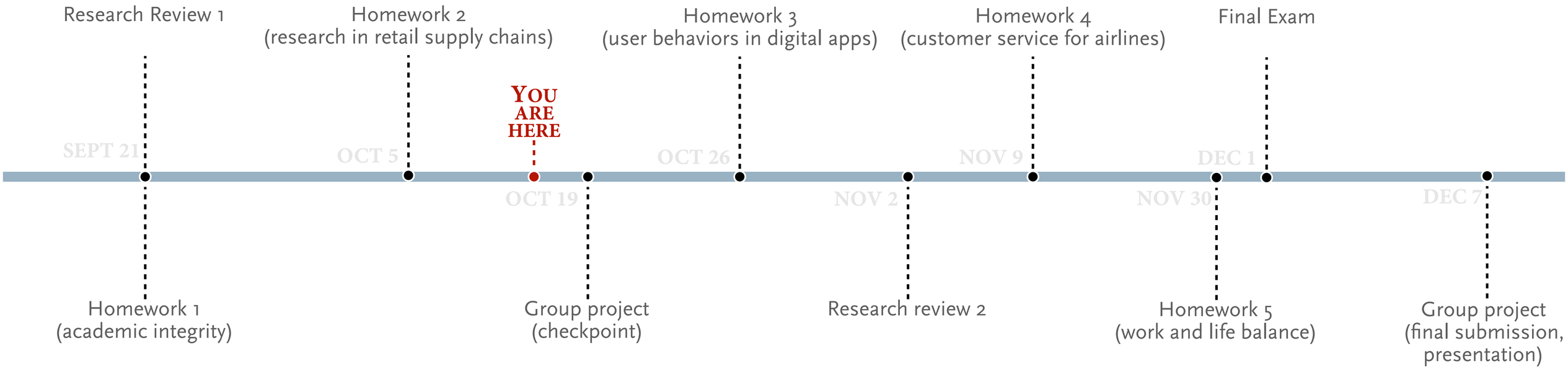
Research Design, Fall 2021

05: statistical tests continued; inference and interpretation

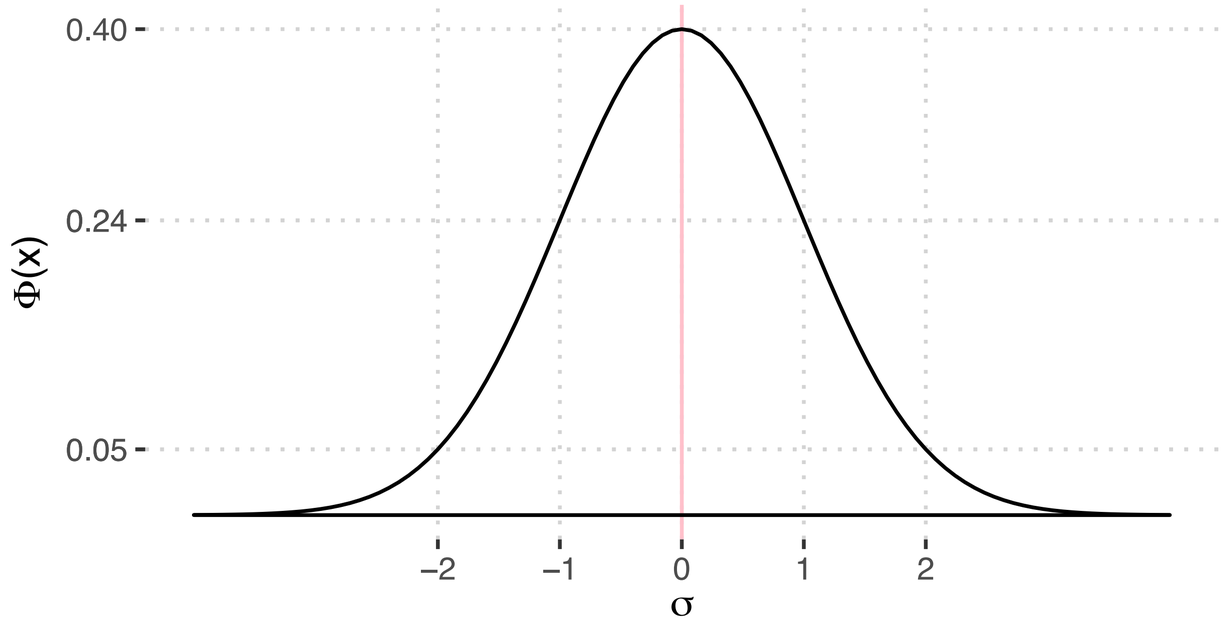
Scott Spencer | Columbia University


Research Review 1
Homework 2
(research in retail supply chains)
Homework 3
(user behaviors in digital apps)
Homework 4
(customer service for airlines)
Final Exam
YOU ARE HERE
SEPT 21
OCT 5
OCT 19
OCT 26
NOV 2
NOV 9
NOV 30
DEC 1
DEC 7
Homework 1
(academic integrity)
Group project
(checkpoint)
Research review 2
Homework 5
(work and life balance)
Group project
(final submission, presentation)

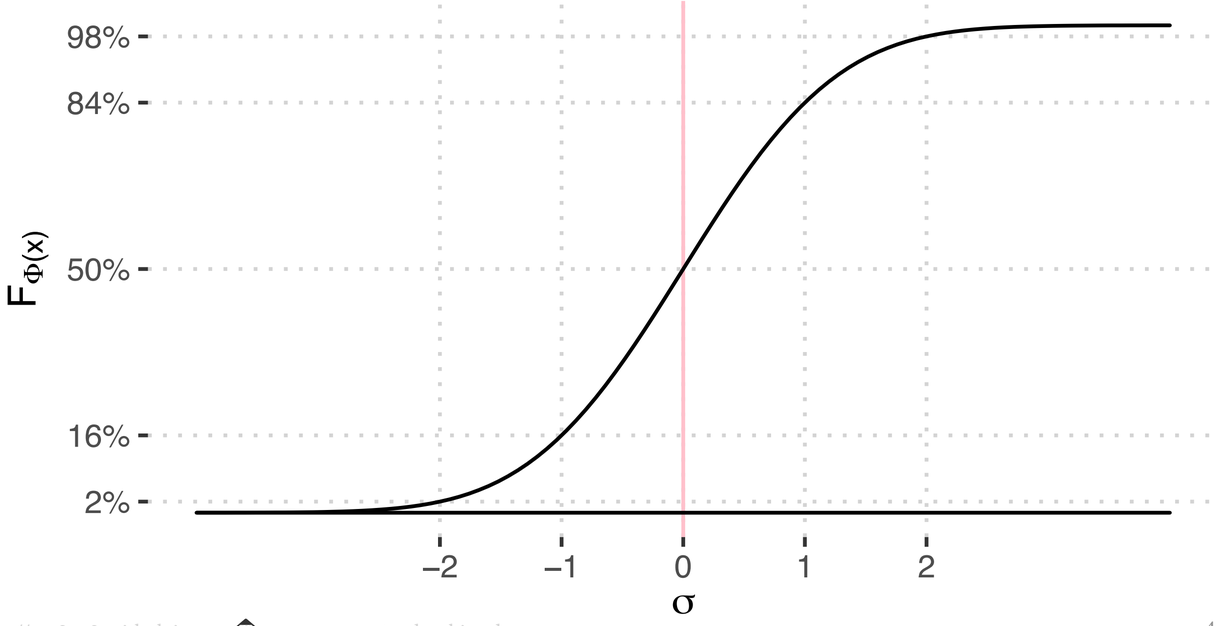
visual recap on *probability density functions* (PDF) and *cumulative distribution functions* (CDF)

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("$\\Phi(x)$"))
```

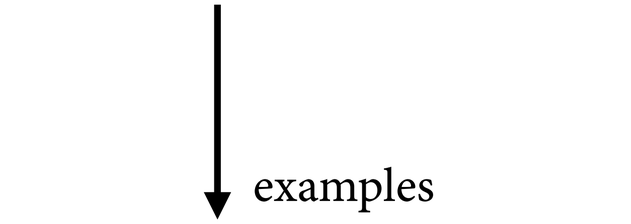



