

Causal Modeling in R: Whole Game

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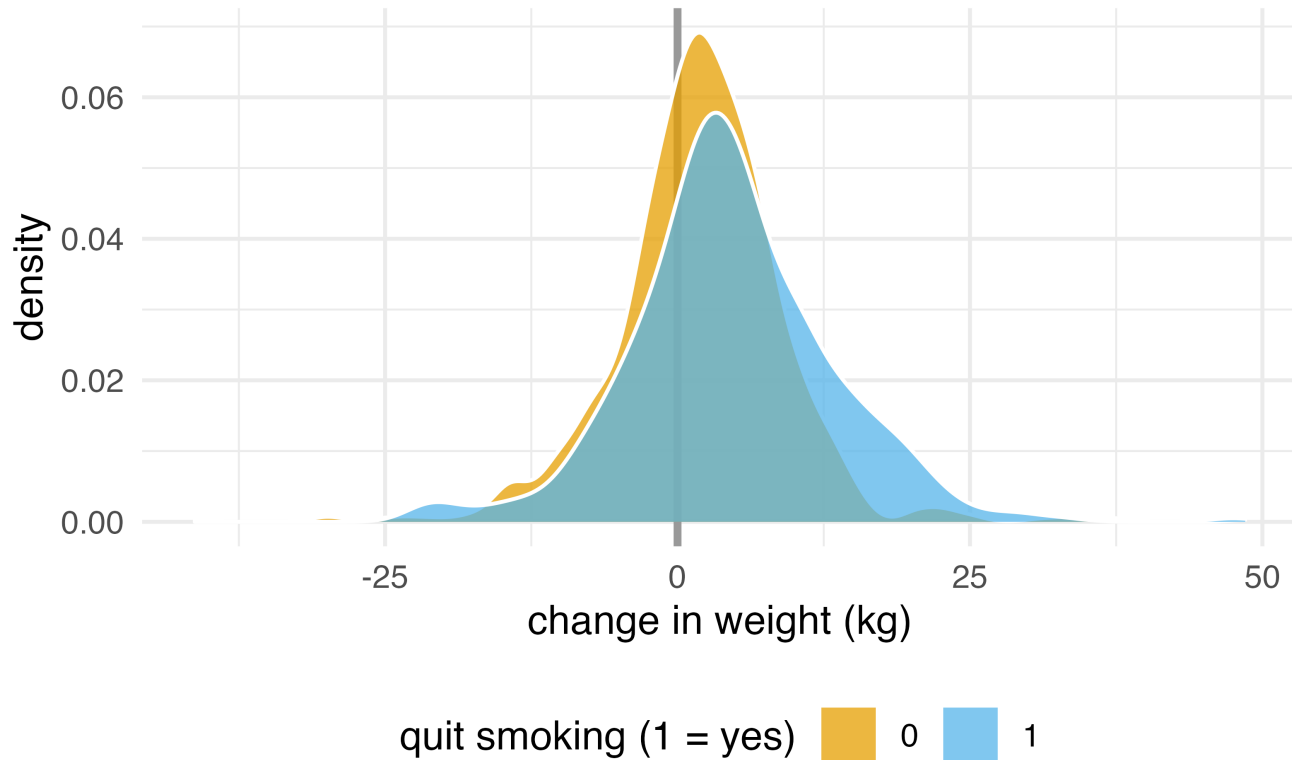
- 1 Specify causal question**
- 2 Draw assumptions (causal diagram)**
- 3 Model assumptions (e.g. propensity score)**
- 4 Analyze propensities (diagnostics)**
- 5 Estimate causal effects (e.g. IPW)**
- 6 Sensitivity analysis (more later!)**

**Do people who quit smoking
gain weight?**

```
library(causaldata)
nhefs_complete_uc <- nhefs_complete %>%
  filter(censored == 0)
nhefs_complete_uc
```

```
## # A tibble: 1,566 × 67
##      seqn  qsmk death yrdth modth dadth  sbp  dbp sex
##      <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <fct>
##  1    233     0     0    NA    NA    NA   175   96 0
##  2    235     0     0    NA    NA    NA   123   80 0
##  3    244     0     0    NA    NA    NA   115   75 1
##  4    245     0     1    85     2    14   148   78 0
##  5    252     0     0    NA    NA    NA   118   77 0
##  6    257     0     0    NA    NA    NA   141   83 1
##  7    262     0     0    NA    NA    NA   132   69 1
##  8    266     0     0    NA    NA    NA   100   53 1
##  9    419     0     1    84    10    13   163   79 0
## 10    420     0     1    86    10    17   184  106 0
## # ... with 1,556 more rows, and 58 more variables: age <dbl>,
## # race <fct>, income <dbl>, marital <dbl>, school <dbl>,
## # education <fct>, ...
```

Did those who quit smoking gain weight?

