Sensitivity and Effective Samples

Drew Dimmery drewd@nyu.edu

February 14, 2014

Plan for today

- First homework
  - Some issues with identification / estimation
- Second homework
  - Some basic asymptotics
- Effective Samples in regression
  - Aronow & Samii (2013)
- Confounding & Sensitivity Analysis
  - Imbens (2003)
  - And generalizations (which are easy)

Identification / Estimation

- The "Four questions" may have been a little confusing.
- Let me re-break down the last two questions as "Identification" and "Estimation"
- "A regression is causal when the CEF it approximates is causal" - MHE
- Identification consists (in this context) as the set of things you need to believe in order to believe the CEF is causal.
- Thus, when we think about identification, we should think about assumptions.
- Estimation is the process you use to estimate the CEF.

In practice

- The Conditional Independence Assumption would fall in identification.
- I'd also throw in assumptions of additivity / linearity in this pot.
- Estimation would include the populations/samples of interest, and all statistical inference.
- But there's a close connection between the two.
- Problems in estimation can lead to changes in identifying assumptions.
- So they aren't completely separable.

Basic Identities and Definitions

- Convergence in probability:
  $X_n \xrightarrow{p} X$ if $\forall \epsilon > 0 \quad \Pr(|X_n - X| > \epsilon) \to 0$ as $n \to \infty$
- A very basic decomposition of variance:
  $\mathrm{var}(X) = E[X^2] - E[X]^2$
- Something we do NOT know: $E[XY] = E[X] \times E[Y]$
- Pretty much everybody assumed this to be true.

Problem Set 2

- We want to find the probability limit of $\frac{D_d' D_d}{N}$
- Pretty much everyone correctly observed that this was:

$$\begin{pmatrix} \frac{1}{N}\sum_i (X_i - \bar{X})^2 & \frac{1}{N}\sum_i (X_i - \bar{X})(Z_i - \bar{Z}) \\ \frac{1}{N}\sum_i (X_i - \bar{X})(Z_i - \bar{Z}) & \frac{1}{N}\sum_i (Z_i - \bar{Z})^2 \end{pmatrix}$$

- We can't simply say that this is equal to the following, though:

$$\begin{pmatrix} \frac{1}{N}\sum_i (X_i - p)^2 & \frac{1}{N}\sum_i (X_i - p)(Z_i - q) \\ \frac{1}{N}\sum_i (X_i - p)(Z_i - q) & \frac{1}{N}\sum_i (Z_i - q)^2 \end{pmatrix}$$

- This is a fact which you should all be able to recognize as false IMMEDIATELY.

Continued

- The sample variance is BIASED when divided by N rather than $N - 1$.
- It is still consistent, though, which is what is relevant to us.
- The simple proof is as follows:
  $\frac{\sum_i (X_i - \bar{X})^2}{N} = \frac{1}{N}\left(\sum_i X_i^2 - 2\sum_i \bar{X} X_i + \sum_i \bar{X}^2\right)$

- We can pull out constants from the sums:
  $\frac{1}{N}\left(\sum_i X_i^2 - 2\bar{X}\sum_i X_i + \bar{X}^2\sum_i 1\right)$
- And simplify some things:
  $\frac{\sum_i X_i^2}{N} - 2\bar{X}^2 + \bar{X}^2 = \frac{\sum_i X_i^2}{N} - \frac{\sum_i \bar{X}^2}{N}$
- This is the point at which we can use the LLN. Averages converge in probability to their expectations.
  $E[X^2] - E[\bar{X}^2]$
- Use this identity: $E[Z^2] = E[Z]^2 + \text{var}(Z)$

- Which gives us: $E[X]^2 + \text{var}(X)$ and $E[\bar{X}]^2 + \text{var}(\bar{X})$
- Substituting in these identities:
  $E[X]^2 + \text{var}(X) - E[\bar{X}]^2 - \text{var}(\bar{X})$
- Which gives us: $p^2 + p(1-p) - p^2 - \frac{p(1-p)}{N} = \frac{N-1}{N}p(1-p)$
- Which converges in probability to $p(1-p)$ (i.e. it is consistent)

Finishing it up:

- After that there weren't many issues
- We know off-diagonals are zero because X and Z are independent.
- This means we have a diagonal matrix, which is easy to invert (just take the inverse of the diagonal elements)
- We then use a similar method to find $D_d'Y$, and multiply them together, which completes the first part.
- For the next part, observe that we know $\text{var}(X_i) = p(1-p)$, so we only need to think about the expectation of the numerator.
- We end up with the following:
  $\text{cov}(X,Y) = E[XY] - E[X]E[Y] = E[Y|X=1]p(X=1) - pE[Y]$
- We then use the law of total probability on $E[Y]$:
  $pE[Y|X=1] - p(pE[Y|X=1] + (1-p)E[Y|X=0])$
- Distribute and collect terms:
  $p(1-p)\left(E[Y|X=1] - E[Y|X=0]\right)$
- By random assignment of X, we have:
  $p(1-p)\left(E[Y_1 - Y_0]\right)$
- So dividing by $p(1-p)$ will leave us with ρ

Effective Samples

- We're going to be investigating how to check the properties of your effective sample in regression.
- The key result is:
  $\hat{\rho}_{reg} \xrightarrow{p} \frac{E[w_i\rho_i]}{E[w_i]}$ where $w_i = \text{var}(D_i|X_i)$

- We estimate these weights with:
  $\hat{w}_i = \hat{D}_i^2$ where D_i^2 is the ith squared residual.
- Because these estimates are "bad" for each unit, using them to reweight the sample is a bad idea.
- Instead, we just use them to get a sense for what the effective sample is by examining the weight allocated to particular strata.
- We will now explore how to do this.

Example paper

- We will be looking at Egan and Mullin (2012)
- This paper explores the effect of local weather variations on belief in global warming.
- Very cool paper! With an interesting randomized treatment.
- But what is the effective sample?
- In other words, where is weather (conditional on covariates) most variable?
- That's what we'll explore.

Load in data

- Get the data from Pat's replication materials here.

. . .

```
require(foreign)
d <- read.dta("gwdataset.dta")

## Warning: value labels ('q2') for 'jan07_q2' are missing

zips <- read.dta("zipcodetostate.dta")
zips <- unique(zips[, c("statenum", "statefromzipfile")])
pops <- read.csv("population_ests_2013.csv")
pops$state <- tolower(pops$NAME)
d$getwarmord <- as.double(d$getwarmord)
# And estimate primary model of interest:
out <- lm(getwarmord ~ ddt_week + educ_hsless + educ_coll + educ_postgrad +
    educ_dk + party_rep + party_leanrep + party_leandem + party_dem + male +
    raceeth_black + raceeth_hisp + raceeth_notwbh + raceeth_dkref + age_1824 +
    age_2534 + age_3544 + age_5564 + age_65plus + age_dk + ideo_vcons + ideo_conservative +
    ideo_liberal + ideo_vlib + ideo_dk + attend_1 + attend_2 + attend_3 + attend_5 +
    attend_6 + attend_9 + as.factor(doi) + as.factor(statenum) + as.factor(wbnid_num),
    d)
# And partial regression:
```

Base Model

- We won't worry about standard errors yet.

. . .

```
summary(out)$coefficients[1:10, ]
```

```
##                 Estimate Std. Error t value  Pr(>|t|)
## (Intercept)     1.945740   0.771479  2.5221 1.169e-02
## ddt_week        0.004858   0.002476  1.9621 4.980e-02
## educ_hsless     0.057740   0.024484  2.3583 1.839e-02
## educ_coll       0.021457   0.027095  0.7919 4.284e-01
## educ_postgrad   0.049387   0.030734  1.6069 1.081e-01
## educ_dk         0.102936   0.250495  0.4109 6.811e-01
## party_rep      -0.243900   0.036627 -6.6591 2.992e-11
## party_leanrep  -0.092809   0.041812 -2.2197 2.648e-02
## party_leandem   0.147409   0.039024  3.7774 1.600e-04
## party_dem       0.175427   0.035267  4.9743 6.725e-07
```

Estimate D^2

- We can simply square the residuals of a partial regression to get D^2:

. . .

```
outD <- lm(ddt_week ~ educ_hsless + educ_coll + educ_postgrad + educ_dk + party_rep +
    party_leanrep + party_leandem + party_dem + male + raceeth_black + raceeth_hisp +
    raceeth_notwbh + raceeth_dkref + age_1824 + age_2534 + age_3544 + age_5564 +
    age_65plus + age_dk + ideo_vcons + ideo_conservative + ideo_liberal + ideo_vlib +
    ideo_dk + attend_1 + attend_2 + attend_3 + attend_5 + attend_6 + attend_9 +
    as.factor(doi) + as.factor(statenum) + as.factor(wbnid_num), d)
D2 <- residuals(outD)^2
```

Effective Sample Statistics

- We can use these estimated weights for examining the sample.

. . .

```
compare_samples <- d[, c("wave", "ddt_week", "ddt_twoweeks", "ddt_threeweeks",
    "party_rep", "attend_1", "ideo_conservative", "age_1824", "educ_hsless")]
compare_samples <- apply(compare_samples, 2, function(x) c(mean(x), sd(x), weighted.mean(x,
    D2), sqrt(weighted.mean((x - weighted.mean(x, D2))^2, D2))))
compare_samples <- t(compare_samples)
colnames(compare_samples) <- c("Nominal Mean", "Nominal SD", "Effective Mean",
    "Effective SD")
compare_samples
```

```
##                   Nominal Mean Nominal SD Effective Mean Effective SD
## wave                   3.09694     1.4253        3.20788       1.5609
## ddt_week               3.83549     5.9047        5.11579      10.8980
## ddt_twoweeks           3.85506     5.4572        5.00137       9.2263
## ddt_threeweeks         3.96720     4.7690        5.10859       8.4348
## party_rep              0.29527     0.4562        0.28978       0.4537
## attend_1               0.11433     0.3182        0.12343       0.3289
## ideo_conservative      0.31133     0.4631        0.29325       0.4553
## age_1824               0.07196     0.2584        0.06881       0.2531
## educ_hsless           0.34151     0.4743        0.31220       0.4634
```

Effective Sample Maps

- But one of the most interesting things is to see this visually.
- Where in the US does the effective sample emphasize?
- To get at this, we'll use some tools in R that make this incredibly easy.
- In particular, we'll do this in ggplot2.

. . .

```
# Effective sample by state
wt.by.state <- tapply(D2, d$statenum, sum)
wt.by.state <- wt.by.state/sum(wt.by.state) * 100
wt.by.state <- cbind(D2 = wt.by.state, statenum = names(wt.by.state))
data_for_map <- merge(wt.by.state, zips, by = "statenum")
# Nominal Sample by state
wt.by.state <- tapply(rep(1, 6726), d$statenum, sum)
wt.by.state <- wt.by.state/sum(wt.by.state) * 100
wt.by.state <- cbind(Nom = wt.by.state, statenum = names(wt.by.state))
data_for_map <- merge(data_for_map, wt.by.state, by = "statenum")
# Get correct state names
require(maps, quietly = TRUE)
data(state.fips)
data_for_map <- merge(state.fips, data_for_map, by.x = "abb", by.y = "statefromzipfile")
```

```
data_for_map$D2 <- as.double(as.character(data_for_map$D2))
data_for_map$Nom <- as.double(as.character(data_for_map$Nom))
data_for_map$state <- sapply(as.character(data_for_map$polyname), function(x) strsplit(x,
    ":")[[1]][1])
data_for_map$Diff <- data_for_map$D2 - data_for_map$Nom
data_for_map <- merge(data_for_map, pops, by = "state")
data_for_map$PopPct <- data_for_map$POPESTIMATE2013/sum(data_for_map$POPESTIMATE2013) *
    100
data_for_map$PopDiffEff <- data_for_map$D2 - data_for_map$PopPct
data_for_map$PopDiffNom <- data_for_map$Nom - data_for_map$PopPct
data_for_map$PopDiff <- data_for_map$PopDiffEff - data_for_map$PopDiffNom
require(ggplot2, quietly = TRUE)
state_map <- map_data("state")
```

