

What interspersion was needed for **our pulse experiment**?

What interspersion would be needed for **the direct estimate version**?

Three alternatives for the pulse experiment

							EU	Replicate
1)	Jill	Sit <div>X</div>	Bob	Stand <div>X</div>	Amy	Sit <div>X</div>	Person	None
2)	T1	Jill <div>Sit</div>	T1	Bob <div>Stand</div>	T1	Amy <div>Sit</div>	Person:Trial	Person
	T2	<div>Stand</div>	T2	<div>Sit</div>	T2	<div>Stand</div>		
3)	Jill	Sit <div>X</div>	Bob	Stand <div>X</div>	Amy	Sit <div>X</div>	Person	None
		<div>X</div> T2		<div>X</div> T2		<div>X</div> T2		

Experimental Unit

The **smallest** unit of experimental material to which a **single treatment** (or treatment combination) is assigned by the experimenter and which is dealt with **independently** of other such systems **under that treatment** at **all stages in the experiment** at which important variation may enter.

Each experimental unit get its treatment **independently**

Each experimental unit is **equally likely** to be assigned each treatment

Experimental units shouldn't **interfere** with each other

Experimental units should be **randomly** selected from a **reference population**

Replicates

Units exposed to all treatment levels where we can construct a direct treatment effect estimate

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2)	T1	Jill <div>Sit</div>	T1	Bob <div>Stand</div>	T1	Amy <div>Sit</div>	Person:Trial	Person
	T2	<div>Stand</div>	T2	<div>Sit</div>	T2	<div>Stand</div>		
3)	Jill	Sit <div>X</div>	Bob	Stand <div>X</div>	Amy	Sit <div>X</div>	Person	None
		<div>X</div> T2		<div>X</div> T2		<div>X</div> T2		

How do we analyze each experiment?

Analytically describe the design

How are treatment effect estimates constructed?

What are the sources of confusion?

controlled and un-controlled

how does each affect the precision of the results?

Empirically analyze data collected from the design

How do we communicate the design to *R*?

R's calculations **do not** follow our analytical processes

How do we estimate the treatment effect?

		Jill		Bob		Amy	EU	Replicate
2)	T1	Sit	T1	Stand	T1	Sit	Person:Trial	Person
	T2	Stand	T2	Sit	T2	Stand		

