# Research Design, Fall 2021

**04: a bit more probability review; sampling; statistical tests**

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general feedback for research reviews

# research reviews, general guidance

Title: homework 1

This paper described A and …

# research reviews, general guidance

~~Title: homework 1~~

Why should I be reading this document? What is the main point?

The authors of ~~this paper~~ described A and …

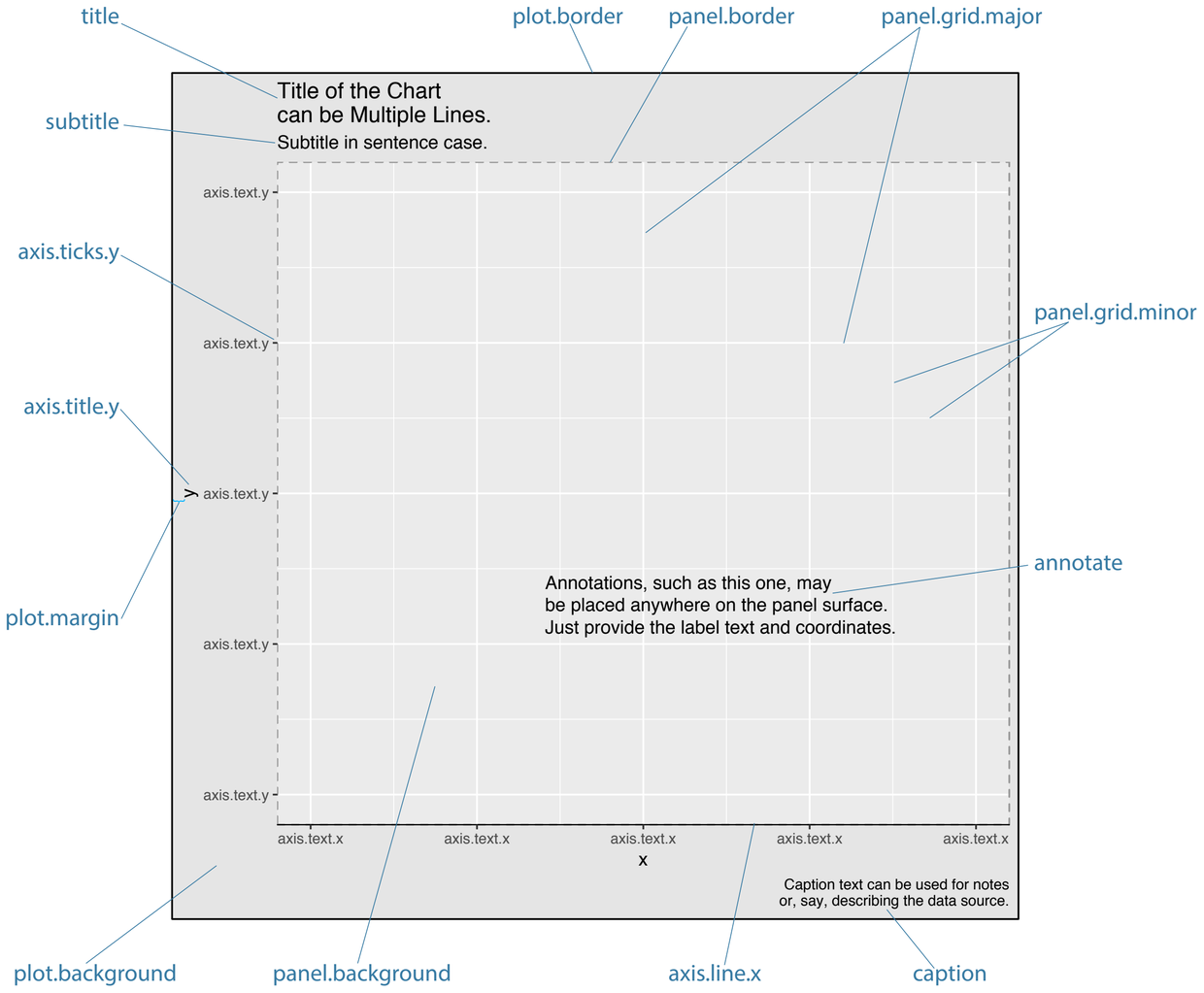
To what paper are you referring? Always introduce new ideas before using language that refers back. And properly cite your sources.

**Also review:**

Harris, Joseph. Rewriting: *How to Do Things with Texts*. Second edition. Logan: Utah State University Press, 2017.

tips on graphics as a tool for exploring and communicating research design

# An aside on graphics to communicate research designs,




# Coding graphic elements, *example in R/GGplot2*

```
# load grammar of graphics
library(ggplot2)

p <-

  # functions for data ink

  ggplot(data = <data>,
         mapping = aes(<aesthetic> = <variable>,
                       <aesthetic> = <variable>,
                       <...> = <...>) +
  geom_<type>(<...>) +
  scale_<mapping>_<type>(<...>) +
  coord_<type>(<...>) +
  facet_<type>(<...>) +
  <...> +

  # functions for non-data ink

  labs(<...>) +
  theme(<...> = <...>) +
  annotate(<...>) +
  <...>
```

```
element_blank()
element_line(<...> = <...>)
element_rect(<...> = <...>)
element_text(<...> = <...>)
```