```
cdf <- ggplot() +
  theme(panel.grid.major = element_line(color = "lightgray", linetype = "dotted")) +
  scale_x_continuous(breaks = seq(-2, 2)) +
  scale_y_continuous(breaks = pnorm(seq(-2, 2)),
                     labels = scales::label_percent(accuracy = 1)) +
  geom_vline(xintercept = 0, color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



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

d<probability function name>	probability density function
p<probability function name>	cumulative distribution function (of probability)
q<probability function name>	quantile function
r<probability function name>	random generation function

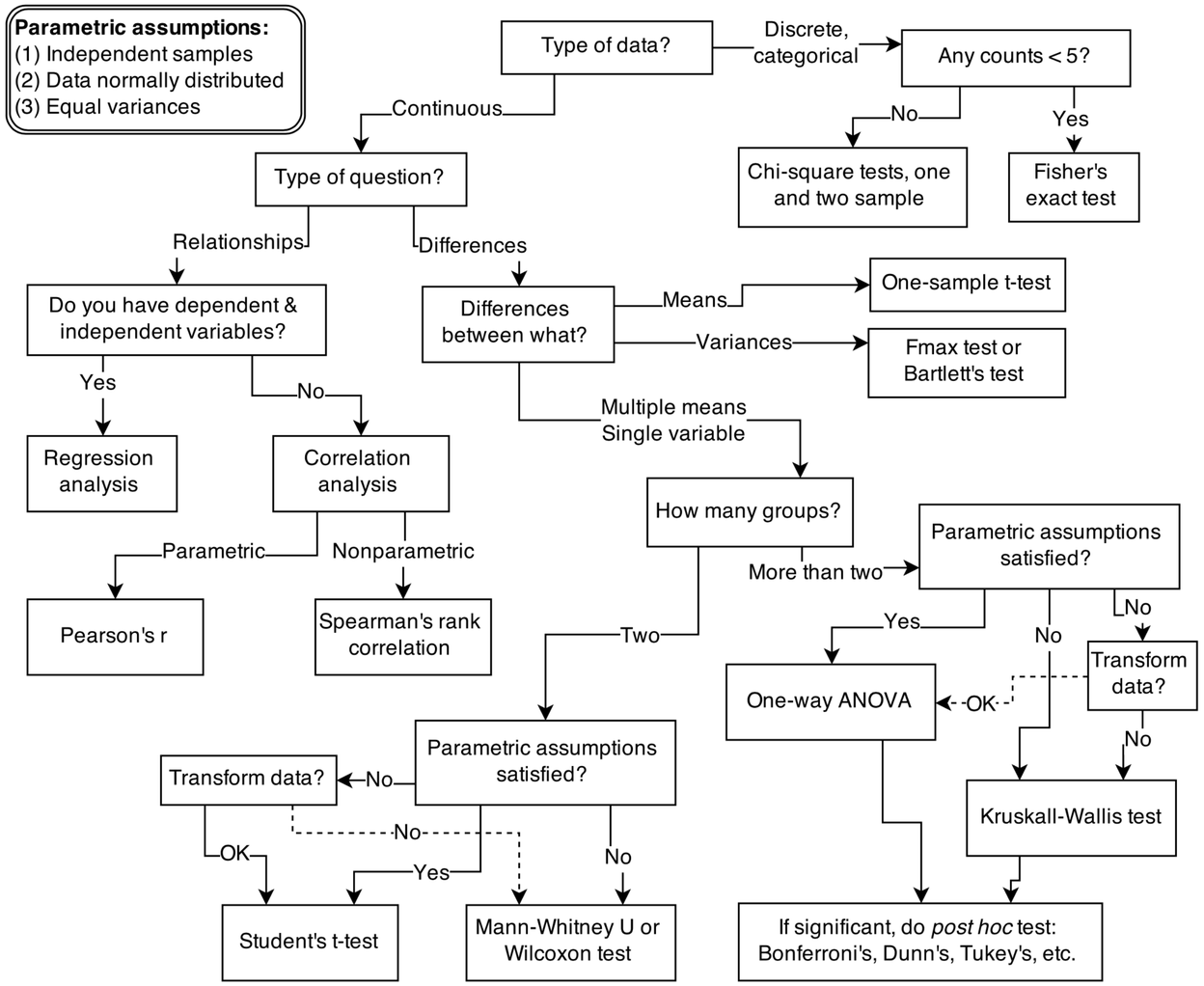


normal	*negative binomial*
student t	*gamma*
bernoulli	*cauchy*
binomial	*100s more*
poisson	…

‘a zoo of pre-constructed golems known as “tests” ’

— Richard McElreath

a zoo of tests, a decision tree for selecting one (and *not all* named or unnamed tests are listed below)



This zoo of tests does share common theories based on probability.

— Casella & Berger 1990; Lehmann & Casella 1998; Lehmann & Romano 2005

a zoo of tests, a decision tree for selecting one, *keeping in mind that classical tests can be **inflexible** and **fragile***

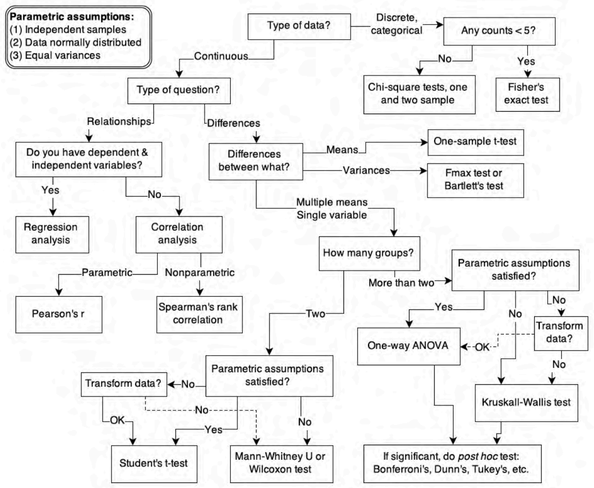


FIGURE 1.1. Example decision tree, or flowchart, for selecting an appropriate statistical procedure. Beginning at the top, the user answers a series of questions about measurement and intent, arriving eventually at the name of a procedure. Many such decision trees are possible.

Sometimes their unyielding logic reveals implications previously hidden to their designers. These implications can be priceless discoveries. Or they may produce silly and dangerous behavior. Rather than idealized angels of reason, scientific models are powerful clay robots without intent of their own, bumbling along according to the myopic instructions they embody. Like with Rabbi Judah's golem, the golems of science are wisely regarded with both awe and apprehension. We absolutely have to use them, but doing so always entails some risk.

There are many kinds of statistical models. Whenever someone deploys even a simple statistical procedure, like a classical *t*-test, she is deploying a small golem that will obediently carry out an exact calculation, performing it the same way (nearly[2]) every time, without complaint. Nearly every branch of science relies upon the senses of statistical golems. In many cases, it is no longer possible to even measure phenomena of interest, without making use of a model. To measure the strength of natural selection or the speed of a neutrino or the number of species in the Amazon, we must use models. The golem is a prosthesis, doing the measuring for us, performing impressive calculations, finding patterns where none are obvious.

However, there is no wisdom in the golem. It doesn't discern when the context is inappropriate for its answers. It just knows its own procedure, nothing else. It just does as it's told.

And so it remains a triumph of statistical science that there are now so many diverse golems, each useful in a particular context. Viewed this way, statistics is neither mathematics nor a science, but rather a branch of engineering. And like engineering, a common set of design principles and constraints produces a great diversity of specialized applications.

This diversity of applications helps to explain why introductory statistics courses are so often confusing to the initiates. Instead of a single method for building, refining, and critiquing statistical models, students are offered a zoo of pre-constructed golems known as "tests." Each test has a particular purpose. Decision trees, like the one in FIGURE 1.1, are common. By answering a series of sequential questions, users choose the "correct" procedure for their research circumstances.