More setup

```
plotEff <- ggplot(data_for_map, aes(map_id = state))
plotEff <- plotEff + geom_map(aes(fill = D2), map = state_map)
plotEff <- plotEff + expand_limits(x = state_map$long, y = state_map$lat)
plotEff <- plotEff + scale_fill_continuous("% Weight", limits = c(0, 16), low = "white",
    high = "black")
plotEff <- plotEff + labs(title = "Effective Sample")
plotEff <- plotEff + theme(legend.position = c(0.2, 0.1), legend.direction = "horizontal",
    axis.line = element_blank(), axis.text = element_blank(), axis.ticks = element_blank(),
    axis.title = element_blank(), panel.background = element_blank(), plot.background = elen
    panel.border = element_blank(), panel.grid = element_blank())

plotNom <- ggplot(data_for_map, aes(map_id = state))
plotNom <- plotNom + geom_map(aes(fill = Nom), map = state_map)
plotNom <- plotNom + expand_limits(x = state_map$long, y = state_map$lat)
plotNom <- plotNom + scale_fill_continuous("% Weight", limits = c(0, 16), low = "white",
    high = "black")
plotNom <- plotNom + labs(title = "Nominal Sample")
plotNom <- plotNom + theme(legend.position = c(0.2, 0.1), legend.direction = "horizontal",
    axis.line = element_blank(), axis.text = element_blank(), axis.ticks = element_blank(),
    axis.title = element_blank(), panel.background = element_blank(), plot.background = elen
    panel.border = element_blank(), panel.grid = element_blank())
```

And the maps

```
require(gridExtra, quietly = TRUE)
grid.arrange(plotNom, plotEff, ncol = 2)
```

Setup Comparison Plot

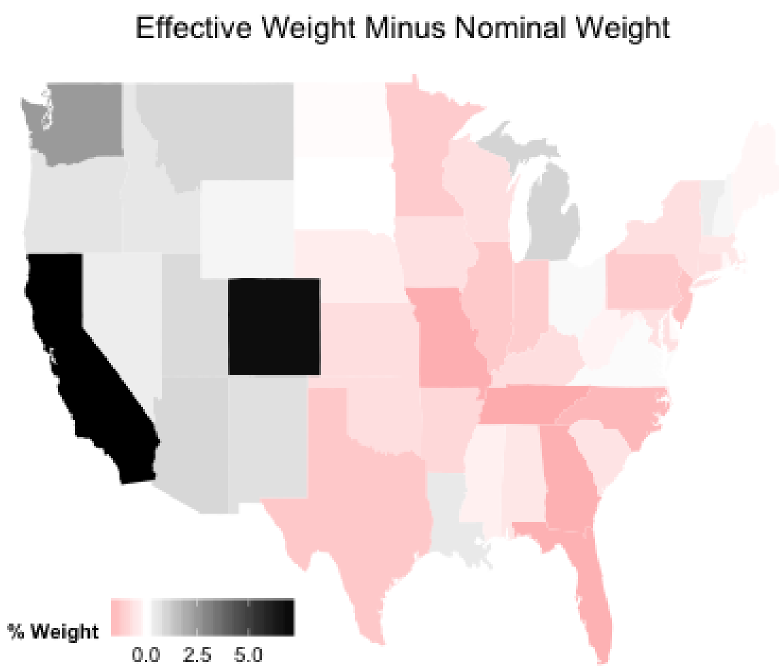
```
plotDiff <- ggplot(data_for_map, aes(map_id = state))
plotDiff <- plotDiff + geom_map(aes(fill = Diff), map = state_map)
plotDiff <- plotDiff + expand_limits(x = state_map$long, y = state_map$lat)
plotDiff <- plotDiff + scale_fill_gradient2("% Weight", low = "red", mid = "white",
    high = "black")
plotDiff <- plotDiff + labs(title = "Effective Weight Minus Nominal Weight")
plotDiff <- plotDiff + theme(legend.position = c(0.2, 0.1), legend.direction = "horizontal",
    axis.line = element_blank(), axis.text = element_blank(), axis.ticks = element_blank(),
    axis.title = element_blank(), panel.background = element_blank(), plot.background = elem
    panel.border = element_blank(), panel.grid = element_blank())
```