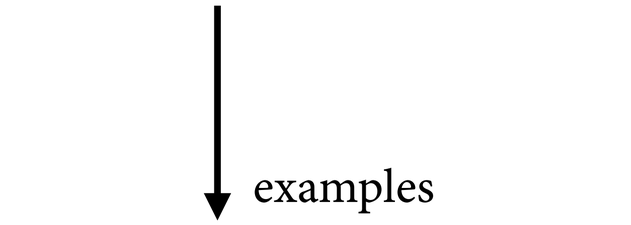
# Drawing functions,

```
stat_function(
  fun  = <function name>,
  args = list(parameter1 = <...>, parameter2 = <...>),
  geom = "<type>",
  ...)
```

a bit more statistics and probability

# R's probability functions, probability density (PDF), cumulative distribution (CDF), quantile, random generation

| | |
|---|---|
| p<probability function name> | probability density function |
| d<probability function name> | cumulative distribution function |
| q<probability function name> | quantile function |
| r<probability function name> | random generation function |




| | |
|---|---|
| *normal* | *negative binomial* |
| *student t* | *gamma* |
| *bernoulli* | *cauchy* |
| *binomial* | *100s more* |
| *poisson* | … |

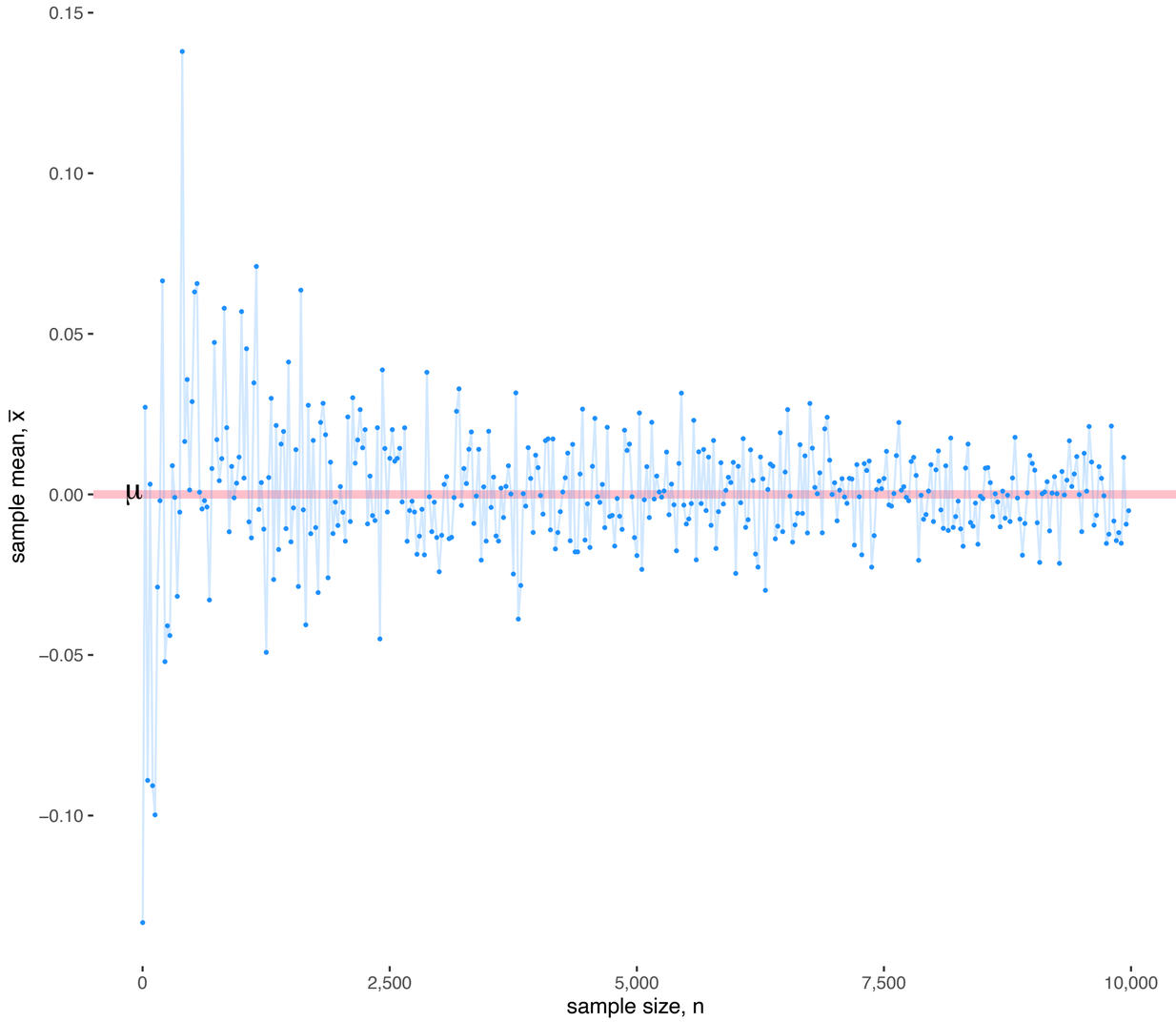
# law of large numbers, as $n \to \infty, \bar{x} \longrightarrow \mu$

```
set.seed(29914)

n     <- seq(1, 10000, by = 25)
mu    <- 0
sigma <- 1
x_bar <- sapply(n, FUN = function(n) {mean( rnorm(n, mu, sigma) )} )
```

```
library(ggplot2); library(ggthemes); library(latex2exp)
theme_set( theme_tufte(base_family = "sans") )

ggplot() +
  scale_x_continuous(labels = scales::comma) +
  geom_hline(yintercept = mu, color = "pink", lwd = 2) +
  geom_point(aes(n, x_bar), size = 0.5, color = "dodgerblue") +
  geom_line(aes(n, x_bar), alpha = 0.2, color = "dodgerblue") +
  annotate("text", 0, mu, hjust = 1, size = 16/.pt, label = TeX("$\\mu$") ) +
  labs(x = "sample size, n", y = TeX("sample mean, $\\bar{x}$"))
```




Experiment with different values of $n$, $\mu$, and $\sigma$ to see how $\bar{x}$ compares with $\mu$.

