Introduction to DeclareDesign

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What is DeclareDesign?

- Framework, R package for formally characterizing research designs
 - Problem: Degree of detail about research design varies greatly in published work, pre-analysis plans etc.
 - Motivation: Create framework capable of characterizing all research designs (any/all methods)
- Tools for analysis of designs
 - Big question: What could we have learned from a design?
 - Ancillary benefits: Create "dummy" datasets with which you can practice different analyses

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What could we have learned from a design?

- A research design at the front-end consists of:
 - Design choices by researcher/nature/dataset maker (depends on method)

- Set of beliefs/assumptions about how the world works
- ▶ We can learn about how a design functions through simulation
 - Logic of Monte Carlo analysis
 - Draw data, analyze, save estimates, repeat many times
 - Diagnoses based on estimates

Six Components of a Research Design

- 1. **Population**: Set of units about which inferences are sought and their characteristics
- 2. **Potential outcomes**: Outcomes each unit might exhibit depending on how causal process changes the world
- 3. **Sampling strategy**: Strategy used to select units to include in study
- 4. **Assignment**: Manner in which units are assigned to reveal one potential outcome or another

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- 5. **Estimand**: Quantities that we want to learn about in the world, in terms of potential outcomes
- 6. **Estimator**: Procedure for generating estimates of the quantities we want to learn about

Population

Start from theory:

- Where should the theory apply?
- Where shouldn't it apply? (scope conditions)
- What is the population that we want to make an inference about?
- Often practical limitations about the population that we can study

- Regardless of method employed
- But stay idealistic for the moment

Sampling Strategy

- How are we selecting units to analyze?
 - How do we choose the case (context)?
 - What does this selection method mean about inference to the population above?
- Types of samples:
 - Population ("big data," very specific populations)
 - Convenience (lab experiments, some surveys etc.)
 - Some sort of random sample (some surveys etc.)
- If we can't make a population inference from a sample, do we:
 - Redefine population?
 - Only worry about sample diagnostics?
- One source of concerns about external validity
 - Unclear (to me) that this is an "experiments" issue...

Potential Outcomes

- Codifies our asssumptions about the relationships between different treatment conditions, baseline covariates, and outcomes
 - Should be rooted in theory
- Functional form of relationships must be specified
 - Should be informed by theory, but often theories are not specific on this point
 - Less difficult in case of binary treatments
 - Another source of concerns about external validity (model-based inference)

- Some difficulties of experimental analysis should be viewed as potential outcomes!
 - (Non)-compliance
 - Spillovers
 - Attrition

Assignment

How is treatment/independent variable of interest assigned?

Experiments:

- Input the randomizations.
- Defaults allow for simple, complete, blocked, clustered, and blocked and clustered randomization, among others
- Quasi-experiments/natural experiments:
 - Treatment assignment requires more assumptions about the assignment process
- Other observational work:
 - Stronger assumptions about the assignment of treatment, assignment could be modeled on covariates

Estimand, Estimator

What do we want to know?

- We've talked about the ATE, various marginal effects, conditional marginal effects
- Other effects of interest: ITT, LATE, CATE
- Estimands not specified frequently (enough) in existing literature
- Snarky comment: Stars don't mean much if we don't know what the coefficient is measuring
- Estimator:
 - ► Too often we utilize estimators without identifying estimand
 - Many estimators consistent with each estimand though some work better than others...

The Guts: Declare Design

```
population <- declare_population()
sampling <- declare_sampling()
assignment <- declare_assignment()
potential_outcomes <- declare_potential_outcomes()
estimand <- declare_estimand()
estimator <- declare_estimator(estimand = estimand)</pre>
```

```
my_design <- declare_design(
    population = population,
    sampling = sampling,
    potential_outcomes = potential_outcomes,
    assignment = assignment,
    estimator = estimator)</pre>
```

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Audience for DeclareDesign

Three-ish audiences:

- 1. **Ninjas:** Advanced R users that (might) specify user-input functions for any design
- 2. **Advanced:** Use built-in functionalities to characterize a wide range of designs
- 3. **Novices:** Use template functions (some here, many forthcoming) to characterize and examine a variety of designs with a few simple arguments.

Using DeclareDesign

```
install.packages("devtools") # run once only!
library(devtools)
install_github("DeclareDesign/DeclareDesign") # run once or
library(devtools)
```

source("templates file.R")

Two templates in this file:

- ► Generalized *m*-arm
- 2 × 2 factorial

See .pdf for detail about all arguments to these functions.

How Can we Use DeclareDesign to Learn Designs?