Unfortunately, while experienced statisticians grasp the unity of these procedures, students and researchers rarely do. Advanced courses in statistics do emphasize engineering principles, but most scientists never get that far. Teaching statistics this way is somewhat like teaching engineering backwards, starting with bridge building and ending with basic physics. So students and many scientists tend to use charts like FIGURE 1.1 without much thought to their underlying structure, without much awareness of the models that each procedure embodies, and without any framework to help them make the inevitable compromises required by real research. It's not their fault.

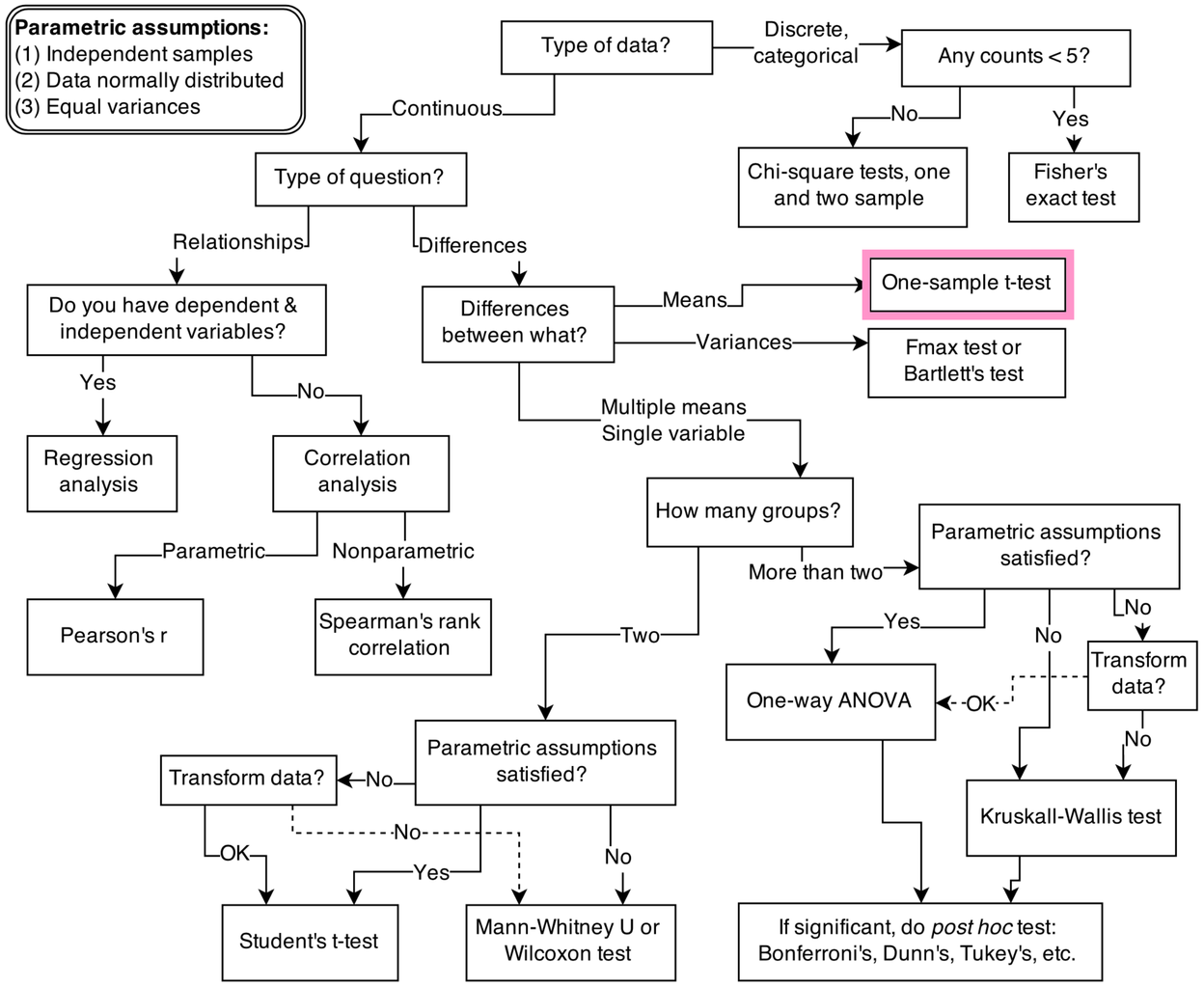
For some, the toolbox of pre-manufactured golems is all they will ever need. Provided they stay within well-tested contexts, using only a few different procedures in appropriate tasks, a lot of good science can be completed. This is similar to how plumbers can do a lot of useful work without knowing much about fluid dynamics. Serious trouble begins when scholars move on to conducting innovative research, pushing the boundaries of their specialties. It's as if we got our hydraulic engineers by promoting plumbers.

Why aren't the tests enough for research? The classical procedures of introductory statistics tend to be inflexible and fragile. By inflexible, I mean that they have very limited ways to adapt to unique research contexts. By fragile, I mean that they fail in unpredictable ways when applied to new contexts. This matters, because at the boundaries of most sciences, it is hardly ever clear which procedure is appropriate. None of the traditional golems has been evaluated in novel research settings, and so it can be hard to choose one and then to understand how it behaves. A good example is *Fisher's exact test*, which applies (exactly) to an extremely narrow empirical context, but is regularly used whenever cell counts are small. I have personally read hundreds of uses of Fisher's exact test in scientific journals, but aside from Fisher's original use of it, I have never seen it used appropriately. Even a procedure like ordinary linear regression, which is quite flexible in many ways, being able to encode a large diversity of interesting hypotheses, is sometimes fragile. For example, if there is substantial measurement error on prediction variables, then the procedure can fail in spectacular ways. But more importantly, it is nearly always possible to do better than ordinary linear regression, largely because of a phenomenon known as OVERFITTING (Chapter 7).

The point isn't that statistical tools are specialized. Of course they are. The point is that classical tools are not diverse enough to handle many common research questions. Every active area of science contends with unique difficulties of measurement and interpretation, converses with idiosyncratic theories in a dialect barely understood by other scientists from other tribes. Statistical experts outside the discipline can help, but they are limited by lack of fluency in the empirical and theoretical concerns of the discipline.

Furthermore, no statistical tool does anything on its own to address the basic problem of inferring causes from evidence. Statistical golems do not understand cause and effect.

zoo & decisions, **comparing $\bar{x}$ to μ, $x \in \mathbb{R}$**



Recall Student's t test — comparing one sample means to μ where we assume a population normal distribution with unknown standard deviation σ.

$$H_0 : \bar{x} = \mu, H_A : \bar{x} < \mu$$

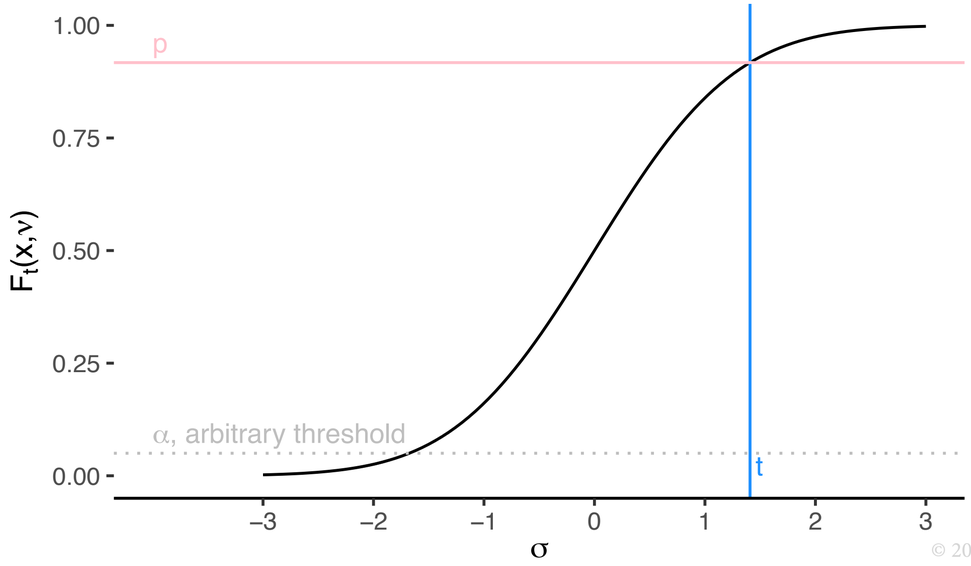
$$t = \frac{\bar{x} - \mu}{s/\sqrt{n}}, \quad \nu = n - 1, \quad p = F_T(t, \nu)$$

```
t.test(x, mu, alternative = "less", conf.level = 0.95)
```

zoo & decisions, **example** — comparing $\bar{x}$ to μ, $x \in \mathbb{R}$

```
set.seed(1)

mu1 <- 4
pop1 <- rnorm(1e5, mean = mu1, sd = 2)

# sample from the population
n1 <- 50
x1 <- sample(x = pop1, size = n1, replace = FALSE)
```

```
# setup the test to calculate manually
xbar1 <- mean(x1)
s1 <- sd(x1)
nu <- n1 - 1

# pretend we know population mu but not sigma
t <- (xbar1 - mu1) / (s1 / sqrt(n1))

# manually get p-value
p <- pstudent_t(q = t, df = nu)
```



