

Supplementary Data

The following annotated R code performs the statistical analysis described in Using Propensity Score Methods to Assess Causal Effects of Mothers' Dieting Behavior on Daughters' Early Dieting Behavior.

R Code

```
#Load the twang package and set the working directory
library(twang)
setwd("C:/Users/dlc30/Documents/working data")

#Import data
GNS <- read.csv(file = "earlydietms.csv", header = TRUE)

#Limit data to those who have not yet begun dieting
GNS <- GNS[GNS$G1DIET == 0, ]
attach(GNS)
set.seed(1234)

#Estimate the propensity scores and include the moderator,
g1ovrcdc

gbm.GNS <- ps(M2CURLS ~ DIABETZ1 + M1AGE1 +
M1BMI + M1DEPRS + M1ESTEEM + M1NOEX +
M1WTCON + M1YRED + MOMHRS1 + M1CURLS +
M1CURMT + M1GSATN + M1MFATCN +
M1GFATCN + M1PCEEXT + M1WGTTES + m1cfqrsp +
m1cfqrst + m1picky + m1dis + m1hung + m1rest +
G1WTCON + g1tottes + g1pFM + D1MNOW + g1ovrcdc,

  data = GNS, estimand = "ATE",
  stop.method = "es.mean",
  n.trees = 10000, interaction.depth = 4, shrinkage = 0.001,
  perm.test.iters = 0, verbose = FALSE)

#More details on the options mentioned may be found in
the tutorial for the twang package
```

```
#Save the propensity scores
GNS$pihat.gbm <- gbm.GNS$ps$es.mean

#Fit a numerator model for the weights that includes only
the moderator, g1ovrcdc
num.mod <- glm(M2CURLS ~ g1ovrcdc, data = GNS,
family = binomial)

#Save the predicted probabilities from the numerator
model
GNS$num <- num.mod$fitted

#Balance assessment diagnostics
plot(gbm.GNS, plots = "boxplot")
plot(gbm.GNS, plots = "es")
bal.table(gbm.GNS)

#Calculate weights and descriptives of weights
GNS$gbm.ipw <- ifelse(GNS$M2CURLS == 1, GNS$num/
GNS$pihat.gbm, (1-GNS$num)/(1-GNS$pihat.gbm))

mean(GNS$gbm.ipw)
range(GNS$gbm.ipw)

#Outcome analysis using GBM weights to estimate causal
effect, early diet is the outcome

#Include the six potential confounders that had absolute
standardized mean differences >0.25 as covariates
design.1 <- svydesign(ids = ~ 1, weights = ~ gbm.ipw,
data = GNS)
mod.1 <- svyglm(earlydiet ~ M2CURLS + g1ovrcdc +
M2CURLS:g1ovrcdc + M1CURLS + M1CURMT +
M1WTCON + G1WTCON + m1rest + M1BMI,
  design = design.1, family = binomial)
summary(mod.1)
```