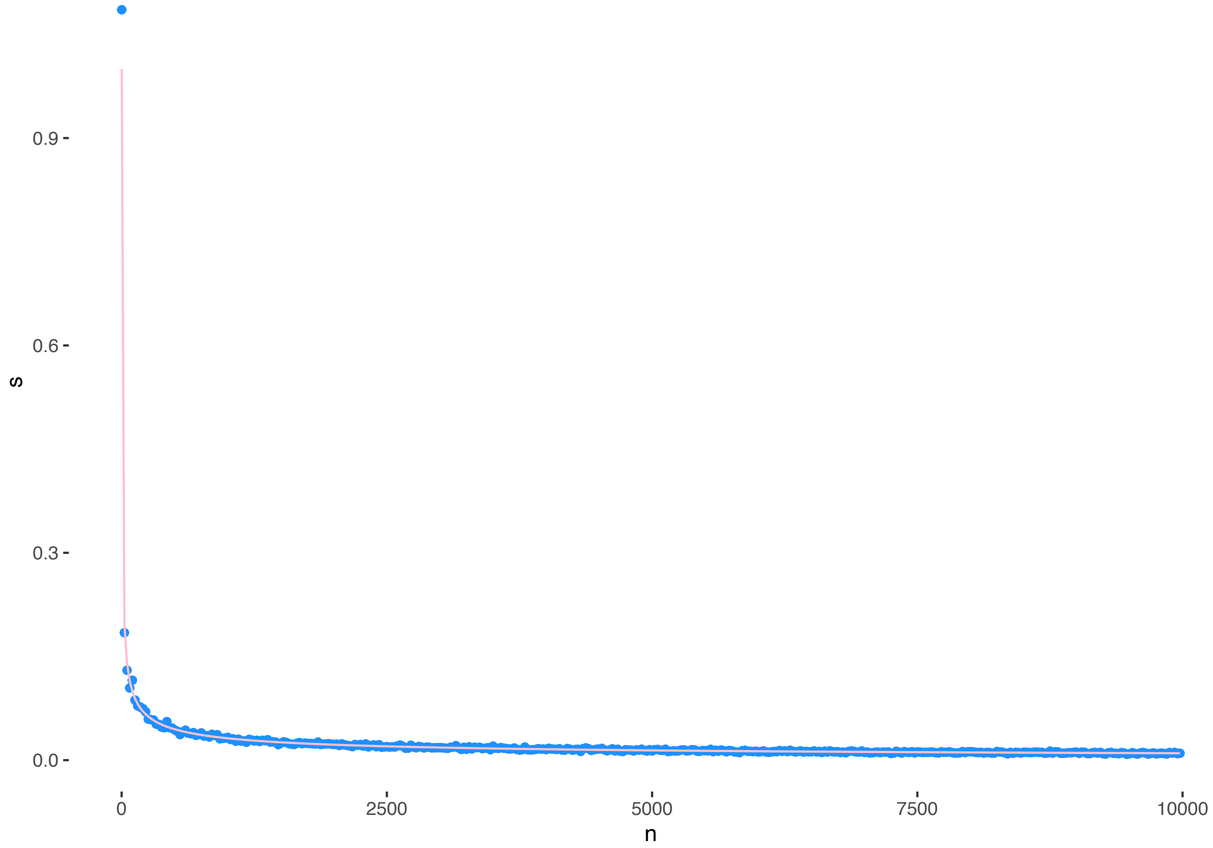
Experiment with different seed values and compare results. How would you describe the uncertainty of $\bar{x}$?