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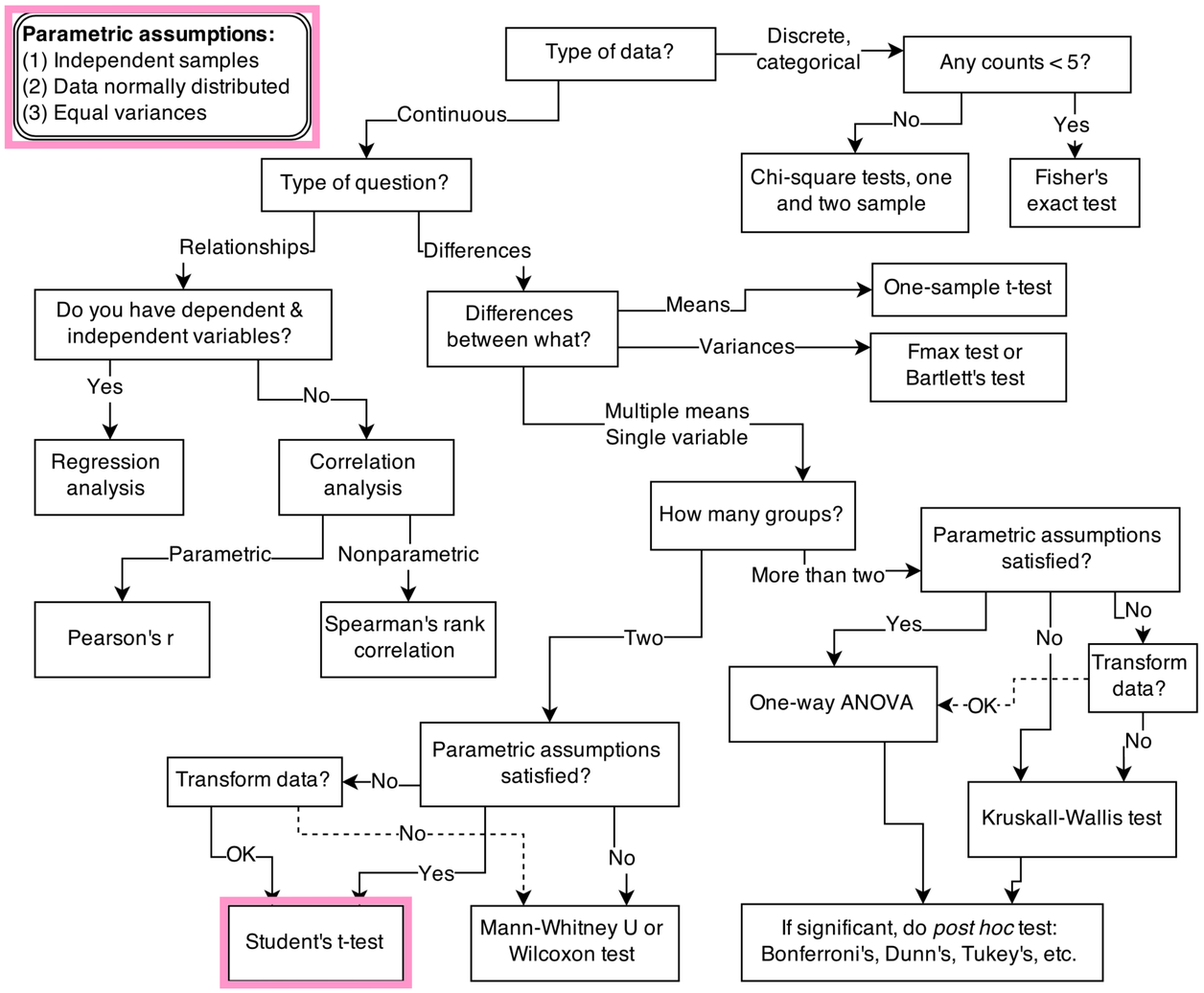


Student's t test — comparing two sample means where we can assume an underlying normal distribution.

$$H_0 : \mu_1 = \mu_2, H_A : \mu_1 < \mu_2$$

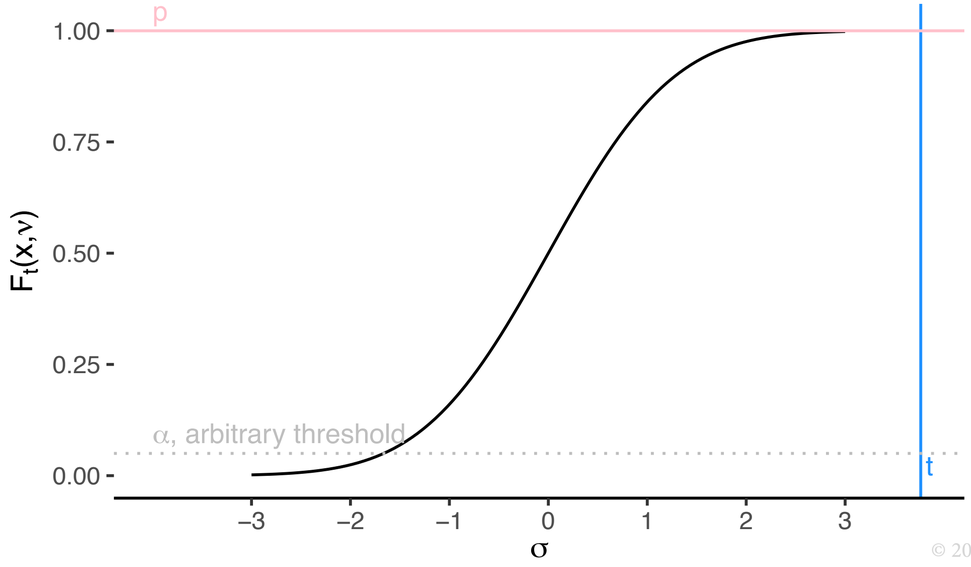
$$t = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{s_1^2/n_1 + s_2^2/n_2}}, \quad \nu = \frac{(s_1^2/n_1 + s_2^2/n_2)^2}{\frac{(s_1^2/n_1)^2}{n_1 - 1} + \frac{(s_2^2/n_2)^2}{n_2 - 1}}, \quad p = F_T(t, \nu)$$

```
t.test(x, y, alternative = "less", var.equal = FALSE, conf.level = 0.95)
```

zoo & decisions, **example** comparing locations, data as $\mathbb{R}$

```
# second population
mu2 <- 2
pop2 <- rnorm(1e5, mean = mu2, sd = 3)

# sample from the second population
n2 <- 50
x2 <- sample(x = pop2, size = n2, replace = FALSE)
```

```
xbar2 <- mean(x2)
s2 <- sd(x2)

t <- ( xbar1 - xbar2 ) / sqrt( s1 ^ 2 / n1 + s2 ^ 2 / n2)

nu <- ( s1 ^ 2 / n1 + s2 ^ 2 / n2 ) ^ 2 /
      ( ( s1 ^ 2 / n1 ) ^ 2 / (n1 - 1) + ( s2 ^ 2 / n2 ) ^ 2 / (n2 - 1) )

p <- pstudent_t(q = t, df = nu)
```