Collect 40 people

Measure each person 1x in each treatment, calculate the difference

$$y_{A1}, y_{B1} \rightarrow d_1$$

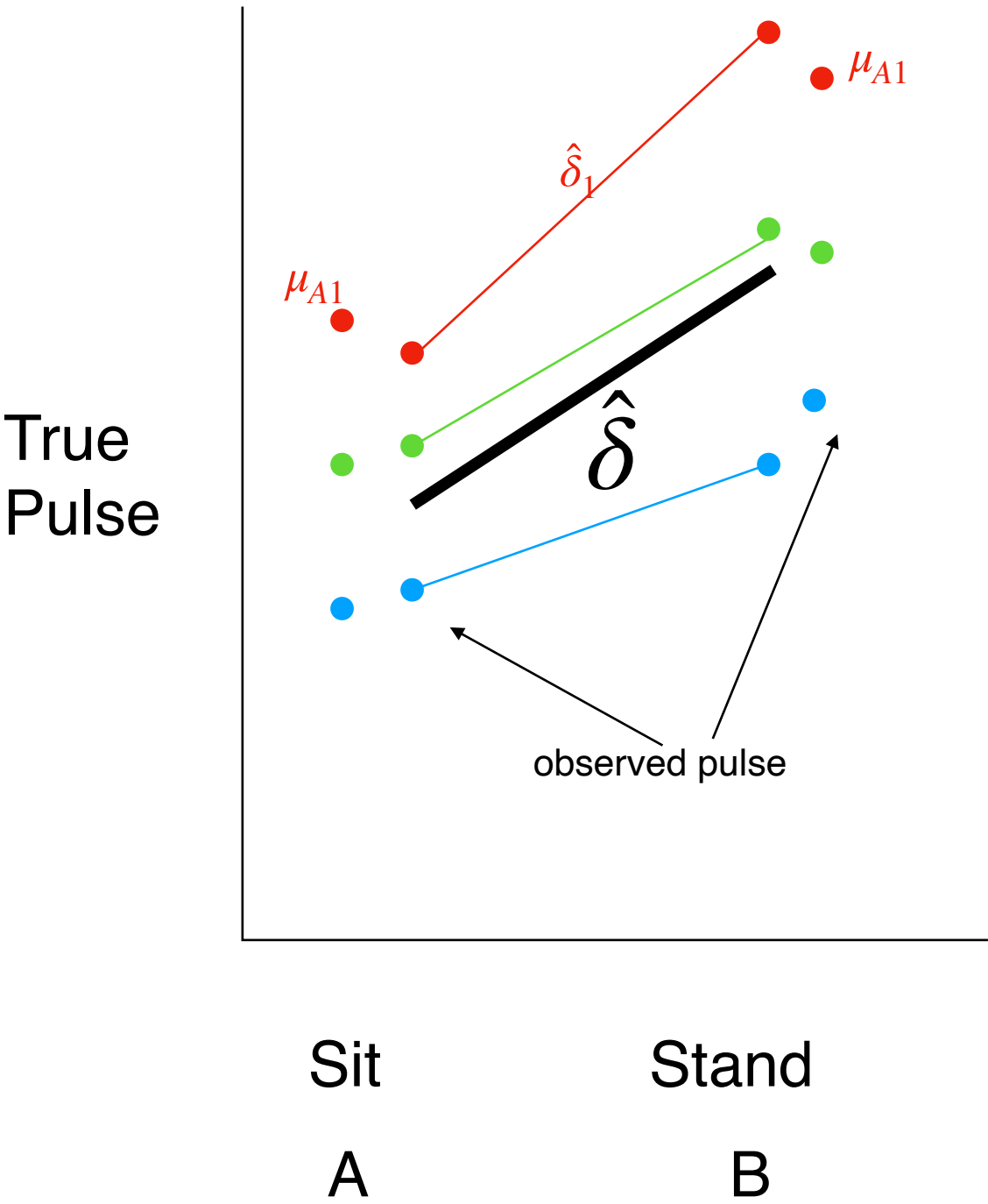
Estimate the treatment effect for each person

