How to ensure that policy experiments are credible and actionable

Jake Bowers February 28, 2018

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A proposed research integrity process

Standard Operating Procedures

- Project Initiation: early ideas about the project are discussed to ensure general feasibility, proper planning, and wise investment of team resources prior to formally initiating a project and committing to a collaboration with agency partners
- ② Design Review: the project design is peer reviewed and then presented to the team, to ensure a sound design that effectively addresses research objectives before we invest resources in fielding a study
- Analysis Plan Commitment: an analysis plan (also known as a "pre-analysis plan" or "pre-specification plan") is finalized, date-stamped, and posted publicly on our website before data are received and analyzed
- **Findings Review**: an initial analysis of results is presented to the team, to ensure that tentative findings are consistent with a sound analysis of the data, that important limitations on the study's findings have been identified, and that alternative explanations have been addressed to the greatest extent possible
- Reanalysis: an internal replication of the initial analysis, to ensure that results and conclusions are sound, reliable, and reproducible
- Pre-Publication Review: to ensure OES maintains transparency, retains materials necessary for reproducibility, and meets all legal and administrative requirements in disseminating knowledge for the whole of government and the public

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2 Standard Operating Procedures

Current DRAFT OES SOP Principles

① Collaborate. Serve the agency partner. Practice humility and listening.

- Work in public as much as possible. (Post code, Post pre-analysis plans, Post results)
- S Randomization is a reasoned basis for statistical inference (i.e. *p*-values should refer to distributions generated by design). (Ramdom sampling, likelihood functions, Bayesian posterior (likelihood+prior) are all reasoned bases as well. But we can much more easily test hypotheses about alternative randomizations than we can justify the other claims.)

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Setup an experiment:

```
set.seed(20180225)
N <- 50
K <- 30
Xdat <- as.data.frame(replicate(K,rnorm(N)))
names(Xdat) <- paste0("X",1:K)
y0 <- Xdat$X1+Xdat$X2+rchisq(N,df=1)
y1 <- y0 + rnorm(N,mean=0,sd=sd(y0))## No treatment effect but different variance
Z <- complete_ra(N,m=15) ## very simple randomization
Y <- Z*y1 + (1-Z) * y0 ## randomization reveals a potential outcome
dat <- data.frame(cbind(Xdat,Y=Y,Z=Z,y0=y0,y1=y1))</pre>
```

Hansen and Bowers (2008) developed an omnibus balance test that refers to a Normal distribution that approximates the randomization-based reference distribution in large-samples. (see the help page for balanceTest for strata() and cluster() arguments for block and/or clustered designs)

```
balfmla <- reformulate(names(Xdat),response="Z")
## See balanceTest help for block and cluster randomized designs
randTest1 <- balanceTest(balfmla,data=dat,report="all",p.adjust.method="none")
signif(randTest1$results[,"p",J,3)[1:5]</pre>
```

X1 X2 X3 X4 X5 0.1430 0.0924 0.3980 0.5700 0.7510

randTest1\$overall[1,]

chisquare df p.value 34.0239 30.0000 0.2799

sum(randTest1\$results[,"p",]<.05,na.rm=TRUE) ## How many false positives</pre>

[1] 3

A common approach with two problems (separation/problems in high dimensions and not-randomization based reference distribution)

```
balfmla <- reformulate(names(Xdat),response="Z")
## See balanceTest help for block and cluster randomized designs
glm1 <- glm(balfmla,data=dat,family=binomial())</pre>
```

Warning: glm.fit: algorithm did not converge

Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

```
glm0 <- glm(Z~1,data=dat,family=binomial())
anova(glm0,glm1,test="Chisq")</pre>
```

```
Analysis of Deviance Table
```

```
Model 1: Z ~ 1
Model 2: Z ~ X1 + X2 + X3 + X4 + X5 + X6 + X7 + X8 + X9 + X10 + X11 +
X12 + X13 + X14 + X15 + X16 + X17 + X18 + X19 + X20 + X21 +
X22 + X23 + X24 + X25 + X26 + X27 + X28 + X29 + X30
Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1     49     61.1
2     19     0.0 30     61.1     0.00068 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Example 1: Randomization Assessment Which to use? How should we choose? (One idea: False Positive Rate)

newExp <- function(N){ complete_ra(N,m=15) }
getPvalues <- function(){
 dat\$newZ <- newExp(N)
 newfmla <- reformulate(names(Xdat),response="newZ")
 bt1 <- balanceTest(newfmla,data=dat,report="all",p.adjust.method="none")
 btp<-bt1\$overall[1,"p.value"]
 theglm1 <- glm(newfmla,data=dat,family=binomial())
 theglm0 <- glm(newZ-1,data=dat,family=binomial())
 theanova <- anova(theglm0,theglm1,test="Chisq")
 anovap <- theanova[2,"Pr(>Chi)"]
 return(c(btp = btp, anovap = anovap))
}