Difference in Weights

```
plotDiff
```

Population Comparison

```
plotEff <- ggplot(data_for_map, aes(map_id = state))
plotEff <- plotEff + geom_map(aes(fill = PopDiffEff), map = state_map)
plotEff <- plotEff + expand_limits(x = state_map$long, y = state_map$lat)
plotEff <- plotEff + scale_fill_gradient2("% Weight", limits = c(-2, 6), low = "red",
    mid = "white", high = "black")
plotEff <- plotEff + labs(title = "Effective Sample")
plotEff <- plotEff + theme(legend.position = c(0.2, 0.1), legend.direction = "horizontal",
    axis.line = element_blank(), axis.text = element_blank(), axis.ticks = element_blank(),
    axis.title = element_blank(), panel.background = element_blank(), plot.background = elem
```

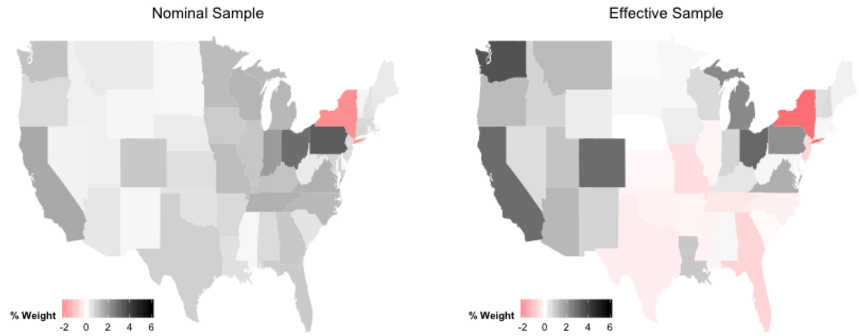

Effective Weight Minus Nominal Weight
% Weight
0.0
2.5
5.0

```
    panel.border = element_blank(), panel.grid = element_blank())

plotNom <- ggplot(data_for_map, aes(map_id = state))
plotNom <- plotNom + geom_map(aes(fill = PopDiffNom), map = state_map)
plotNom <- plotNom + expand_limits(x = state_map$long, y = state_map$lat)
plotNom <- plotNom + scale_fill_gradient2("% Weight", limits = c(-2, 6), low = "red",
    mid = "white", high = "black")
plotNom <- plotNom + labs(title = "Nominal Sample")
plotNom <- plotNom + theme(legend.position = c(0.2, 0.1), legend.direction = "horizontal",
    axis.line = element_blank(), axis.text = element_blank(), axis.ticks = element_blank(),
    axis.title = element_blank(), panel.background = element_blank(), plot.background = elen
    panel.border = element_blank(), panel.grid = element_blank())
```