$$\hat{\delta}_1$$

Estimate the average treatment effect

$$\hat{\delta}_{B-A} = \frac{1}{n} \sum \hat{\delta}_j$$

Direct estimate of δ

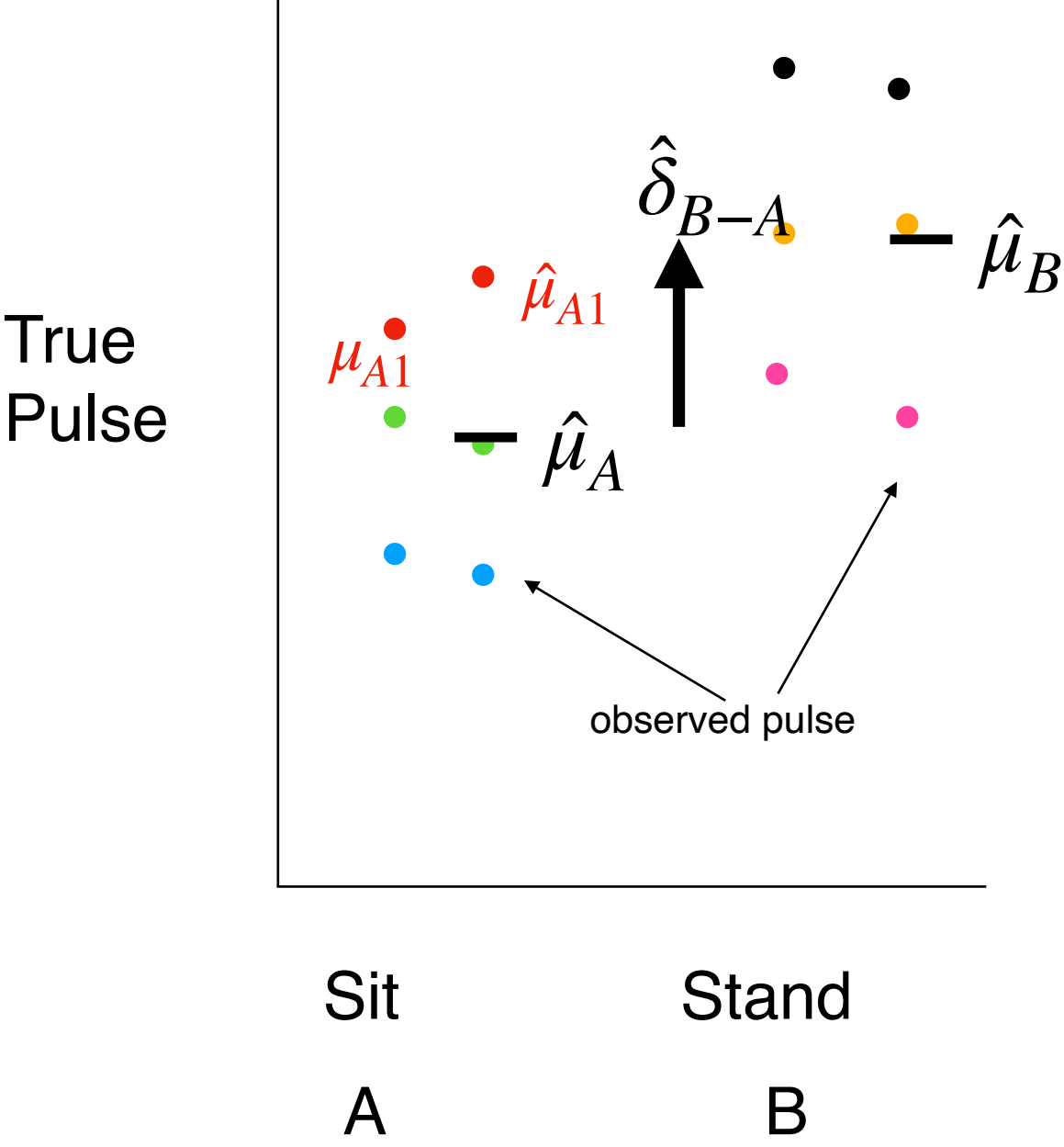


How do we estimate the treatment effect?

		EU					
		Sit		Stand		Sit	
1)	Jill	<input checked="" type="checkbox"/>		Bob	<input checked="" type="checkbox"/>	Amy	<input checked="" type="checkbox"/>
						Person	

Collect 40 people for Sitting group and 40 people for standing group. These are our EU

Measure each person 1x after applying the appropriate treatment level
 y_{A1}, y_{B2}, \dots



Estimate the average pulse of each group

$$\hat{\mu}_A = \frac{1}{n_A} \sum \hat{\mu}_{Aj} \quad \hat{\mu}_B = \frac{1}{n_B} \sum \hat{\mu}_{Bj}$$

