} \frac{\hat{p} - p}{\sqrt{\hat{p}(1 - \hat{p})}} \approx N(0, 1)$$

instead of

$$\sqrt{n} \frac{\hat{p} - p}{\sqrt{p(1 - p)}} \sim N(0, 1)$$

which was the correct statement.

- ▶ **Boss:** I can't write *kind of* in my report. Can't you give me a more exact interval?

- ▶ **You:** I can say exactly that

$$\sqrt{n} \frac{\hat{p} - p}{\sqrt{\hat{p}(1 - \hat{p})}} \sim t_{n-1}$$

where  $t_{n-1}$  is another distribution (called *Student's t* distribution).

- ▶ **Boss:** Where did you come up with that distribution from?
- ▶ **You:** Okay let me explain.

## How is the $T$ -distribution Related to Estimation?

Let  $X_1, X_2, \dots, X_n$  be a random sample from a  $N(\mu, \sigma^2)$  popn.

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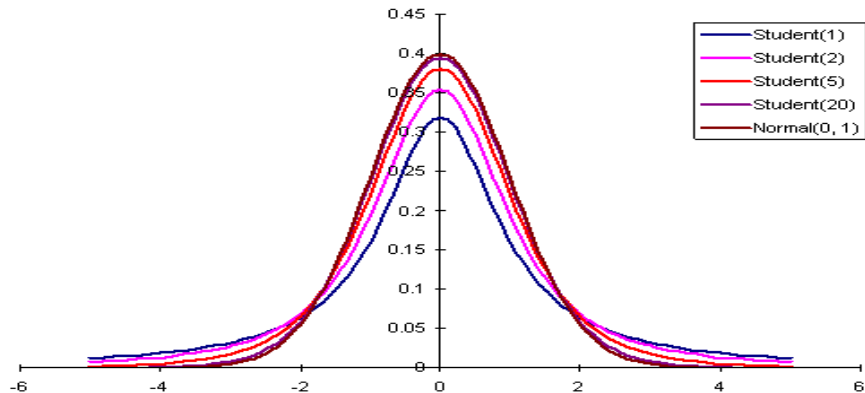
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The t-distribution is nice because it is well-documented, meaning there is a table for  $t_{n-1}$  of the probabilities just as there is a table for  $N(0, 1)$  as you must be familiar with by now.

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$$95 \% \text{ CI for } p(t) : [0.554, 0.725]$$

## t distribution

A random variable  $T \sim t_{n-1}$  distribution

$$Pr [-1.979 < T_{(n-1)=123} < 1.979] = 0.95$$

We know

$$Pr [-1.959 < Z < 1.959] = 0.95$$

$$Pr[\hat{p} - 1.98 \frac{\sqrt{\hat{p}(1 - \hat{p})}}{\sqrt{n}} < p < \hat{p} + 1.98 \frac{\sqrt{\hat{p}(1 - \hat{p})}}{\sqrt{n}}] = 0.95$$

$$95 \% CI \text{ for } p(t) : [0.554, 0.725]$$

$$95 \% CI \text{ for } p(z) : [0.56, 0.72]$$



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# Hypothesis testing

- ▶ **Boss:** Okay I am reporting that I am 95% confident that  $p$  lies in  $[0.5685, 1]$ .
- ▶ **You:** Sure.
- ▶ **Boss:** So we can say now that there is effect of leaning on right with kissing .
- ▶ **You:** Yes you can. Thats because the 95% CI does not contain 0.5.
- ▶ **Boss:** Ohh, how did you work that out?

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## General idea: Bootstrapping/ Resampling

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We know if  $n$  is large, then this sampling distribution is normal, and

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If  $n$  is not so large though, normality is not a good assumption for sampling distribution.

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You can use this technique for any parameter of interest!



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- ▶ The proportion gives you the estimated p-value.
- ▶ For CI, find the region that contains 95% of the  $T$  in the Bootstrap samples (for 2-sided the region between the 2.5 th quantile and 97.5 th quantile of the Bootstrap  $T$  samples, for 1-sided the region beyond 5 th quantile)

You can use this technique to test your hypothesis or build

```
obs.samp <- c(rep(1,80), rep(0, 44));  
bootstrap_counts <- replicate(1000, sum(sample(obs.samp, replace  
summary(bootstrap_counts)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
65.0	77.0	80.0	80.2	84.0	95.0

```
bootstrap_prop <- bootstrap_counts/124;  
## 2-sided
```

```
quantile(bootstrap_prop, 0.025)
```

```
2.5%  
0.5645
```

```
quantile(bootstrap_prop, 0.975)
```

```
97.5%  
0.7258
```

```
## 1-sided  
quantile(bootstrap_prop, 0.05)
```

```
5%  
0.5806
```



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- ▶ To be continued....

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	$H_0$ is true	$H_a$ is true
Reject $H_0$	Type I error $\alpha$	Correct decision $1 - \beta = \pi$
Not reject $H_0$	Correct decision $1 - \alpha$	Type II error $\beta$

- ▶  $\alpha = P(\text{Type I Error}) = P(\text{Reject } H_0 | H_0 \text{ is true}) =$   
Significance level
- ▶  $\beta = P(\text{Type II Error}) = P(\text{Not reject } H_0 | H_a \text{ is true})$
- ▶ We also define **power** as

$$\begin{aligned}
 \pi &= 1 - \beta \\
 &= P(\text{Reject } H_0 | H_a \text{ is true}) \\
 &= \text{Ability to Detect the Alternative Hypothesis}
 \end{aligned}$$

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$$\alpha = Pr(\text{Reject } H_0 | p = 0.5)$$

Assume we reject  $H_0$  if p-value is  $< 0.05$ , this means if true  $p$  under null hypothesis  $H_0$  does not lie in the 95% confidence interval, put  $\hat{p} = 0.64$ ,  $p = 0.5$ ,

$$Pr \left[ p - 1.96 \frac{\sqrt{p(1-p)}}{\sqrt{n}} < \hat{p} < p + 1.96 \frac{\sqrt{p(1-p)}}{\sqrt{n}} \right] = [0.552, 0.728]$$

$p = 0.5$  does not belong in this