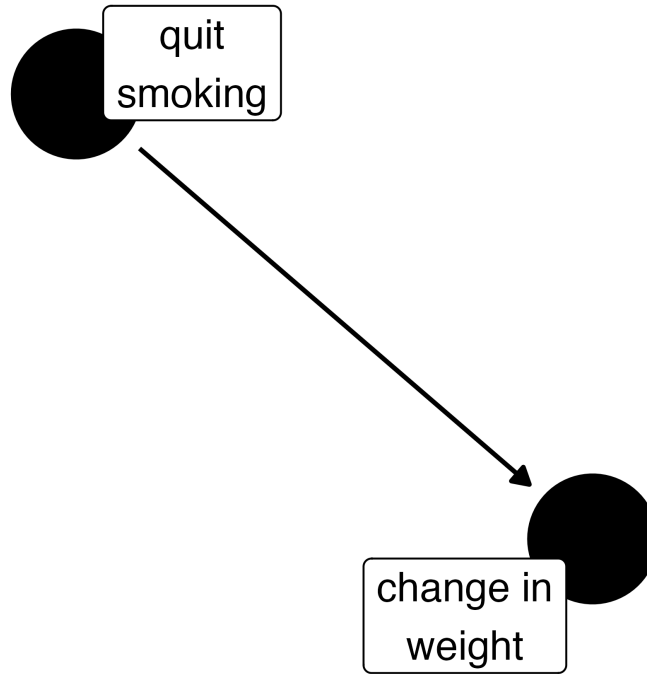


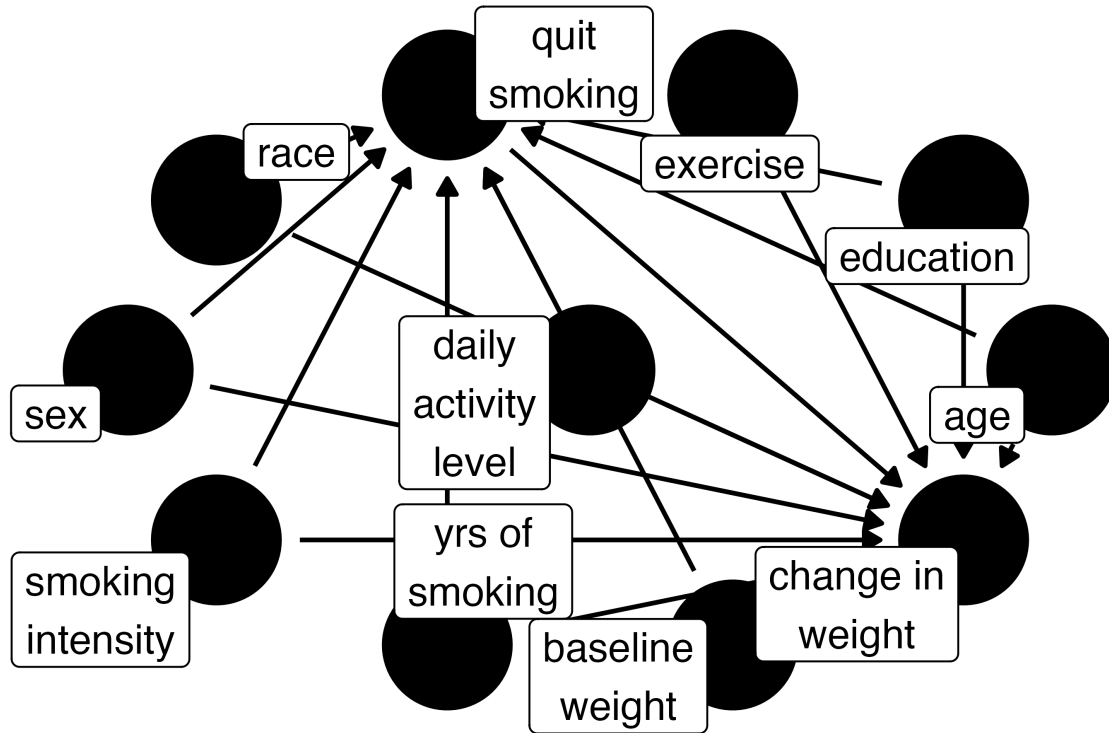
Did those who quit smoking gain weight?

```
# ~2.5 KGs gained for quit vs. not quit
nhfs_complete_uc %>%
  group_by(qsmk) %>%
  summarize(
    mean_weight_change = mean(wt82_71),
    sd = sd(wt82_71),
    .groups = "drop"
  )
```

```
## # A tibble: 2 × 3
##   qsmk mean_weight_change    sd
##   <dbl>          <dbl> <dbl>
## 1     0              1.98  7.45
## 2     1              4.53  8.75
```

