

Experimental Design

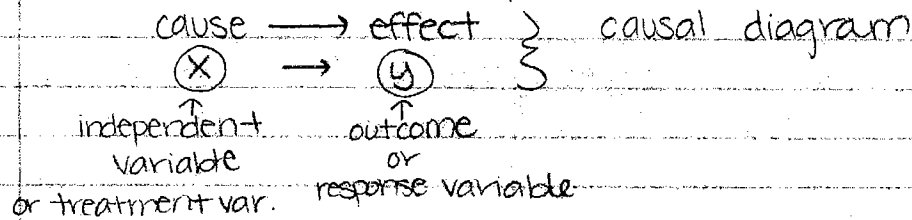
10/9

* H.W. due Oct 21 (pg. 39-41 in reader)

2 types of data-gathering 1. sample survey → deer disease

2. experiments

* Cause + Effect relationships



X = psychological env. Y = brain anatomy

* Science article (reader pg. 54) *

X = dichotomous → Enriched: ^(Anerds) grew w/ 12 in cage, toys to play w/, mazes
 → Deprived: 1 to a cage, no toys, no handling by human
 * all food + H₂O they wanted

* Design 0 = Bad design → prove nothing b/c need to make comparison
 ↳ what's a "bunch" of rats, how long is "awhile"

* Berkeley brain anatomy (good exp.) n = 120 rats "bunch"
 "awhile" = adult maturity

* Causal Inference

before:

Rat number	Cortex Weight	
	Enrich	deprive
1	6881	?
2	6856	?
3	⋮	⋮
⋮	⋮	⋮
120	6491	?

this row all guesses b/c design 0 only looked at rats in enriched env. Instead, this exp. should have split the rats in half (1/2 enrich, 1/2 deprive)

(5) mean = 683mg
 (5) SD = 32mg

Design 1: Controlled Exp.

population

rats

experiment rats

T

C

* start w/ 120 rats: should but 60 in T + 60 in C. Wait til mature, then measure cortex weights

treatment

Control

Rat Number	T or C status	Cortex Weight	
		Enrich	Deprive
...	T	689	?
60	T	649	?
61	C	?	657
...
120	C	?	602

* making comparison

mean $\bar{y}_1 = 683$ $\bar{y}_2 = 647$ (mg)
 $s_1 = 32$ $s_2 = 30$ (mg)

(T-C) difference $683 - 647 = +36$ mg

Does this difference seem large in biological terms?

(absolute comparison) $\bar{T} - \bar{C} = +36$ mg

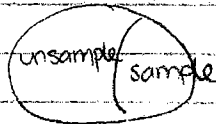
(relative comparison) $\rightarrow \frac{\bar{T} - \bar{C}}{\bar{C}} = \frac{+36 \text{ mg}}{647 \text{ mg}} = 5.6\%$

* mean cortex weight of T animals was 5.6% larger than mean cortex weight of C animals.
 ↳ This seems large in practical terms

*NOTE Randomization doesn't guarantee 100% comparability of \textcircled{T} + \textcircled{C}

goal: WANT \textcircled{T} + \textcircled{C} to be as similar as possible in all possible ways (except for $\textcircled{T}/\textcircled{C}$ distinctions)

Ex: Deers



idea: assign experimental subjects to T/C at RANDOM: randomized control trial (RCT)

treatment: enriched vs. deprived
(x) \textcircled{T} \textcircled{C}

outcome: cortex weight (mg)
(y)

- often can identify third variable \textcircled{Z} that has potential to be associated with both \textcircled{X} + \textcircled{Y} .
- 2 variables u + v are associated if when one goes up or down the other tends to go up or down with it.

→ \textcircled{Z} is called a potential confounding factor (PCF)
↳ PCF = ENEMY in exp. design b/c they can bias the results

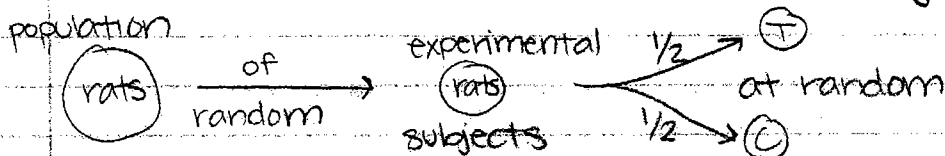
- bias = a systematic tendency to over or under estimate the truth.

• Z (PCF) = genetic predisposition to small or large cortex

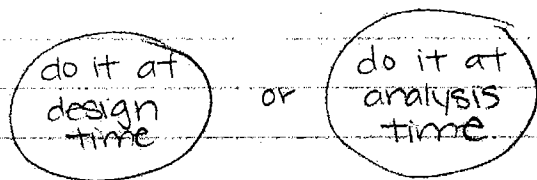


Randomization will tend to defeat enemy of PCFs by promoting comparability of \textcircled{T} + \textcircled{C} .

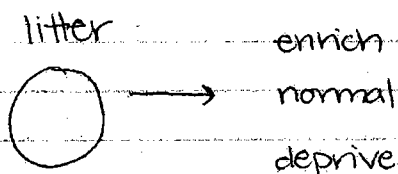
• Randomized controlled trial \leftrightarrow completely randomized design



• How to defeat a PCF: Hold it constant



actual design: from 60 litters from genetically pure strain of rat they chose 2 rats at random from each litter + assigned to T/C at random: matched pairs
 \rightarrow special case of randomized block design



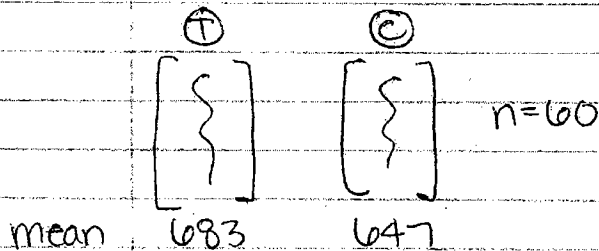
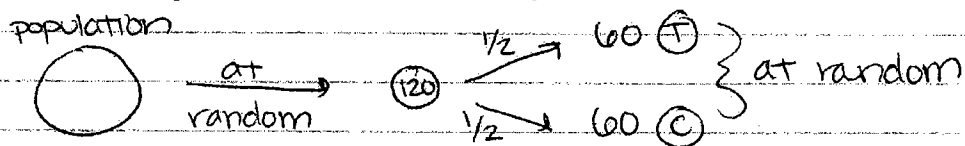
matched pairs design \rightarrow special case of randomized blocks w/ block size 2

Pair #	E (T)	D (C)	D = T - C
1	708	655	+53
2	683	655	+36
...
60	699	688	+11

focus on column of differences (T-C)

* one row for each pair
 here is a matched pairs design
 ★ This better b/c hold z constant ★

completely randomized design:



1 row for each rat

~~these rats are~~ Here (b/c not pairs)
no linkage + therefore no
meaning in Difference ($D = T - C$)

120 diff. rats w/ no connection

*matched pair designs: tend to be more accurate than completely randomized design.

harder to do b/c need to know genetics

- a design is valid if it introduces no bias into the process of estimating cause + effect ~~correct~~ correctly

→ both matched pairs + completely randomized designs are valid, but the former tends to be more accurate (and also more complicated/expensive).