# central limit theorem, standard deviation $s$ of $\bar{x} = \frac{\sigma}{\sqrt{n}}$

```
sample_mean <- function() {
  sapply(n, FUN = function(n) {mean( rnorm(n, mu, sigma) )} )
  }

x_bar <- replicate(1000, sample_mean() )
s <- apply(x_bar, 1, sd)

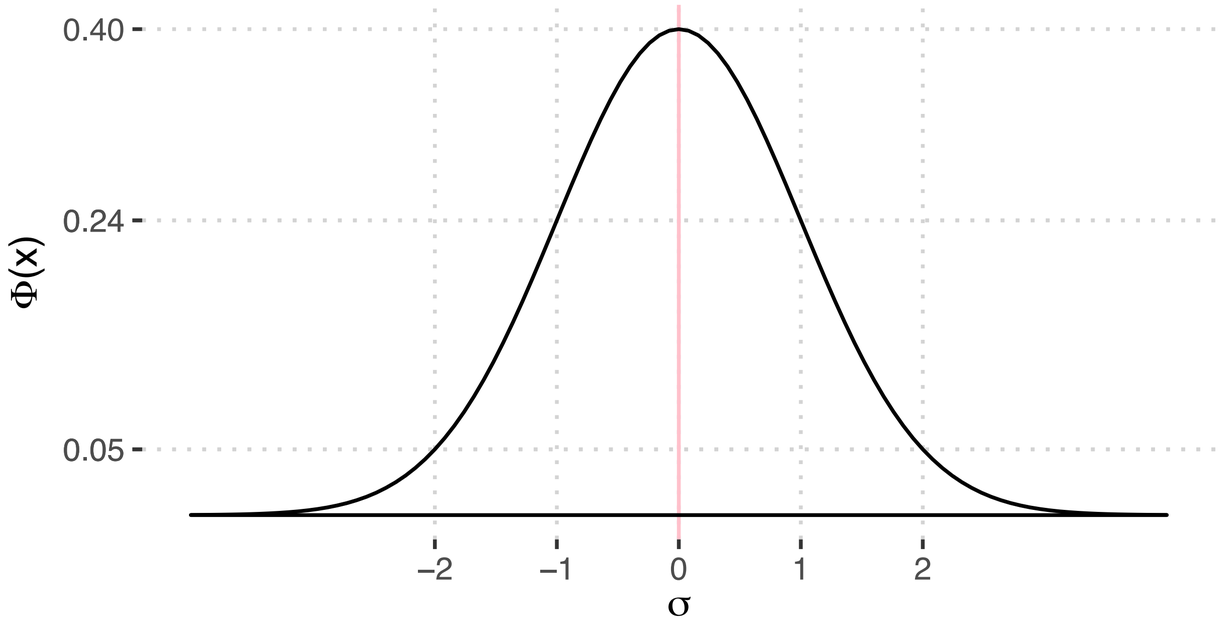
ggplot() +
  geom_point(aes(n, s), color = "dodgerblue") +
  geom_line(aes(n, sigma / sqrt(n) ), color = "pink")
```




Experiment with different values of $\sigma$ and $\mu$ and replications to check the relationships empirically.

# probability, probability density functions v. continuous distribution functions — e.g., the standard normal Φ

```
pdf <- ggplot() +
  theme(panel.grid.major = element_line(color = "lightgray", linetype = "dotted")) +
  scale_x_continuous(breaks = seq(-2, 2)) +
  scale_y_continuous(breaks = dnorm(seq(-2, 2)), labels = scales::comma) +
  geom_vline(xintercept = 0, color = "pink") +
  stat_function(fun  = dnorm,
                args = list(mean = 0, sd = 1),
                geom = "density",
                xlim = c(-4,4)) +
  labs(x = TeX("$\\sigma$"), y = TeX("$\\Phi(x)$"))
```