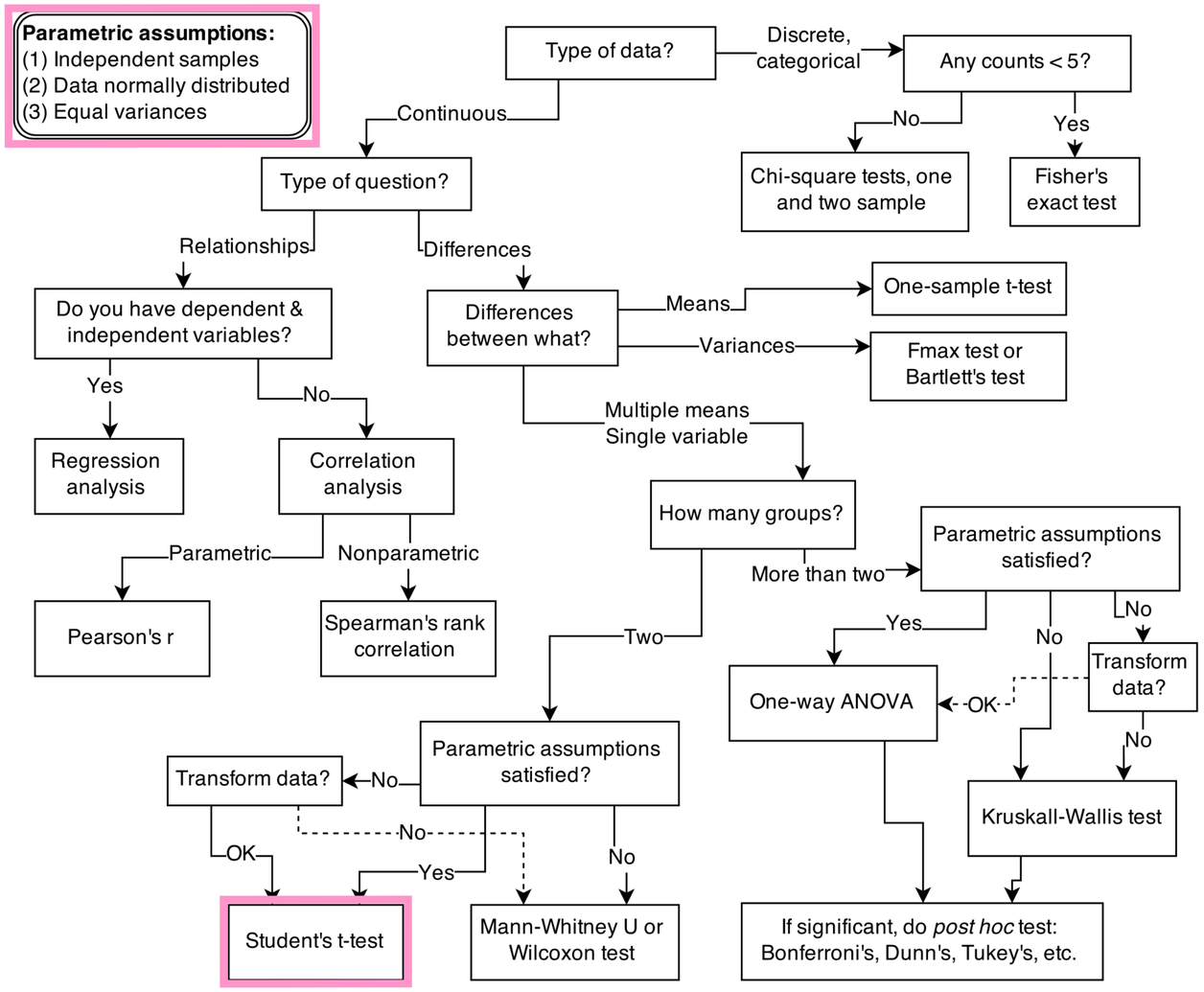


Student's t test — comparing two sample means where we can assume an underlying normal distribution.

$$H_0 : \mu_1 = \mu_2, H_A : \mu_1 < \mu_2$$

$$t = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{s_1^2/n_1 + s_2^2/n_2}}, \quad \nu = \frac{(s_1^2/n_1 + s_2^2/n_2)^2}{\frac{(s_1^2/n_1)^2}{n_1 - 1} + \frac{(s_2^2/n_2)^2}{n_2 - 1}}, \quad p = F_T(t, \nu)$$

```
a <- t.test(x1, x2, alternative = "less", var.equal = FALSE, conf.level = 0.95)
p == a$p.value
```



Proportions are distributed as binomial, which tends to approximate a normal with sufficient n

comparing observed proportion to probability

$$H_0 : \pi = \pi_0, H_A : \pi \neq \pi_0$$

$$z = \frac{\hat{p} - \pi}{\sqrt{\frac{\pi(1-\pi)}{n}}}, p = F_\Phi(z)$$

comparing two observed proportions

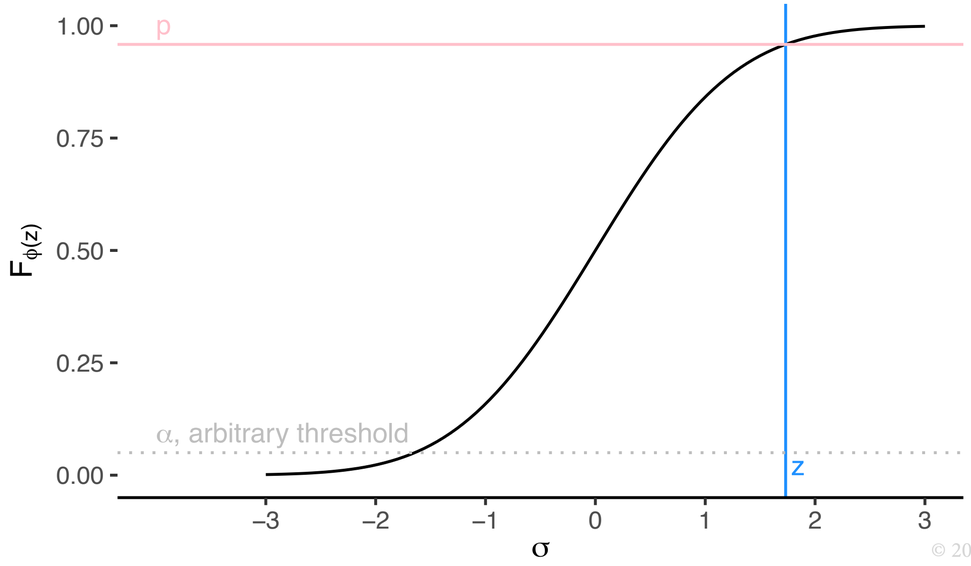
$$H_0 : \pi_1 - \pi_2 = \delta, H_A : \pi_1 - \pi_2 \neq \delta$$

$$z = \frac{\hat{p}_1 - \hat{p}_2 - \delta}{\sqrt{p_0(1-p_0)(\frac{1}{n_1} + \frac{1}{n_2})}} \text{ where } p_0 = \frac{x_1 + x_2}{n_1 + n_2}, p = F_\Phi(z)$$

zoo & decisions, **comparing locations, data as $\mathbb{R} \in [0,1]$**

```
# population proportion
pi <- 0.4

# population of proportions
pop1 <- rbinom(n = 1e5, size = 1, prob = pi)

# observed proportion (sample or experiment)
p1 <- sample(pop1, size = n1)
```

```
phat1 <- mean(p1)

# calculate test statistic
z <- ( phat1 - pi ) / sqrt( pi * (1 - pi) / n1 )

# get location on cdf of standard normal distribution
p <- pnorm(q = z)
```



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$$H_0 : \pi = \pi_0, H_A : \pi \neq \pi_0$$

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comparing two observed proportions