Population Comparison Plots

```
grid.arrange(plotNom, plotEff, ncol = 2)
```

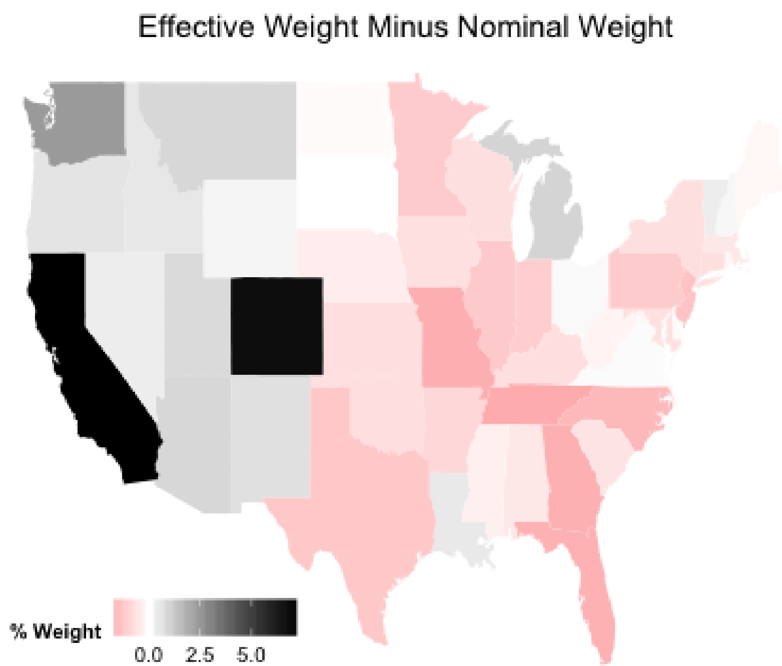


Setup New Comparison Plot

```
plotDiff <- ggplot(data_for_map, aes(map_id = state))
plotDiff <- plotDiff + geom_map(aes(fill = PopDiff), map = state_map)
plotDiff <- plotDiff + expand_limits(x = state_map$long, y = state_map$lat)
plotDiff <- plotDiff + scale_fill_gradient2("% Weight", low = "red", mid = "white",
    high = "black")
plotDiff <- plotDiff + labs(title = "Effective Weight Minus Nominal Weight")
plotDiff <- plotDiff + theme(legend.position = c(0.2, 0.1), legend.direction = "horizontal",
    axis.line = element_blank(), axis.text = element_blank(), axis.ticks = element_blank(),
    axis.title = element_blank(), panel.background = element_blank(), plot.background = elen
    panel.border = element_blank(), panel.grid = element_blank())
```

Plot Difference

```
plotDiff
```



Sensitivity Analysis

- The homework mentions a couple places to find pre existing code.
- I'm going to walk you through how to do a generalized version of the Imbens (2003) method.
- It may be easier to use one of the canned routines for your homework, though.
- We're going to keep working with Pat's data, since we already have it handy.
- Imbens process:
  - Simulate (or imagine simulating) an unobserved confounder like the following:

$Y_d|X, U \sim \mathcal{N}(\tau d + \beta' X + \delta U, \sigma^2)$
$D|X, U \sim f(\gamma' X + \alpha U)$ (with f known)

- That is, $Y_1, Y_0 \perp D|X, U$
- So we want to generate an additively linear confounder with both D and Y.

Generate a confounder

- For our analysis, Y is belief in global warming and D is local variation in temperature.
- We want to standardize these variables first.

. . .

```
d$getwarmord <- scale(d$getwarmord)
d$ddt_week <- scale(d$ddt_week)
genConfound <- function(alpha, delta) {
    e <- rnorm(nrow(d), 0, 1)
    U <- alpha * d$ddt_week + delta * d$getwarmord + e
    return(U)
}
```

. . .

- So we can vary partial correlations with D and Y by varying `alpha` and `delta`.

. . .

```
U1 <- genConfound(0, 2)
U2 <- genConfound(10, 10)
c(D = cor(U1, d$ddt_week), Y = cor(U1, d$getwarmord))
```

```
##      D      Y
## 0.0305 0.8913
```

```
c(D = cor(U2, d$ddt_week), Y = cor(U2, d$getwarmord))
```

```
##      D      Y
## 0.7192 0.7208
```

```
X <- "educ_hsless+educ_coll+educ_postgrad+educ_dk+party_rep+party_leanrep+party_leandem+part
c(D = coef(lm(paste0("ddt_week~U1+", X), d))["U1"], Y = coef(lm(paste0("getwarmord~U1+",
    X), d))["U1"])
```

```
##     D.U1     Y.U1
## 0.005302 0.388986
```

```
c(D = coef(lm(paste0("ddt_week~U2+", X), d))["U2"], Y = coef(lm(paste0("getwarmord~U2+",
    X), d))["U2"])
```

```
##    D.U2    Y.U2
## 0.03226 0.06704
```

Continued

- More importantly, we can see how this changes our estimate of the treatment effect:

. . .

```
out <- lm(paste0("getwarmord~ddt_week+", X), d)
coef(out)["ddt_week"]
```

```
## ddt_week
##  0.03618
```

```
coef(lm(paste0("getwarmord~ddt_week+U1+", X), d))["ddt_week"]
```

```
## ddt_week
##  0.01399
```

```
coef(lm(paste0("getwarmord~ddt_week+U2+", X), d))["ddt_week"]
```

```
## ddt_week
##  -0.9855
```