# probability, probability density functions v. continuous distribution functions — e.g., the standard normal Φ

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pdf <- ggplot() +
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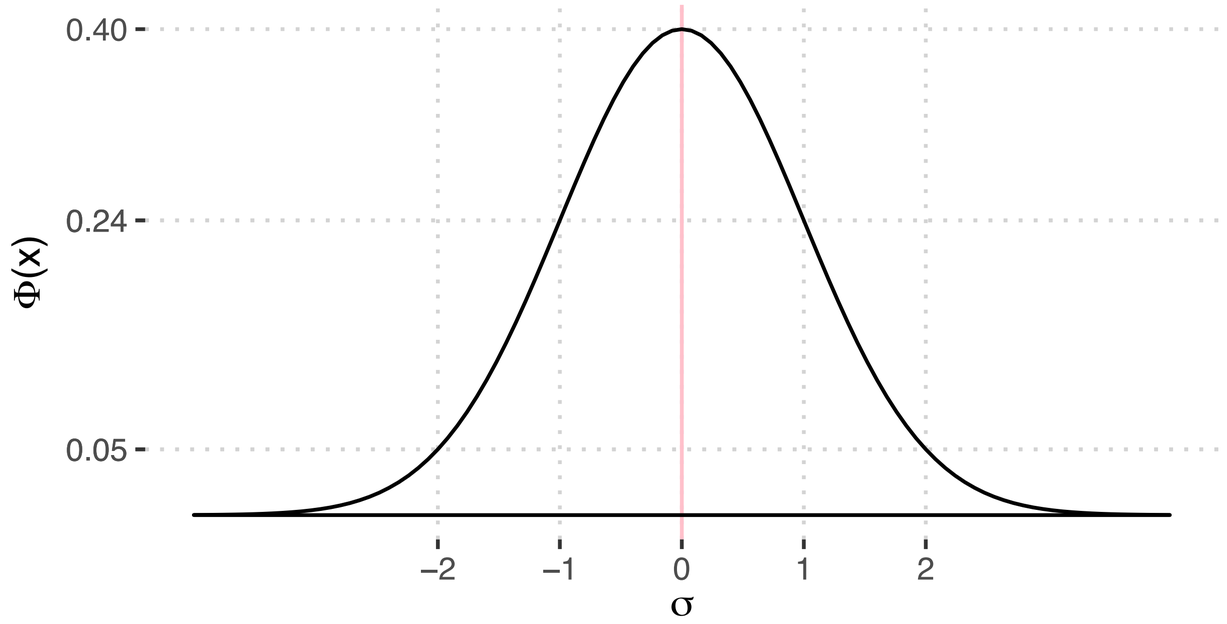
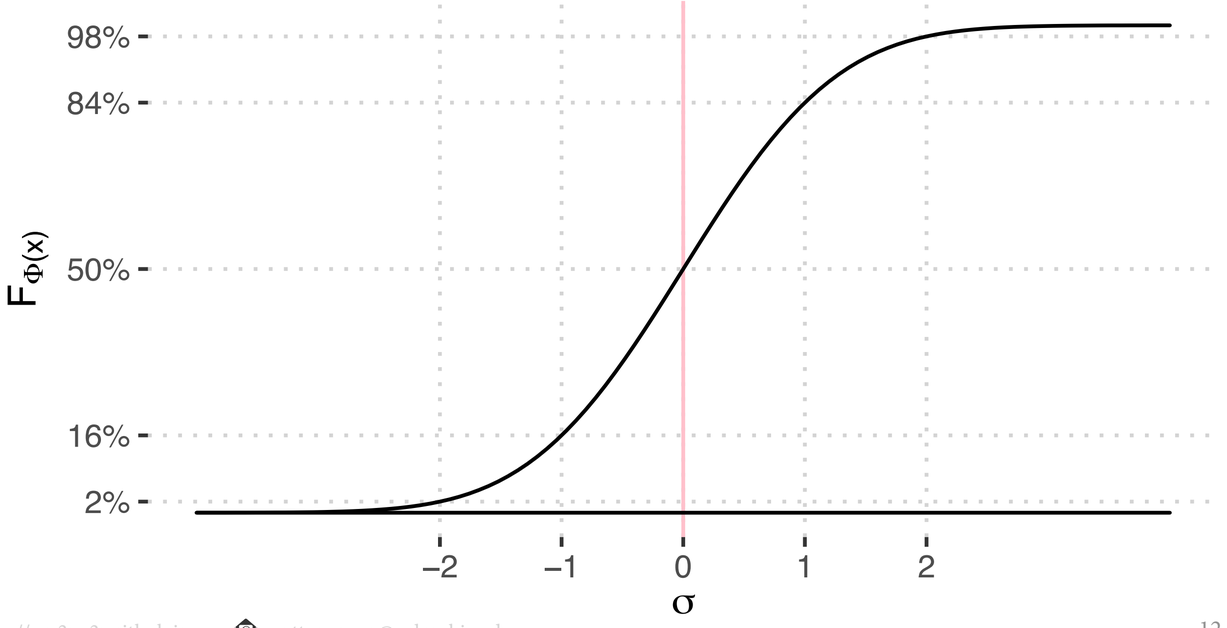
  scale_x_continuous(breaks = seq(-2, 2)) +
  scale_y_continuous(breaks = dnorm(seq(-2, 2)), labels = scales::comma) +
  geom_vline(xintercept = 0, color = "pink") +
  stat_function(fun  = dnorm,
                args = list(mean = 0, sd = 1),
                geom = "density",
                xlim = c(-4,4)) +
  labs(x = TeX("$\\sigma$"), y = TeX("$\\Phi(x)$"))
```