Estimate the average treatment effect

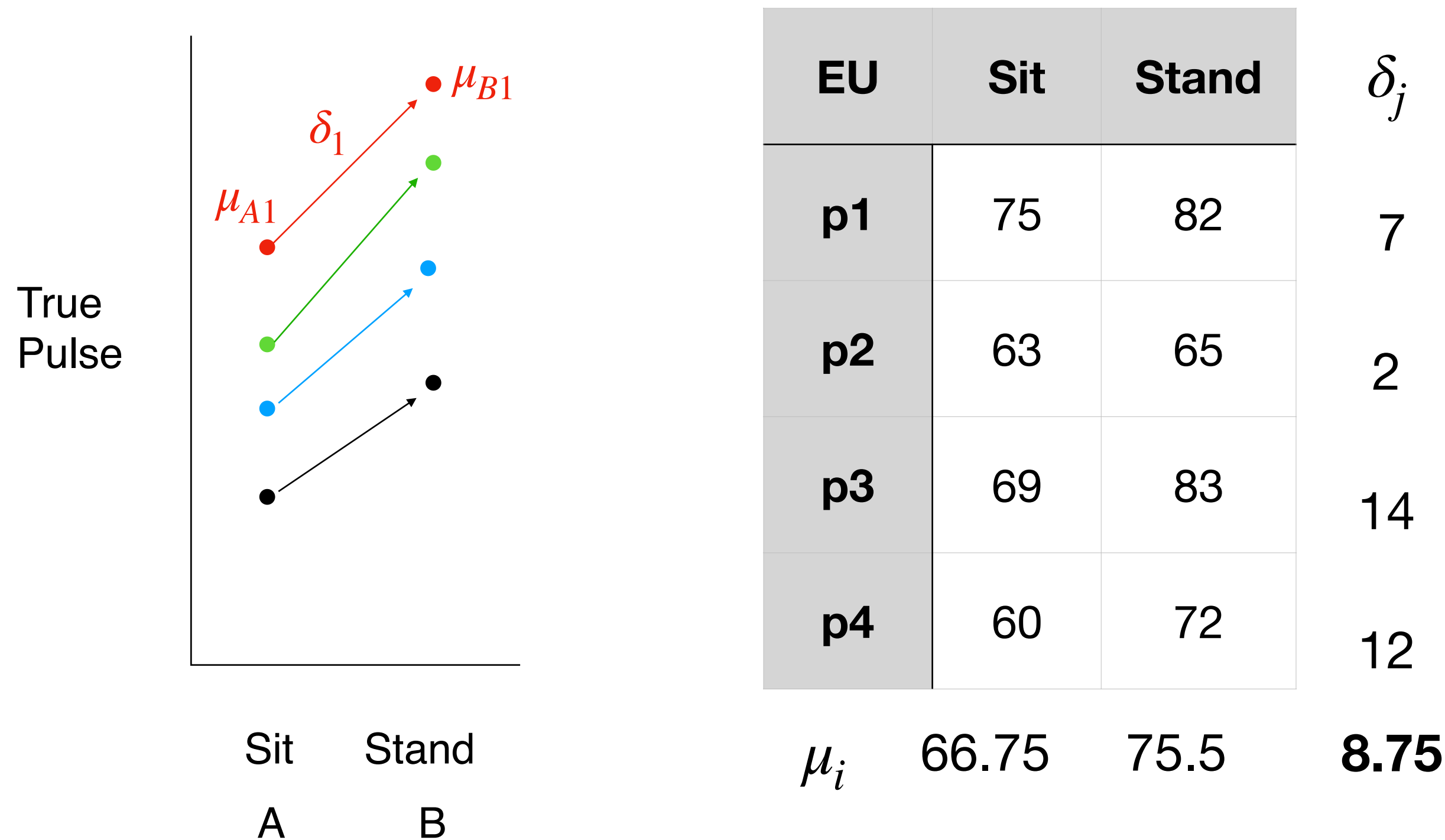
$$\hat{\delta}_{B-A} = \hat{\mu}_B - \hat{\mu}_A$$

Indirect estimate of δ
Through direct estimates of μ_B and μ_A

Why are these both **valid** methods to estimate δ ?

		EU			Replicate
1)		Sit	Stand	Sit	
	Jill	X	Bob X	Amy X	Person
2)		Jill	Bob	Amy	
	T1	Sit	Stand	Sit	Person:Trial
	T2	Stand	Sit	Stand	
					Person