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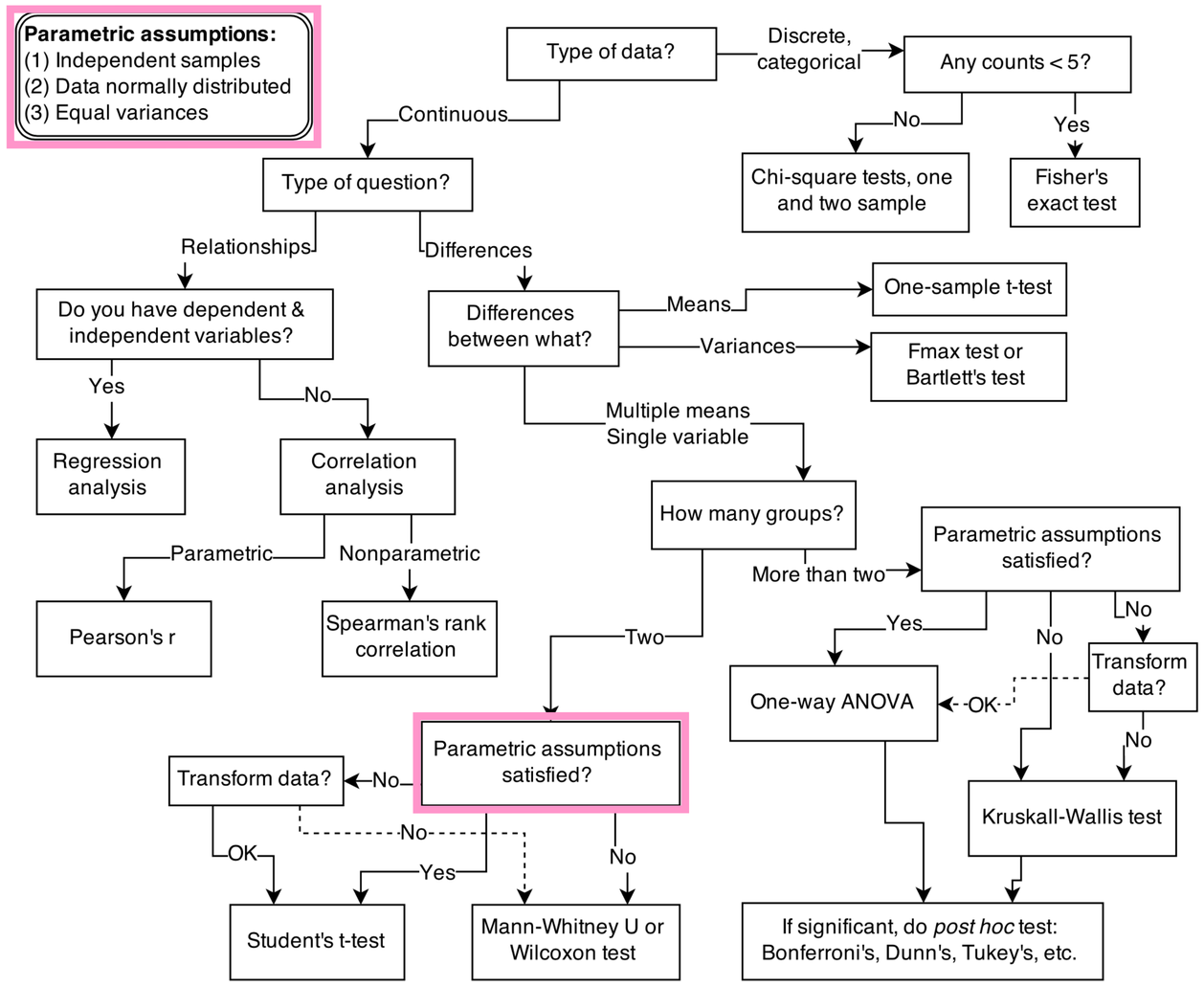
$$z = \frac{\hat{p}_1 - \hat{p}_2 - \delta}{\sqrt{p_0(1-p_0)(\frac{1}{n_1} + \frac{1}{n_2})}} \text{ where } p_0 = \frac{x_1 + x_2}{n_1 + n_2}, p = F_\Phi(z)$$

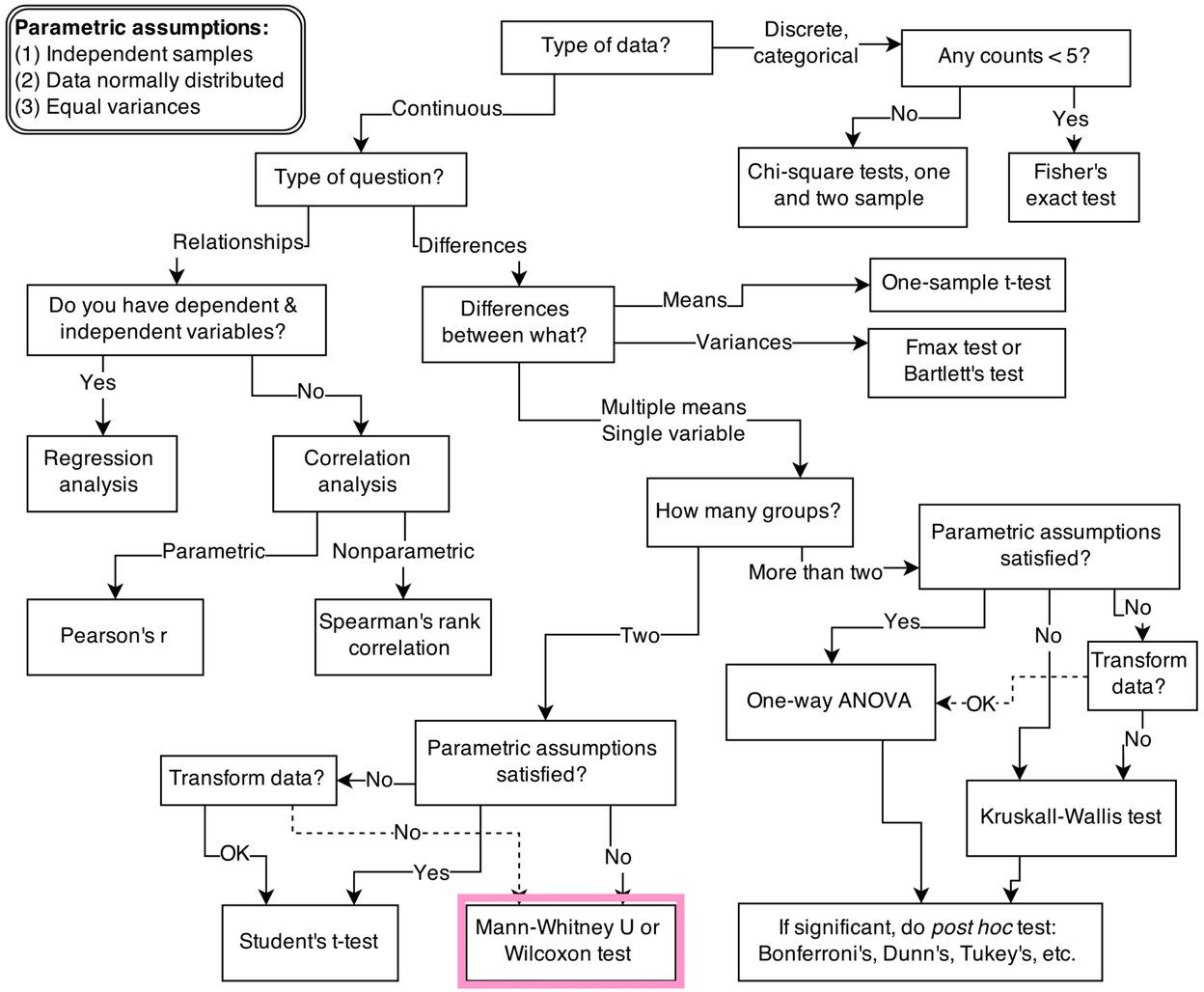
```
prop.test(...)
```

zoo & decisions, **comparing locations, data as an unknown or skewed distribution**



But what if we have *no reason to assume* the population is normally distributed?

zoo & decisions, **comparing locations, data as an unknown or skewed distribution**



Some tests, like *Wilcoxon–Mann–Whitney*, do not rely on parametric assumptions. *WMW* assumes independence of observations and outcomes are ordinal or continuous.

