Voleria, Jeffrey

Stat 145, Tue 19-Oct-2021 -- Tue 19-Oct-2021
Biostatistics
Spring 2021

Binary categorical vars? Is Perocrat? X same as p.

Tuesday, October 19th 2021 -----Due:: WW NormalDists due at 11 pm ------Tuesday, October 19th 2021 ------Wk 8, Tu

Topic:: Inference for proportions Read:: Lock5 6.1-6.3

 $\widetilde{\chi} = \frac{1}{n} \left(X_1 + X_2 + \dots + X_n \right)$

Central Limit Theorem 5.2

In summary, here is the take-away from the **Central Limit Theorem**.

Suppose you have a random sample of size *n* that is either

- i.i.d., or
- an SRS, with the sample size *n* being no more than 10% of the size of the population.

In the case that

- 1. the variable under consideration is quantitative, having population mean μ and standard deviation σ , then the sampling distribution for the sample mean \overline{X} is approximately Norm $(\mu, \sigma / \sqrt{n})$ for *n* large enough.
- 2. the variable under consideration is binary categorical, having population proportion p, then the sampling distribution for the sample proportion \hat{p} is approximately Norm $(p, \sqrt{p(1-p)/n})$ for n large enough.

Since

- null distributions
- randomization distributions
- bootstrap distributions

are all specialized versions of sampling distributions, then so long as the sample statistic in question is the sample's *mean* \overline{X} or the sample *proportion* \hat{p} , we can expect the CLT to apply to these as well.

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Explorations using apps at
 https://shiny.calvin.edu:3838/scofield/samplingDists/
 https://shiny.calvin.edu:3838/scofield/cltProportions/
or, for means, use script samplingDistOfSampleMeanExperiments.R
 require(mosaic)
  require(gridExtra)
  # Create a population
                                                 # left-skewed
 mypop <- 50 - rexp(10000, rate=.15)</pre>
  #mypop <- rgamma(10000, shape=1.6, rate=.1) # right-skewed</pre>
  #mypop <- rnorm(10000, mean=25, sd=6)</pre>
                                                 # normal
 print(favstats(~mypop))
  # Simulate the sampling distribution for the sample mean
  sampleSize = 20
 manyMeans <- do(5000) * mean(~sample(mypop, sampleSize, replace=TRUE))</pre>
 print(favstats(~mean, data=manyMeans))
 p1 <- gf_density(~mypop) %>% gf_refine(scale_x_continuous(limits=c(0,55)))
 p2 <- gf_density(~mean, data=manyMeans) %>%
    gf_refine(scale_x_continuous(limits=c(0,55)))
 grid.arrange(p1, p2, nrow=2)
```

Ex. | Suppose we ask 450 students if they are left-headed,
47 say yes.
So
$$\hat{p} = \frac{47}{450} = 0.104$$

Q: Car I assume \hat{p} has a nearly normal dist?
 $n\hat{p} = 450 \left(\frac{47}{450}\right) = 47 \ge 10$

$$n(1-\hat{p}) = 450 \left(\frac{450-47}{456}\right) = 403 \ge 10$$

A: Yes. So $\hat{p} \sim Norm\left(p, \sqrt{\frac{p(1-p)}{5n}}\right)$

 $Vsc \hat{p}: SE = \sqrt{\frac{\hat{p}(1-\hat{p})}{n}}$

 $= \sqrt{\frac{(.04)(0.896)}{450}}$

 $= 0.0144$

So, a 95% CI for p





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Chapter 6 overview
 - Scenarios are all ones we have discussed
    univariate (one population)
      proportion arising from binary categorical variable
      mean arising from quantitative variable
    2 populations
      difference of proportions
      difference of means investigated using
        two independent samples
        matched pairs
 - Deferred to later chapter: 2 quant vars
 - Can see Chapter 6 as something of a history lesson
 - Relies entirely on facts from Central Limit Theorem
Sections 1-3: single proportion
Confidence interval construction
 - review how done using bootstrapping (Ch. 3)
 - refining the z*-value
    in past, stats students used tables of Z-scores
      see https://www.math.arizona.edu/~jwatkins/normal-table.pdf
    compare with pnorm(), qnorm() calculations
 - formula for SE
Practice:
 - obtaining critical z* values for
    96% confidence
    90% confidence
    99% confidence
 - doing inference (CI and hypothesis testing) with datasets
    1. in 119 games of rock-paper-scissors, player did rock 66 times
    2. in 70 out of 120 soccer games, the home team won
    3. suppose that 42% of people have 0+ blood. sample shows 65 out of 192
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