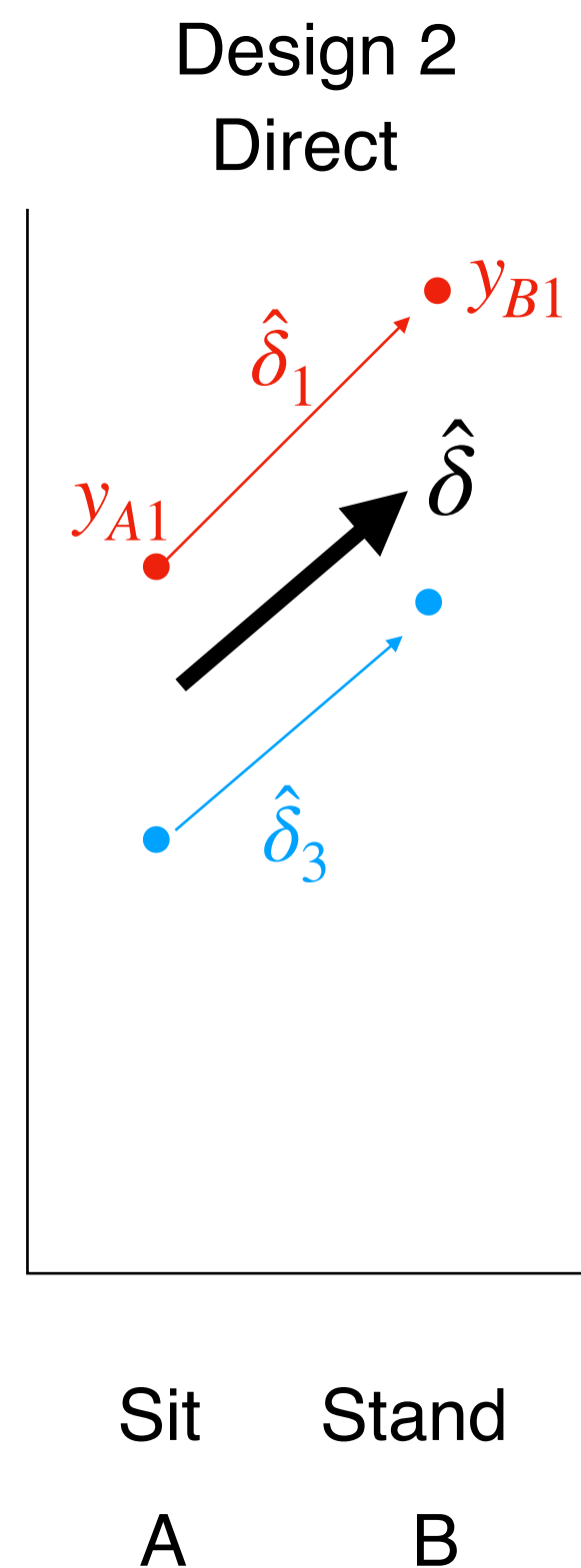
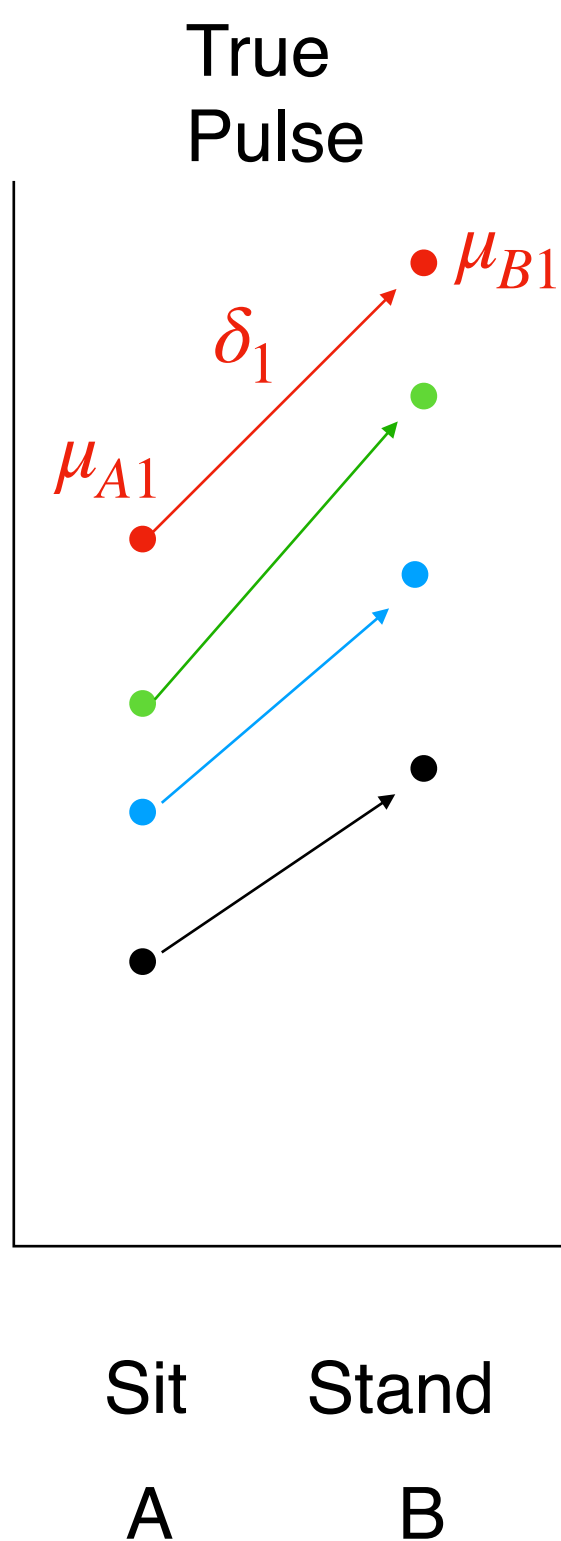