- Suppose you want to extend Chong, De la O, Karlan, Wantchekon (2014) to a different context.
- Three treatment arms
 - 1. Pure control (no flyer)
 - 2. Placebo (flyer about the federal transfer)
 - 3. Treatment (flyer about federal transfer with results of corruption audit)
- DV: Turnout
- 600 municipalities are candidates for evaluation
- You can only afford to implement treatment and do data collection in 450 municipalities
- Hypothesized treatment effect comes from Chong et al. (2014) findings

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Design 1: No Pretreatment Covariate

Assume the following Potential Outcomes Function:

 $Turnout_i = 60 - 1.5 \times Treatment_i + 0.5 \times Placebo_i + \epsilon_i$

We can enter this entire design with the following code:

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Estimands are ATEs, Estimator is OLS

Design 2: Lagged Turnout as Pretreatment Covariate Assume the following Potential Outcomes Function:

 $\mathsf{Turnout}_i = 28.5 - 1.5 \times \mathsf{Treatment}_i + 0.5 \times \mathsf{Placebo}_i + 0.5 \times \mathsf{Turnout}_{t-1} + \epsilon_i$

Declare design without covariate adjustment:

three_arm_des_2 <-	- m_arm_template	(
Ν	= 600,	# 600 in population	
n	= 450,	# 450 in sample	
m	= 3,	# 3 arms, 150/arm	
mu_YO	= 28.5,	<i># basline in ctrl</i>	
ATEs	= c(-1.5, 0.5),	<pre># Treatment effects</pre>	
noise_scale	= 4,	# SD of error term	
coef_X	= 0.5,	<pre># Coef. on turnout,</pre>	t-1
<pre>location_scale_X</pre>	= c(65, 8),	# Mean, SD of turnou	t, t
cov_adjustment	= FALSE)	# No covariate adjus	tmen

Design 3: Lagged Turnout as Pretreatment Covariate Assume the following Potential Outcomes Function:

 $\mathsf{Turnout}_i = 28.5 - 1.5 \times \mathsf{Treatment}_i + 0.5 \times \mathsf{Placebo}_i + 0.5 \times \mathsf{Turnout}_{t-1} + \epsilon_i$

Declare design with covariate adjustment:

three_arm_des_3 <-	- m_arm_template	(
N	= 600,	# 600 in population	
n	= 450,	# 450 in sample	
m	= 3,	# 3 arms, 150/arm	
mu_YO	= 28.5,	<i># basline in ctrl</i>	
ATEs	= c(-1.5, 0.5),	<i># Treatment effects</i>	
noise_scale	= 4,	# SD of error term	
coef_X	= 0.5,	# Coef. on turnout, $t-1$	
<pre>location_scale_X</pre>	= c(65, 8),	<pre># Mean, SD of turnout,</pre>	t
cov_adjustment	= TRUE)	# No covariate adjustmen	t
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On what basis should we be comparing designs?

Assume that we run the analysis N times, collecting estimates $\hat{\theta}_1, \hat{\theta}_2, ..., \hat{\theta}_N$

Most important/standard:

- Bias: $\mathbb{E}[\hat{\theta} \theta]$
- RMSE: $\sqrt{\mathbb{E}[(\hat{\theta} \theta)^2]}$
- Coverage: Proportion of simulations in which this estimated 95% confidence intervals contains true estimand (θ)
- ▶ Power: Proportion of simulations in which $\hat{\theta}$ is significant at the $\alpha = 0.05$ level

Others:

- Type-S error rate: Proportion of simulations in which the sign of $\hat{\theta}$ is different from the true estimand θ
- Exaggeration ratio: $\mathbb{E}[\hat{\theta}]/\theta$

Diagnosis of designs:

Ancillary benefit:

data <- draw_data(three_arm_des_1) # Not diagnosis</pre>

Diagnosis of designs

d1 <- diagnose_design(three_arm_des_1, population_draws = 5
d2 <- diagnose_design(three_arm_des_2, population_draws = 5
d3 <- diagnose_design(three_arm_des_3, population_draws = 5
</pre>

Comparison of 3 designs

 Compare just the ATE of the treatment (corruption information) versus pure control

knitr::kable(df, digits = 3)

	Design_1	Design_2	Design_3
Mean, SATE	-1.500	-1.500	-1.500
S.D., SATE	0.000	0.000	0.000
Mean Sample RMSE	0.928	0.651	0.455
Mean Sample Bias	0.087	0.012	0.028
Mean Sample Coverage	0.916	0.948	0.936
Mean Sample Type S Rate	0.068	0.008	0.000
Mean Sample Exaggeration Ratio	0.942	0.992	0.981
Mean, Power	0.308	0.624	0.884
S.D., Power	0.190	0.234	0.122
Mean, Estimate	-1.413	-1.488	-1.472
S.D., Estimate	0.985	0.687	0.473

Take Aways

- 1. Framework to think about complete research designs
 - Move toward qustion "what could I learn given my design"
 - Way to conceptualize differences between different approaches
- 2. Tools for examining research designs ex-ante
 - Creating mock datasets
 - Diagnosing designs
- 3. Further steps (that I know of)
 - Development of templates for different research designs (suggestions welcome)
 - Some ammendments to current package to improve functionality/eliminate some issues
 - Programming work to increase speed of simulations, potentially expand to Stata