```
theps <- replicate(1000,getPvalues())
theps[,1:5]</pre>
```

[,1] [,2] [,3] [,4] [,5] btp 0.1384167 0.2308195 0.5880233 0.2045699 0.1915891 anovap 0.0006787 0.0006787 0.0006787 0.0006787 0.0006787

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apply(theps,1,function(x){ mean(x<=.05) })</pre>

btp anovap 0 NA

Example 2: Pre-registration

We pre-register that we will look at the effect of the treatment moderated by X1:

```
lm1 <- lm(Y-Z*X1,data=dat)
lm1ci <- coefci(lm1,vcov=vcovHC(lm1,type="HC2"))
lm1p <- coeftest(lm1,vcov=vcovHC(lm1,type="HC2"))[4,4]</pre>
```

vs we hunt for a statistically significant moderating effect:

Example 2: Pre-registration

How often will we make a false positive error in each case?

```
preRegProcedure <- function(newZ){</pre>
  lm1 <- lm(Y~newZ*X1.data=dat)</pre>
  lm1p <- coeftest(lm1,vcov=vcovHC(lm1,type="HC2"))[4,4]</pre>
  return(lm1p)
pHuntProcedure <- function(newZ){
  theres <- sapply(dat[,names(Xdat)],function(thex){</pre>
                      thelm<-lm(Y~newZ*thex.data=dat)
                      lm1p <- coeftest(thelm.vcov=vcovHC(thelm.tvpe="HC2"))[4,4]</pre>
                      return(lm1p)
})
  anx <- names(theres[theres==min(theres)])
  afmla <- as.formula(paste0("Y~newZ*",anx))
  alm <- lm(afmla.data=dat)
  almp <- coeftest(alm,vcov=vcovHC(alm,type="HC2"))[4,4]</pre>
  return(almp)
}
assessPs <- function(newZ){
  preRegP <- preRegProcedure(newZ = newZ)
  pHuntP <- pHuntProcedure(newZ = newZ)
  return(c(preregp=preRegP, phuntp = pHuntP))
```

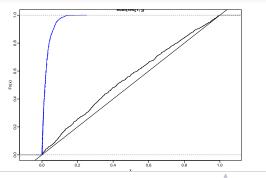
Example 2: Pre-registration

Notice that we could have similar kinds of issues with covariance adjustment and not moderating effects.

```
res <- replicate(1000,assessPs(newZ=complete_ra(N=50,m=15)))
apply(res,1,function(x){ mean(x <=.05) })</pre>
```

```
preregp phuntp
0.065 0.852
```

```
plot(ecdf(res[1,]))
plot(ecdf(res[2,]),add=TRUE,col="blue")
abline(0,1)
```



Example 3: Covariance Adjustment Avoiding Bias

We often use OLS to estimate the ATE using β_1 (below).

$$Y_i = \beta_0 + \beta_1 Z_i$$

$$\hat{\beta}_1 = \Upsilon \overline{Z} = 1 - \Upsilon \overline{Z} = 0 = \frac{\operatorname{cov}(\Upsilon, Z)}{\operatorname{var}(Z)}$$

And we know:

$$E_R(\hat{\beta}_1) = \beta_1 \equiv \mathsf{ATE}$$

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Example 3: Covariance Adjustment Avoiding Bias

Now, what about when we have a covariate X_i and we use it as would be normal in the analysis of non-experimental data:

$$Y_i = \beta_0 + \beta_1 Z_i + \beta_2 X_i$$

What is β_1 in this case? Well, we all know the matrix representation here $(X^T X)^{-1} X^T y$, but here is the scalar formula for this case:

$$\hat{\beta}_1 = \frac{\operatorname{var}(X)\operatorname{cov}(Z, Y) - \operatorname{cov}(X, Z)\operatorname{cov}(X, Y)}{\operatorname{var}(Z)\operatorname{var}(X) - \operatorname{cov}(Z, X)^2}$$

In very large experiments $cov(X, Z) \approx 0$ however in any given finite sized experiment $cov(X, Z) \neq 0$ so this does not reduce to the unbiased estimator of the bivariate case. Is it itself unbiased?

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References