

A: Spread: variability of observations:

sample variance: $s^2 = \Sigma(X_i - \bar{X})^2 / (n - 1)$

why $(n - 1)$? Data used twice: to compute \bar{X} and then to compute s^2

account for this by adjusting the sample size

called “degrees of freedom” or df. More later

standard deviation: $s = \sqrt{\text{Variance}}$

coefficient of variation, cv: s/\bar{X} , measures relative variation.

B: Inference: two types: Confidence interval, hypothesis test

Spoiler: multiple opinions and lots of controversy.

Lots of tricky epistemological and practical issues.

I give the traditional approach

Some perspectives in the references to extra material section of the non-canvas web site

C: Hypothesis test and p-values:

Assume something (null hypothesis) is correct, ask whether observations are unusual

If so, either a fluke happened or the null hypothesis assumption is probably wrong

p-value: probability of observing data or something more extreme given null hypothesis

Scale of evidence: Display 2.12, applied to difference of two group means

Null hypothesis is no difference in means \Leftrightarrow equal means

$p > 0.10$: no evidence of a difference

not: “null is true”, e.g., not: “X has no effect”, not “Two groups have the same mean”

$0.05 < p < 0.10$: weak evidence of a difference

$0.01 < p < 0.05$: evidence of a difference

$0.001 < p < 0.01$: strong evidence of a difference

$p < 0.001$: very strong evidence of a difference

Mis-interpretations of p-values:

Frequently mis-interpreted, leading many to reject any use of p-values

Does not prove null hypothesis (even if p-value large)

Does not show that alternative more likely than null.

Limited knowledge: small p only tells you parameter not zero (for most frequent H0).

D: Randomization test: design-based inference

randomly reassign labels, compute $S =$ statistic of interest

e.g., difference in means or absolute value of difference in means: $|\bar{Y}_A - \bar{Y}_B|$

$p = P[\text{obs } S \text{ more extreme than random } S]$, e.g., (two-sided hypothesis)

$P[|\bar{Y}_A - \bar{Y}_B| \geq \text{random } |\bar{Y}_A - \bar{Y}_B|]$

One- and two-sided null hypotheses:

Notation:

δ = population difference in the means

d = sample estimated difference in averages

two-sided: $H_0: \delta = 0$, $H_a: \delta \neq 0$

reject H_0 when d sufficient large ($d > 0$) or sufficiently small ($d < 0$)

one-sided: two possibilities, depending on which “side”

$H_0: \delta \leq 0$, $H_a: \delta > 0$

reject H_0 when d sufficient large ($d > 0$)

$H_0: \delta \geq 0$, $H_a: \delta < 0$

reject H_0 when d sufficient small ($d < 0$)

p-value for two-sided test “counts” both tails

Twice the smaller one-sided p-value

Two-sided tests much more common, even when only one-side is interesting

Less opportunity to “fudge” the result

Can't pick the side after seeing the data

Two very similar versions of a randomization test:

permutation test: enumerate all possible treatment arrangements

randomization test: randomly sample from all possible treatment arrangements

want/need to sample when too many possibilities:

creativity: $>16,123,800,000,000$ arrangements

Calculating the p-value from a permutation or randomization test:

need to know:

R : number of as or more extreme randomizations,

N : number of randomizations

permutation: observed arrangement is one of the possibilities: $p = R/N$

randomization: observed arrangement is one more possibility: $p = (R + 1)/(N + 1)$

which is why commonly see 999 or 9999 randomizations

Randomization/Permutation tests can be very useful, especially for simple studies:

logic is clear

no model, few assumptions.

key assumptions:

random assignment of treatments to each unit

observations are independent \Leftrightarrow treatment assigned separately to each observation

applicable when standard models aren't easy:

e.g., inference on difference of medians or ratio of means

But can be (very) hard to implement for non-simple (most) studies

E: How precise are estimates?

standard deviation: estimated variability in **observations**

does not get systematically smaller with larger sample sizes

standard error: estimated precision of a statistic (e.g., mean)

for simple random sample: $se_{average} = s/\sqrt{n}$

Generally smaller with larger sample sizes

Can use se to determine number of replicates to use in a study

Spoiler: sd and se can be defined in multiple ways. My use focuses on the “endpoints”.

you might see “standard deviation of the mean”: se, but with known sd, not estimated

Which should you report?

My suggestion: what do you want to describe?

variability in observations: report sd

precision of the average (or other statistic): report se

Correctly say which statistic you are reporting

editor’s note on Med diet retraction:

reviewed 934 manuscripts in NEJM

found 11 with curious results.

5 of those were because se was incorrectly reported as sd or vice-versa

When reporting an average, should you report 106.4 or 106.3867190?

Kelley’s rule: Science 60:524 (1924)

report a statistic (e.g., an average) to the leading digit of $se/3$

Estimate from computer: 106.3867190,	se	se/3	report:
	0.0008	0.00026	106.3867
	0.02	0.0066	106.387
	0.06	0.02	106.39
	9	3	106
	50	17	110

F: Model based inference: T-test

$$T = \frac{\text{statistic} - H_0 \text{ parameter}}{\text{se of statistic}}$$

Many T distributions: which depends on (error) degrees of freedom

$T > 2$ or $< -2 \Rightarrow$ two-sided $p < 0.05$ (approximately, unless df small)

Need to know se of various statistics

se for mean from a single population: $se = s/\sqrt{n}$

Now, need to know se for a difference of two means

SE of a difference of two means

Two independent samples: statistic is difference in averages

$$se = \sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}, \text{ when variances unequal}$$

$$= \sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$$

$$se = \sigma \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}, \text{ when variances equal}$$

$$= s_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}, \text{ estimated pooled variance}$$

Pooled error variance:

$$s_p^2 = \frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2}$$

Degrees of freedom: how much information used to estimate a variance (or sd)

n observations in a group minus number of estimates

one group: need to estimate mean (1 parameter), so $n - 1$ for one group

$n_1 + n_2 - 2$ for two groups (estimate two means)

G: Paired data:

compute difference for each subject (pair).

compute mean difference and sd of differences (across subjects)

$$se = s/\sqrt{n}$$

$$df = n - 1$$

Hypothesis test really doesn't tell you much

if p small, parameter is not zero.

even though p values are all over the scientific literature

H: Confidence interval: tells you both location and precision of a statistic.

a 95% interval includes all parameters for which $p\text{-value} > 0.05$

Many statistics: estimate $\pm T_{\text{quantile}} \times se$

T_{quantile} approx 2 for 95% interval unless df small

95% interval includes 0 $\Rightarrow p\text{-value for test of } 0 > 0.05$

95% interval does not include 0 $\Rightarrow p\text{-value for test of } 0 < 0.05$