```
cdf <- ggplot() +
  theme(panel.grid.major = element_line(color = "lightgray", linetype = "dotted")) +
  scale_x_continuous(breaks = seq(-2, 2)) +
  scale_y_continuous(breaks = pnorm(seq(-2, 2)),
                     labels = scales::label_percent(accuracy = 1)) +
  geom_vline(xintercept = 0, color = "pink") +
  stat_function(fun  = pnorm,
                args = list(mean = 0, sd = 1),
                geom = "density",
                xlim = c(-4,4)) +
  labs(x = TeX("$\\sigma$"), y = TeX("$F_\\Phi(x)$"))
```



more on sampling

# sampling, a few of many approaches

simple random

convenience

interval

cluster

quota

stratified

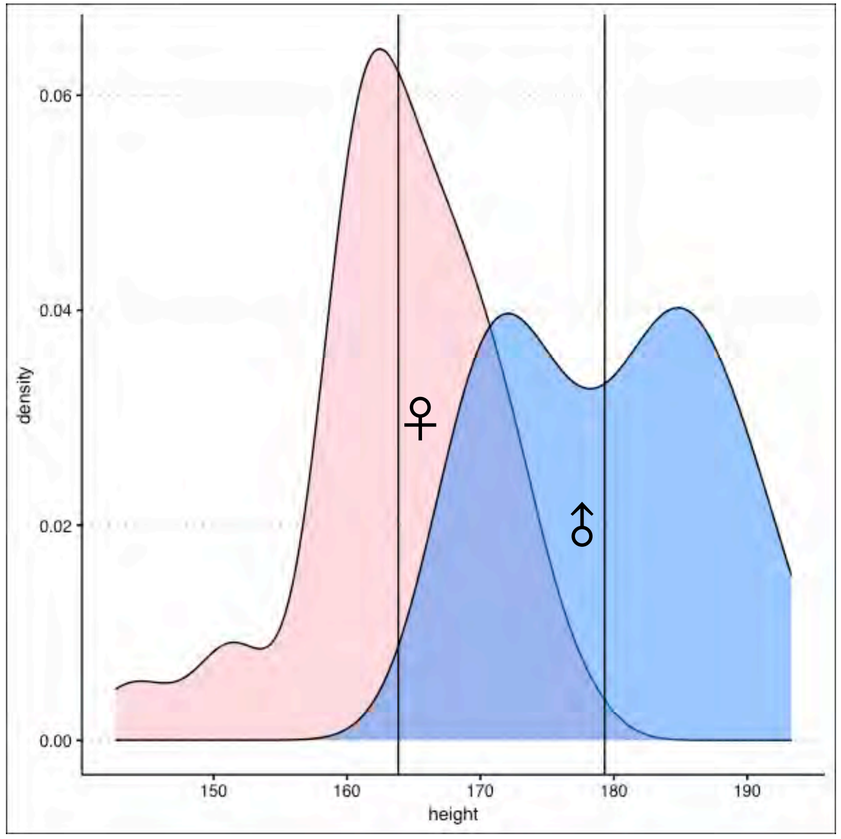
quasi-experimental

statistical tests

## Example, recall our random sample of heights in NYC

Sample mean for both groups,

| male | x_bar |
|---|---|
| FALSE | 163.8453 |
| TRUE | 179.3198 |




How do we decide whether to reject $H_0$ in favor of $H_A$?

$$H_0 : \overline{\text{height}}_{\text{men}} = \overline{\text{height}}_{\text{women}}$$

$$H_A : \overline{\text{height}}_{\text{men}} \neq \overline{\text{height}}_{\text{women}}$$

We need some kind of test!

# A general procedure for a statistical test

Assume an appropriate *probability model* to describe the behavior of the random variable under investigation.

Define a *null* hypothesis and an *alternative* hypothesis that permits meaningful conclusions.

Specify a *test statistic*.

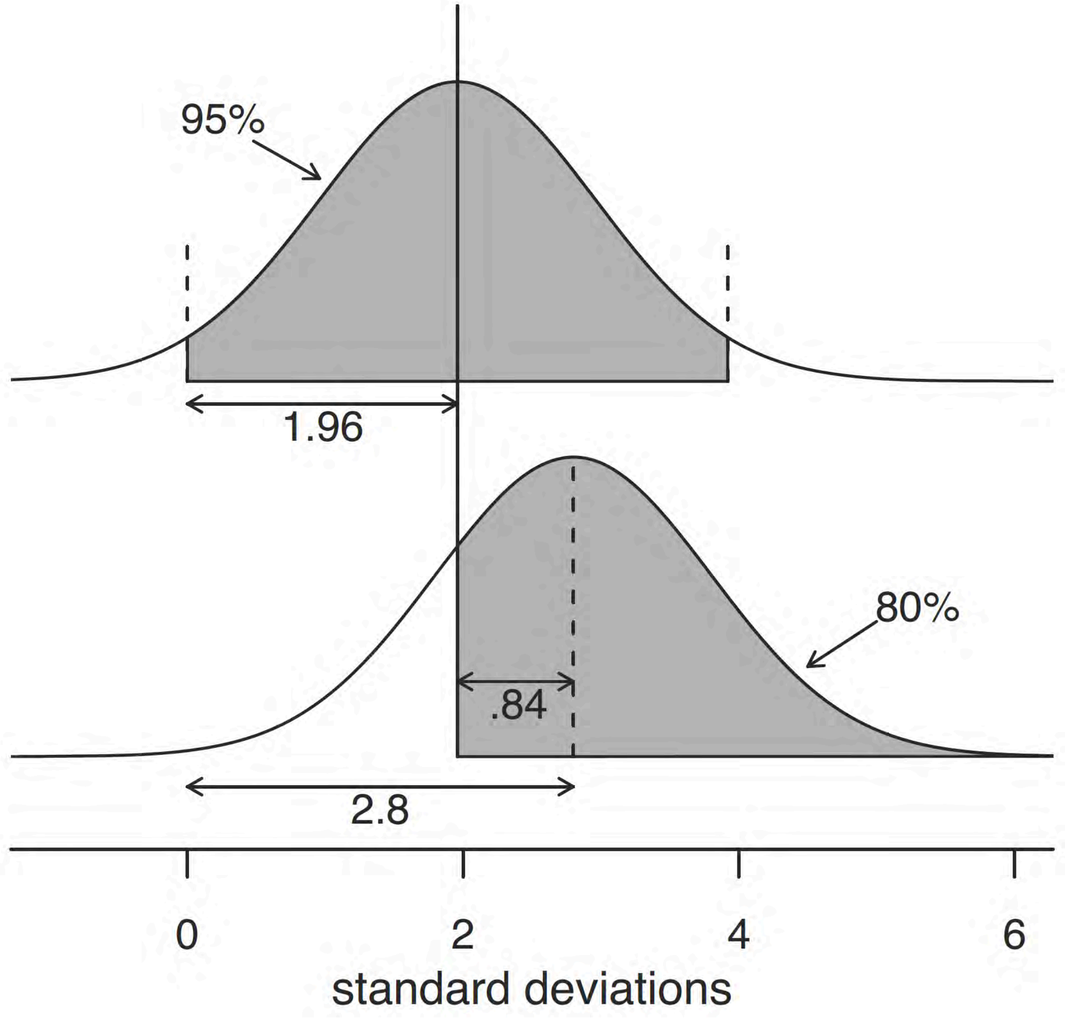
Choose a *level of significance* $\alpha$ for the test.

Determine a *distribution* and *critical region* of the test statistic.

*Calculate a value* of the test statistic from a random sample of data.

*Accept of reject* $H_0$ by comparing the calculated value of the test statistic with the values defining the critical region.

# Generic normal distribution, distance to zero, at a 95 percent *confidence interval* and 80 percent *power*



# statistical tests, comparing sample mean to normal distribution with known $\mu$ and $\sigma$ — *z-statistic*

$$H_0 : \mu = 2.7, H_A : \mu < 2.7$$