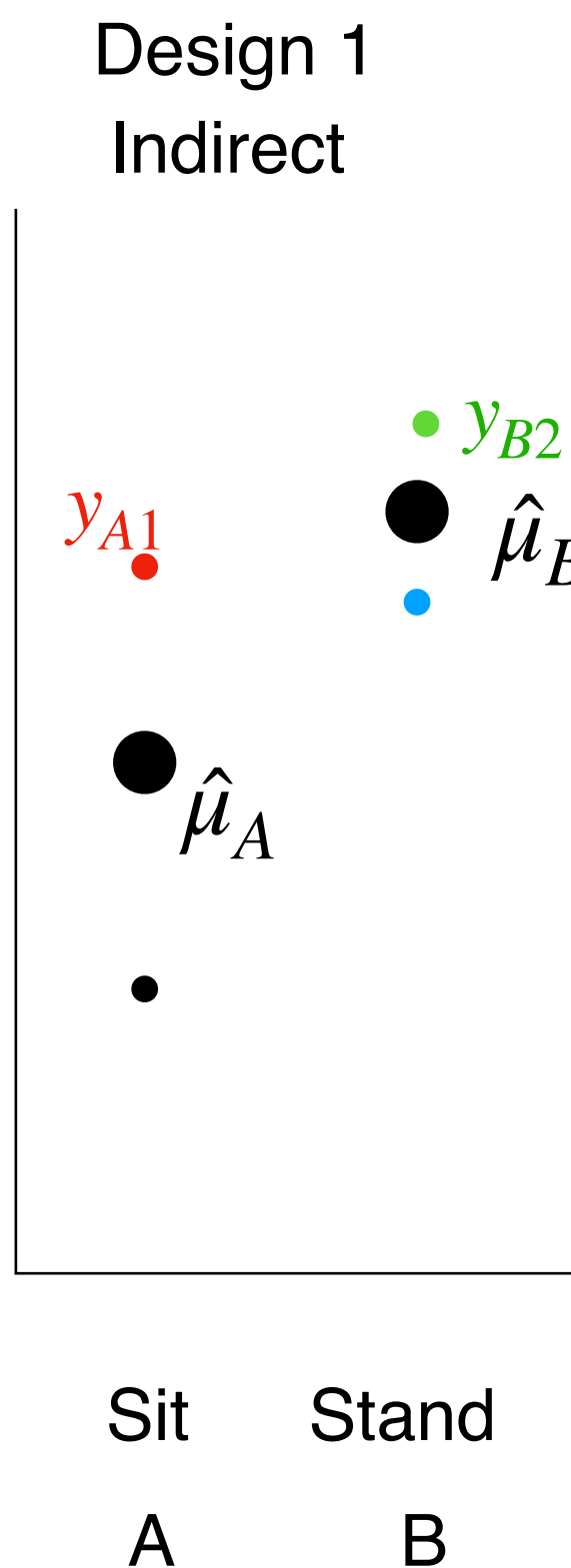
Say this was **the whole population** ...