$H_0 : P(x_i > y_j) = 1/2$ (*i.e.*, populations have same central tendency)
$H_A : P(x_i > y_j) \neq 1/2$ (*i.e.*, central tendencies not same)

Simplified procedure — rank all $(n_1 + n_2)$ observations in ascending order; assign ties their average rank; sum each of the two rankings, T_a and T_b; calculate the U statistic:

$$U_a = n_1 n_2 + \frac{n_1(n_1+1)}{2} - T_a\,, \quad U_b = n_1 n_2 + \frac{n_2(n_2+1)}{2} - T_b$$

then $U = \min(U_a, U_b)$. For $n > 20$,

$$z = \frac{U - \mathbb{E}(U)}{\sigma}, \quad \mathbb{E}(U) = \frac{n_1 n_2}{2}, \quad \sigma^* = \sqrt{\frac{n_1 n_2 (n_1 + n_2 + 1)}{12}}, \quad p = F_\Phi(z)$$

*An adjustment to σ is needed for intergroup ties.

zoo & decisions, *Wilcoxon–Mann–Whitney*, simplified code, simulated example:

```
# simulate samples from experiment, samples from different distributions
n <- 10

set.seed(1)
sample1 <- rbeta(n, 2, 2)
sample2 <- rbeta(n, 2, 5)
```

```
d <-
  data.frame(
    sample = rep(1:2, each = n),
    values = c(sample1, sample2)
  ) %>%
  arrange(values) %>%
  mutate(order = seq(nrow(.))) %>%
  group_by(values) %>%
  mutate(rank = mean(order))

Ta <- filter(d, sample == 1) %>% .$rank %>% sum()
Tb <- filter(d, sample == 2) %>% .$rank %>% sum()

n1 <- with(d, sum(sample == 1))
n2 <- with(d, sum(sample == 2))

Ua <- n1 * n2 + (n1 * (n1 + 1)) / 2 - Ta
Ub <- n1 * n2 + (n2 * (n2 + 1)) / 2 - Tb
U <- min(Ua, Ub)

EU <-  n1 * n2 / 2
sigma <- sqrt( n1 * n2 * (n1 + n2 + 1) / 12 )

z <- (U - EU) / sigma
p <- pnorm(z)
```

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*An adjustment to σ is needed for intergroup ties.

zoo & decisions, *Wilcoxon–Mann–Whitney*, simplified code, simulated example, comparing results with r function

```
a <- wilcox.test(x = sample1, y = sample2,
            correct = FALSE, exact = FALSE,
            alternative = "greater")

p == a$p.value
```

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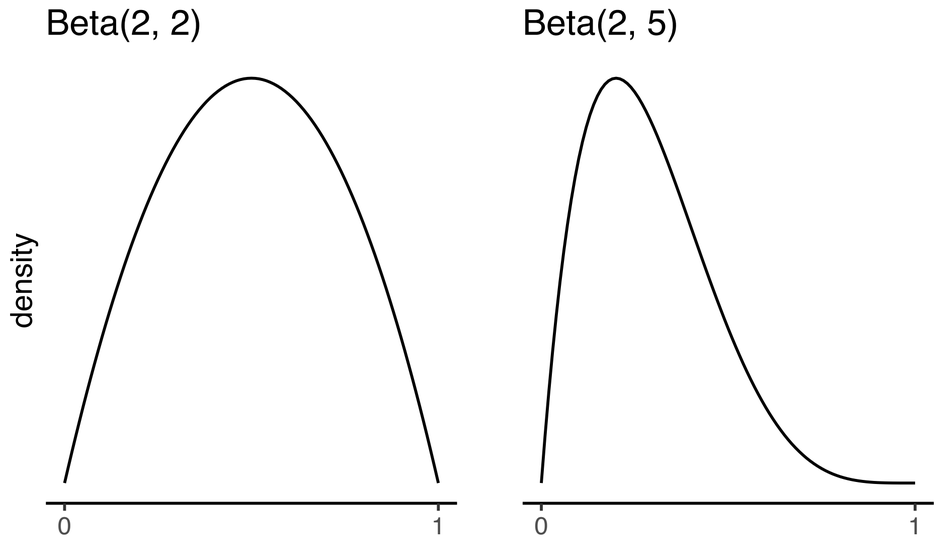

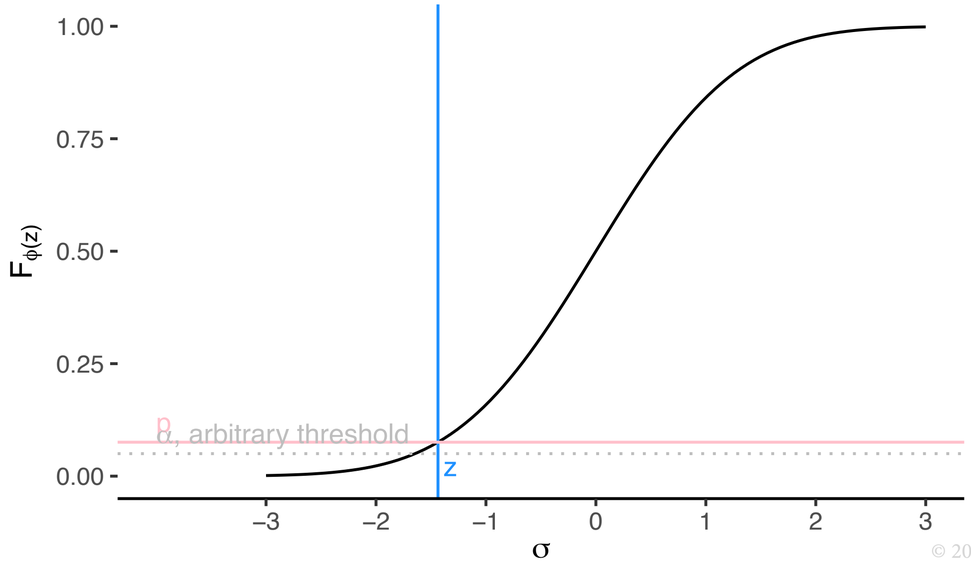

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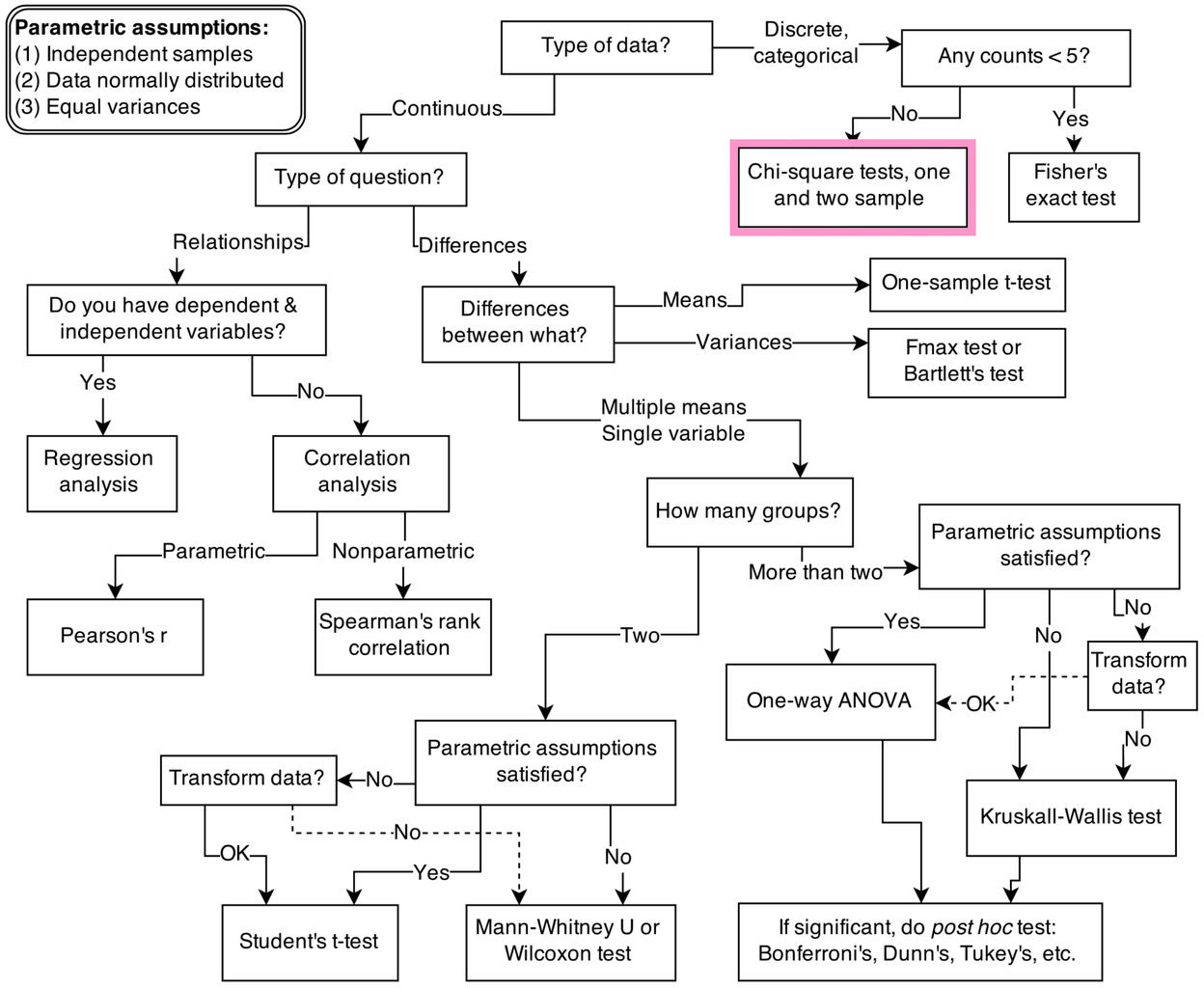
*An adjustment to σ is needed for intergroup ties.