```
set.seed(92)

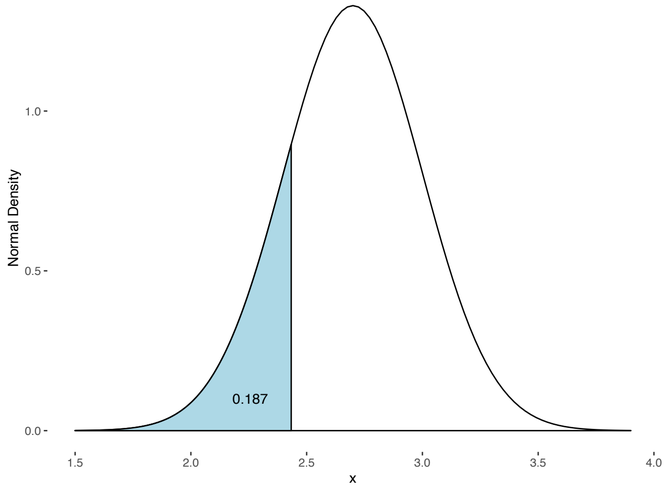
n <- 30
mu <- lambda <- 2.7
sigma <- sqrt(lambda)
x <- rpois(n, lambda)
```

$$z = \frac{\bar{x} - \mu}{\sigma/\sqrt{n}}, \; p = F_\Phi(z)$$

```
x_bar <- mean(x)

z <- ( x_bar - mu ) / ( sigma / sqrt(n) )
p <- pnorm(z)
```

Given the null hypothesis, about
19 percent of experiments have $\bar{x} \leq 2.4\bar{3}$

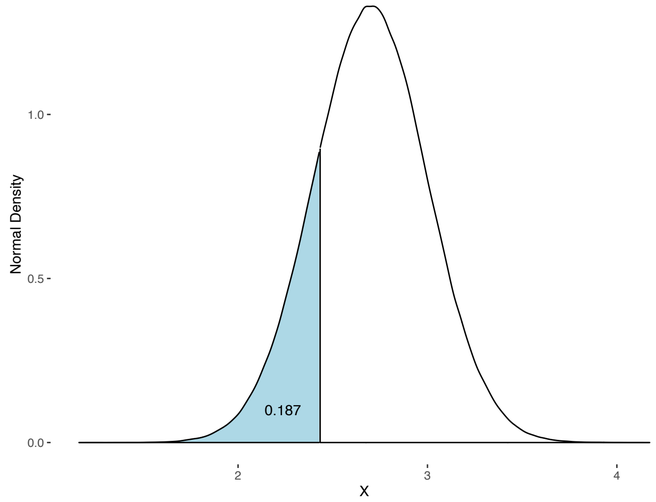



```
ggplot() +
  stat_function(fun  = dnorm,
                args = list(mean = mu, sd = sigma  / sqrt(n)),
                geom = "density",
                fill = "white",
                xlim = c(mu - 4 * sigma / sqrt(n),
                         mu + 4 * sigma / sqrt(n)) ) +
  stat_function(fun  = dnorm,
                args = list(mean = mu, sd = sigma / sqrt(n)),
                geom = "density",
                fill = "lightblue",
                xlim = c(mu - 4 * sigma / sqrt(n), x_bar)) +
   annotate("segment", x = x_bar, xend = x_bar,
            y = 0, yend = dnorm(x_bar, mu, sigma  / sqrt(n))) +
   annotate("text", x = x_bar - 0.1, y = 0.1, hjust = 1,
            label = format(p, digits = 3)) +
   scale_x_continuous(breaks = seq(-1.5, 4, by = 0.5)) +
   labs(y = "Normal Density")
```

$$H_0 : \mu = 2.7, H_A : \mu < 2.7$$

```
X <- rnorm(1e6, mu, sigma / sqrt(n) )

d <- data.frame( density(X)[1:2] )
```




$$z = \frac{\bar{x} - \mu}{\sigma/\sqrt{n}}, \; p = F_\Phi(z)$$

```
ggplot(d) +
  theme(legend.position = "") +
  geom_ribbon(aes(x = x,
                  ymin = 0,
                  ymax = y,
                  fill = x < x_bar),
              color = "black") +
  scale_x_continuous(breaks = seq(-1.5, 4, by = 0.5)) +
  scale_fill_manual(values = c("white", "lightblue")) +
  annotate("segment", x = x_bar, xend = x_bar,
           y = 0, yend = dnorm(x_bar, mu, sigma  / sqrt(n))) +
  annotate("text",
           x = x_bar - 0.1, y = 0.1, hjust = 1,
           label = format( mean( X < x_bar ), digits = 3 ) ) +
  labs(x = "X", y = "Normal Density")
```

**Simulation gives us the same answer:**
given the null hypothesis, about 19 percent of experiments have $\bar{x} \leq 2.4\bar{3}$

statistical tests, if **unknown** $\sigma$, can use sample standard deviation $s$ and student's t distribution — *t-statistic*

$$z = \frac{\bar{x} - \mu}{\sigma/\sqrt{n}},\ p = F_{\Phi}(z) \qquad t = \frac{\bar{x} - \mu}{s/\sqrt{n}},\ p = F_T(t)$$

Of note: as $s \to \sigma \mid n \to \infty$, $t \to z$ and student's t distribution converges towards the normal distribution.

For ease of specifying student-t distribution parameters, here are functions for its four functions, just wrapping the base R versions:

```
dstudent_t <-
  function(x, df, mu = 0, sigma = 1, log = FALSE) {
  if (log) {
    dt( (x - mu) / sigma, df = df, log = TRUE ) - log(sigma)
  } else {
    dt( (x - mu) / sigma, df = df ) / sigma
  }
}

pstudent_t <-
  function(q, df, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE) {
  pt( (q - mu) / sigma, df = df, lower.tail = lower.tail, log.p = log.p )
}

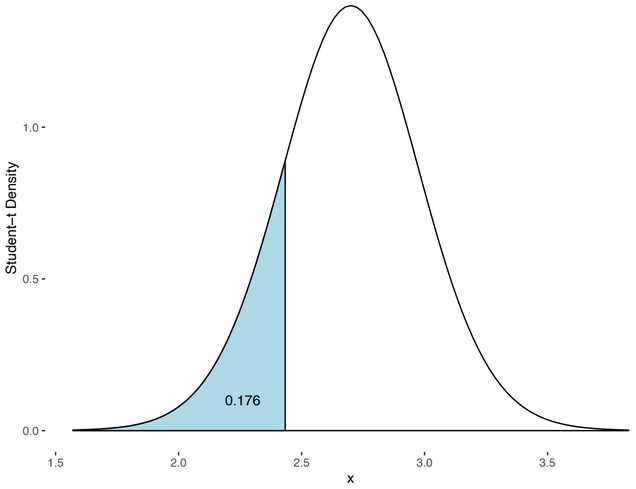
qstudent_t <-
  function(p, df, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE) {
  qt( p, df = df, lower.tail = lower.tail, log.p = log.p ) * sigma + mu
}

rstudent_t <-
  function(n, df, mu = 0, sigma = 1) {
  rt( n, df = df ) * sigma + mu
}
```

# statistical tests, if **unknown** $\sigma$, can use sample standard deviation $s$ and student's t distribution — *t-statistic*

$$H_0 : \mu = 2.7, H_A : \mu < 2.7$$

$$t = \frac{\bar{x} - \mu}{s/\sqrt{n}},\ p = F_T(t)$$




```
s <- sd(x)

t <- ( x_bar - mu ) / ( s / sqrt(n) )
p <- pstudent_t(t, df = n - 1)
```

Given the null hypothesis, about
17 percent of experiments have $\bar{x} \leq 2.4\bar{3}$

```
ggplot() +
  stat_function(fun  = dstudent_t,
                args = list(df = n - 1, mu = mu, sigma = s  / sqrt(n)),
                geom = "density",
                fill = "white",
                xlim = c(mu - 4 * s / sqrt(n),
                         mu + 4 * s / sqrt(n)) ) +
  stat_function(fun  = dstudent_t,
                args = list(df = n - 1, mu = mu, sigma = s  / sqrt(n)),
                geom = "density",
                fill = "lightblue",
                xlim = c(mu - 4 * s / sqrt(n), x_bar)) +
  annotate("segment", x = x_bar, xend = x_bar,
           y = 0, yend = dstudent_t(x_bar, n - 1, mu, s  / sqrt(n))) +
  annotate("text", x = x_bar - 0.1, y = 0.1, hjust = 1,
           label = format(p, digits = 3)) +
  labs(y = "Student-t Density")
```

Firstly,

$$P(D \mid H) \neq P(H \mid D)$$

$$P(H \mid D) = \frac{P(D \mid H)P(H)}{P(D \mid H)P(H) + P(D \mid \neg H)P(\neg H)}$$

Secondly,

**Dichotomous tests** are common in the literature. We typically read comparisons that ask whether the probability of obtaining a value more "extreme" than the sample mean from the null hypothesis, and compare this to an ***arbitrary*** p value of 0.05 (conventionally denoted $\alpha$), rejecting the null hypothesis if this z or t value of smaller, not rejecting otherwise.

But — again — this threshold test is ***arbitrary***. Consider that a difference between probabilities 0.049 and 0.051, for example, is not itself typically significant.

At least report the probability of obtaining the sample value given the selected null probability distribution, *not* just the result of some dichotomous test, and consider the probability of obtaining the sample value if the hypothesis is *not* true. That's a future topic.

breakout session for group project kickoff

# References

**Blitzstein**, Joseph K., and Jessica Hwang. *Introduction to Probability*. Second edition. Boca Raton: Taylor & Francis, 2019.

**Gelman**, Andrew, Jennifer Hill, and Aki Ventari. *Regression and Other Stories*. S.l.: Cambridge University Press, 2020.

**Gelman**, Andrew. "The Problems With P-Values Are Not Just With P-Values." The American Statistician, April 2016, 1–2.

**Harris**, Joseph. *Rewriting: How to Do Things with Texts*. Second edition. Logan: Utah State University Press, 2017.

**McShane**, Blakeley B., David Gal, Andrew Gelman, Christian Robert, and Jennifer L. Tackett. "Abandon Statistical Significance." The American Statistician 73, no. sup1 (March 29, 2019): 235–45.