- 1) Calculate the treatment effects for each person
- 2) Calculate the **mean** treatment effect
- 3) Calculate the **means** of each **treatment level**
- 4) Calculate the **difference between means**

Why are these both **valid** methods to estimate δ ?

						EU	Replicate	
1)	Jill	Sit	Bob	Stand	Amy	Sit	Person	None
		X		X		X		
2)	T1	Jill	T1	Bob	T1	Amy	Person: Trial	Person
		Sit		Stand		Sit		
		T2		T2		T2		
		Stand		Sit		Stand		



$\hat{\mu}_i$ has sampling error
due to:

- missing some individuals
- measurement error

But each is **unbiased** for μ_i

And errors are **uncorrelated**

$\hat{\delta}$ has sampling error
due to:

- missing some individuals
- measurement error

But it is **unbiased** for δ

Why are these both **valid** methods to estimate δ ?

						EU	Replicate	
1)	Jill	Sit	Bob	Stand	Amy	Sit	Person	None
		X		X		X		
<hr/>								
2)	Jill		Bob		Amy		Person:Trial	Person
	T1	Sit	T1	Stand	T1	Sit		
	T2	Stand	T2	Sit	T2	Stand		

Both designs are **valid** because:

$$\begin{aligned}\delta &= \frac{\sum \delta_j}{N} \\ &= \frac{\sum (\mu_{Bj} - \mu_{Aj})}{N} \\ &= \frac{\sum \mu_{Bj}}{N} - \frac{\sum \mu_{Aj}}{N} \\ &= \mu_B - \mu_A\end{aligned}$$

Mean difference
equals the **difference**
of the means

Three alternatives for the pulse experiment

							EU	Replicate
1)	Jill	Sit <div>X</div>	Bob	Stand <div>X</div>	Amy	Sit <div>X</div>	Person	None
<hr/>								
2)	T1 T2	Jill <div>Sit Stand</div>	T1 T2	Bob <div>Stand Sit</div>	T1 T2	Amy <div>Sit Stand</div>	Person:Trial	Person
<hr/>								
3)	Jill	Sit <div>X</div> <div>X</div> T1 T2	Bob	Stand <div>X</div> <div>X</div> T1 T2	Amy	Sit <div>X</div> <div>X</div> T1 T2	Person	None

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2)	T1 T2	Jill <div>Sit Stand</div>	T1 T2	Bob <div>Stand Sit</div>	T1 T2	Amy <div>Sit Stand</div>	Person:Trial	Person
3)	Jill	Sit <div>X</div> <div>X</div> T1 T2	Bob	Stand <div>X</div> <div>X</div> T1 T2	Amy	Sit <div>X</div> <div>X</div> T1 T2	Person	None

Design Table

Structure	Variable	Type	#levels	Replicate	EU
Treatment					
Design					
Response					

Describe how our Experimental Design relates to our Data

Translate the table into R code

Experiment 1: 1 measurement per person

						# people	# measures	#EU	
		Sit	Stand		Sit				
1)	Jill	<div>X</div>	Bob	<div>X</div>	Amy	<div>X</div>	80	80	80

Person	Posture	Pulse
Jill	Sit	60
Bob	Stand	72
Amy	Sit	106
⋮		

Structure	Variable	Type	#levels	Replicate	EU
Treatment	Posture	Cat	2	None	Person
Design	Person	Cat	80		
Response	Pulse	Num	80		

Each column of your table = Variable

Type = Categorical or Numeric

#levels = number of unique values in the column of the data

Only Treatment variables get Replicates and EU

Experiment 2: each person measured in each treatment

		Jill		Bob		Amy	# people	# measures	#EU
2)	T1	Sit	T1	Stand	T1	Sit	40	80	80
	T2	Stand	T2	Sit	T2	Stand			

Person	Posture	Pulse	Trial	Person: Trial
Jill	Sit	60	T1	Jill:T1
Jill	Stand	74	T2	Jill:T2
Bob	Stand	72	T1	Bob:T1
Bob	Sit	78	T2	Bob:T2
Amy	Sit	106	T1	Amy:T1
Amy	Stand	109	T2	Amy:T2
⋮				