zoo & decisions, **goodness of fit**



Tests can suggest whether ***a whole probability distribution fits some count of categorical outcomes.***

H_0 : distribution fits data

H_A : distribution doesn't fit data

$k \in \{1,...,K\}$ outcome categories

O_k observed counts for category k

p_k probability of category k

$E_k = n \cdot p_k$, expected counts for category k

w test statistic, variations from expected counts

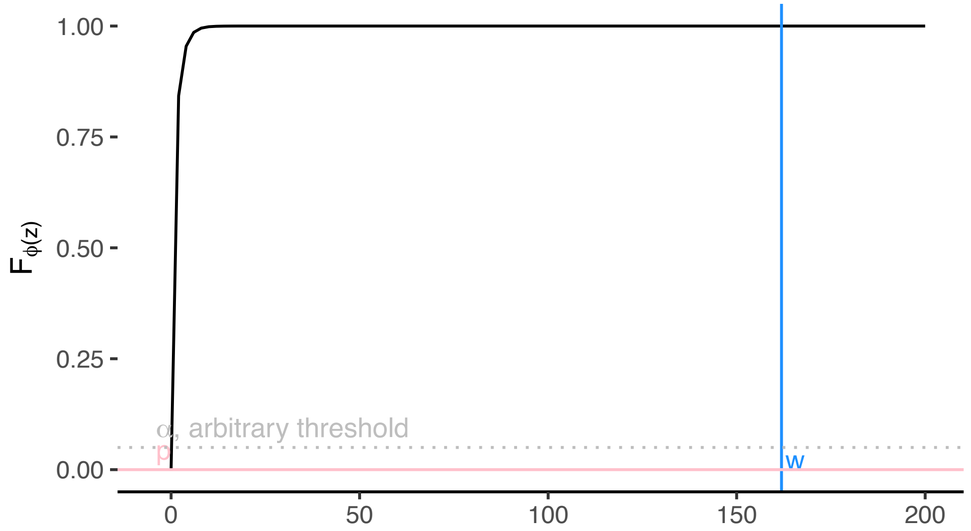
$$w = \sum_{k=1}^{K} \frac{(O_k - E_k)^2}{E_k}, \quad \nu = K - 1, \quad p = F_{\chi^2}(w, \nu)$$

zoo & decisions, **goodness of fit**

```
# Example — test equality of proportions of male and female applicants to Berkeley

data(UCBAdmissions)

UCBAdmissions %>% as.data.frame() %>%
  group_by(Gender) %>%
  summarise(O = sum(Freq)) %>%
  ungroup() %>%
  mutate(E = mean(O)) %>%
  summarise(w = sum((O - E) ^2 / E),
            nu = n_distinct(Gender) - 1) %>%
  mutate(p = pchisq(w, nu, lower.tail = FALSE))
```



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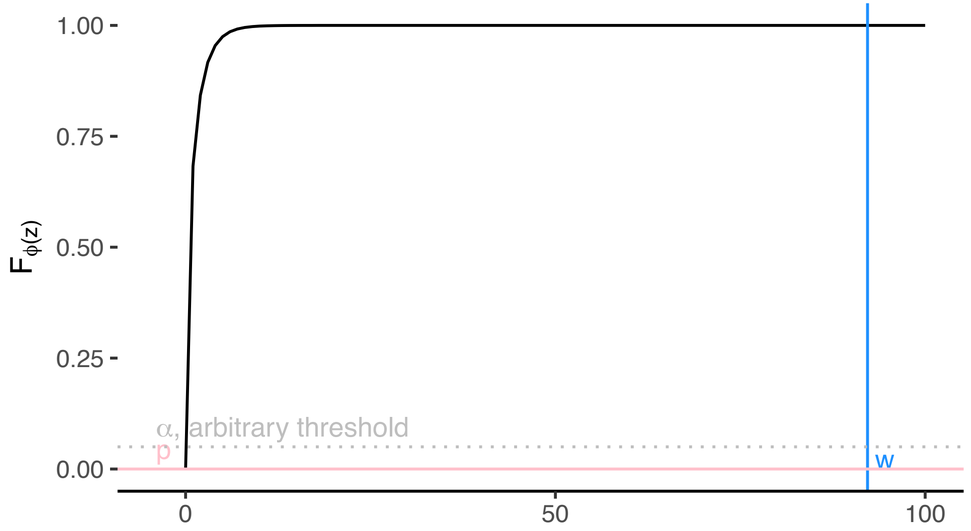
zoo & decisions, **independence**

```
# Example — H0 : P(Admit | Gender) = P(Admit) and P(Gender | Admit) = P(Gender)

UCBAdmissions %>% as.data.frame() %>%
  mutate(Admit_pct = sum(ifelse(Admit == "Admitted", Freq, 0) ) / sum(Freq)) %>%
  group_by(Gender) %>%
  mutate(E = sum(Freq) * ifelse(Admit == "Admitted", Admit_pct, 1 - Admit_pct)) %>%
  group_by(Gender, Admit) %>%
  summarise(O = sum(Freq),
            E = mean(E)) %>%
  ungroup() %>%
  summarise(w = sum((O - E)^2 / E),
            nu = (n_distinct(Admit) - 1) * (n_distinct(Gender) - 1)) %>%
  mutate(p = pchisq(w, nu, lower.tail = FALSE))
```



Tests can suggest whether *variables are independent*.

$H_0 : P(Y|X) = P(Y)$ and $P(X|Y) = P(X)$

$H_A : P(Y|X) \neq P(Y)$ or $P(X|Y) \neq P(X)$

$k \in \{1,...,K\}$ categories

$j \in \{1,...,J\}$ different levels in each category

O_{jk} observed counts for each level j in category k

p_k probability of category k

$E_k = n \cdot p_k$, expected counts for category k

w test statistic, variations from expected counts

$$w = \sum_{j=1}^{J}\sum_{k=1}^{K}\frac{(O_{jk} - E_{jk})^2}{E_{jk}}, \quad \nu = (J-1)(K-1), \quad p = F_{\chi^2}(w, \nu)$$

describing variation in our tests: confidence intervals

confidence intervals

$$\left[(\bar{X} - \bar{Y}) + t_{\alpha/2}\sigma, (\bar{X} - \bar{Y}) + t_{(1-\alpha)/2}\sigma \right]$$

group project work!

References

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