- Now we want to do this over a larger number of values of `alpha` and `delta`

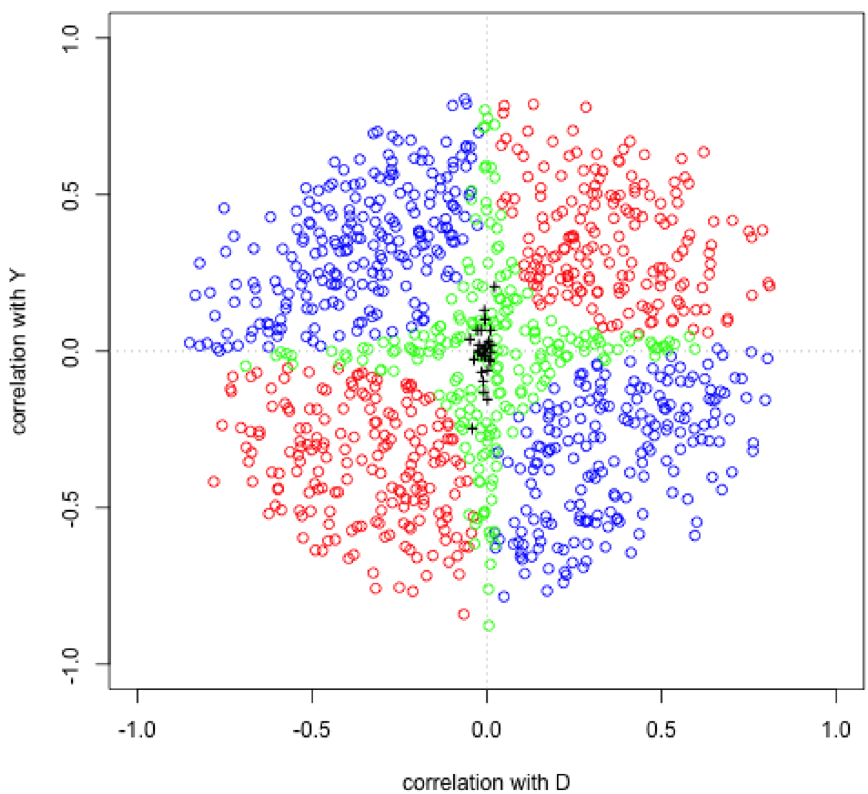
. . .

```r
alphas <- rnorm(1000, 0, 0.5)
deltas <- rnorm(1000, 0, 0.5)
results <- NULL
for (i in seq_len(length(alphas))) {
    U <- genConfound(alphas[i], deltas[i])
    corD <- cor(U, d$ddt_week)
    corY <- cor(U, d$getwarmord)
    estTE <- coef(lm(paste0("getwarmord~ddt_week+U+", X), d))["ddt_week"]
    names(estTE) <- NULL
    res <- c(estTE = estTE, corD = corD, corY = corY)
    results <- rbind(results, res)
}
results <- cbind(results, TEchange = (results[, "estTE"] - coef(out)["ddt_week"]))
```

Plot Simulation Code

```r
color <- ifelse(results[, "estTE"] <= 0.5 * coef(out)["ddt_week"], "red", NA)
color <- ifelse(is.na(color) & results[, "estTE"] >= 1.5 * coef(out)["ddt_week"],
    "blue", color)
color <- ifelse(is.na(color), "green", color)
plot(results[, "corD"], results[, "corY"], col = color, xlab = "correlation with D",
    ylab = "correlation with Y", xlim = c(-1, 1), ylim = c(-1, 1))
vars <- strsplit(X, "[+]", perl = TRUE)[[1]]
vars <- vars[grep("factor", vars, invert = TRUE)]
for (v in vars) {
    corD <- with(d, cor(get(v), d$ddt_week))
    corY <- with(d, cor(get(v), d$getwarmord))
    points(corD, corY, pch = "+", col = "black")
}
abline(v = 0, col = "grey", lty = 3)
abline(h = 0, col = "grey", lty = 3)
```

Plot of the Results


1.0
0.5
0.0
-0.5
-1.0
correlation with Y
-1.0
-0.5
0.0
0.5
1.0
correlation with D