Structure	Variable	Type	#levels	Replicate	EU
Treatment	Posture	Cat	2	Person	Person: Trial
Design	Person	Cat	40		
	Trial	Cat	2		
	Person: Trial	Cat	80		
Response	Pulse	Num	80		

“Person: Trial” is a **Combination Variable**

We don’t have to create it in our data table (but we can)

Experiment 3: each person measured 2x in one treatment

		Sit		Stand		Sit		# people	# measures	#EU
3)	Jill	<div><div>X</div><div>X</div></div> <div>T1 T2</div>		Bob	<div><div>X</div><div>X</div></div> <div>T1 T2</div>	Amy	<div><div>X</div><div>X</div></div> <div>T1 T2</div>	40	80	40

Person	Posture	Pulse	Trial	Person: Trial
Jill	Sit	60	T1	Jill: T1
Jill	Sit	64	T2	Jill: T2
Bob	Stand	72	T1	Bob: T1
Bob	Stand	68	T2	Bob: T2
Amy	Sit	106	T1	Amy: T1
Amy	Sit	112	T2	Amy: T2
⋮				

Structure	Variable	Type	#levels	Replicate	EU
Treatment	Posture	Cat	2	None	Person
Design	Person	Cat	40		
	Trial	Cat	2		
	Person: Trial	Cat	80		
Response	Pulse	Num	80		

The first 4 columns are the same!

Fitting models in R

- 1) Write the model
- 2) Pass it to the function to fit the model: **lm()** or **lmer()**
- 3) Pass the result to a function to get estimates, SE, CI, etc
emmeans(), **contrasts()**, etc

Writing the model

- 1) Response ~ model

model: every variable in Treatment + Design
with # levels < # responses
combined with “+”

- 2) Any variable that is a **Replicate** or **EU** gets declared with (1|X)
+ Variable => + (1|Variable)
call these “random”

Replicates are declared as + (1|Replicate:Treatment)

- 3) If any random variable is included, use **lmer()**. Otherwise use **lm()**

1) Response ~ model

model: every variable in Treatment + Design, combined with “+”
with # levels < # responses

2) Any variable that is a **Replicate** or **EU** gets declared with (1|X)

+ Variable => + (1|Variable)

call these “random”

Replicates are declared as + (1|Replicate:Treatment)

3) If any random variable is included, use lmer(). Otherwise use lm()

Structure	Variable	Type	#levels	Replicate	EU
Treatment	Posture	Cat	2	None	Person
Design	Person	Cat	80		
Response	Pulse	Num	80		

lm(Pulse ~ Posture)

Structure	Variable	Type	#levels	Replicate	EU
Treatment	Posture	Cat	2	Person	Person:Trial
Design	Person	Cat	40		
	Trial	Cat	2		
	Person:Trial	Cat	80		
Response	Pulse	Num	80		

lm(Pulse ~ Posture + Person + Trial)

For Tuesday:

3)

	Sit		Stand		Sit		# people	# measures	#EU												
Jill	<table><tr><td>X</td><td>T1</td></tr><tr><td>X</td><td>T2</td></tr></table>	X	T1	X	T2	Bob	<table><tr><td>X</td><td>T1</td></tr><tr><td>X</td><td>T2</td></tr></table>	X	T1	X	T2	Amy	<table><tr><td>X</td><td>T1</td></tr><tr><td>X</td><td>T2</td></tr></table>	X	T1	X	T2		40	80	80
X	T1																				
X	T2																				
X	T1																				
X	T2																				
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X	T2																				

Structure	Variable	Type	#levels	Replicate	EU
Treatment	Posture	Cat	2	None	Person
Design	Person	Cat	40		
	Trial	Cat	2		
	Person: Trial	Cat	80		
Response	Pulse	Num	80		

Write the model for Design 3

Read the remainder of Hurlbert 1984

What type of **pseudoreplication** are we committing if we don't declare Person as Random in this experiment?