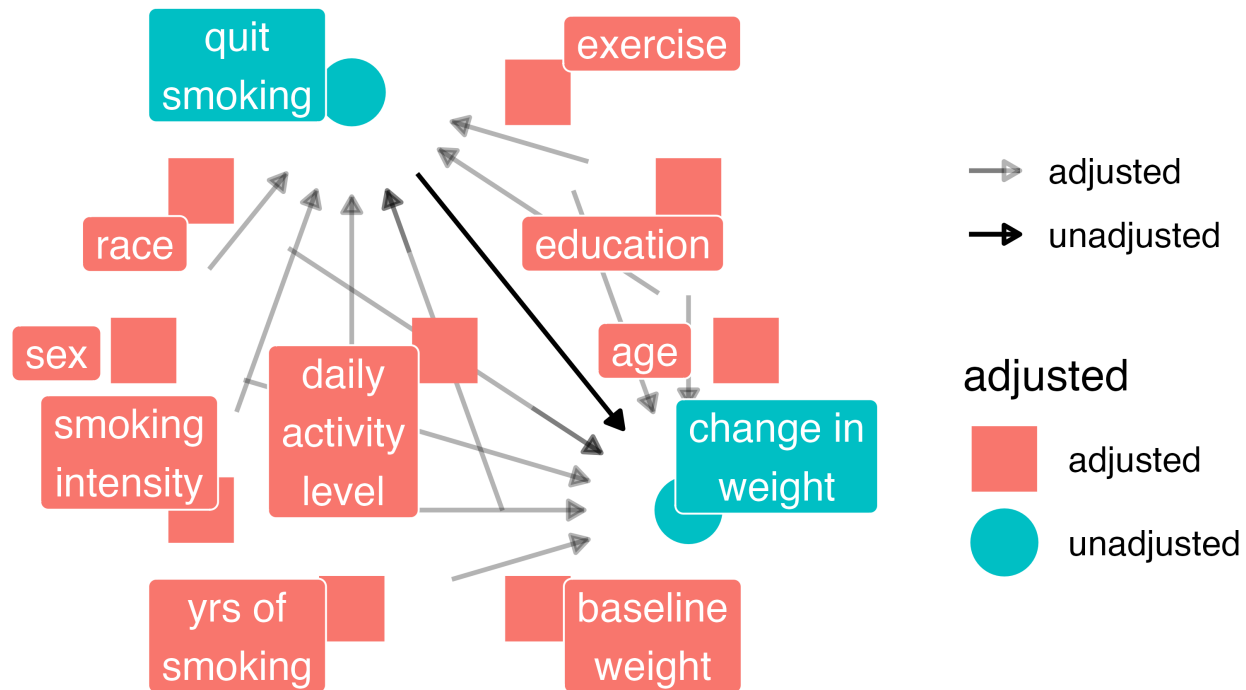
draw your assumptions





What do I need to control for?

cation, exercise, race, sex, smokeintensity,



Multivariable regression: what's the association?

```
lm(
  wt82_71~ qsmk + sex +
    race + age + I(age^2) + education +
    smokeintensity + I(smokeintensity^2) +
    smokeyrs + I(smokeyrs^2) + exercise + active +
    wt71 + I(wt71^2),
  data = nhefs_complete_uc
) %>%
  tidy(conf.int = TRUE) %>%
  filter(term == "qsmk")
```

Multivariable regression: what's the association?

```
lm(
  wt82_71~ qsmk + sex +
    race + age + I(age^2) + education +
    smokeintensity + I(smokeintensity^2) +
    smokeyrs + I(smokeyrs^2) + exercise + active +
    wt71 + I(wt71^2),
  data = nhefs_complete_uc
) %>%
  tidy(conf.int = TRUE) %>%
  filter(term == "qsmk")
```

```
## # A tibble: 1 × 7
```

| ## | term | estimate | std.error | statistic | p.value | conf.low |
|----|--------|----------|-----------|-----------|----------|----------|
| ## | <chr> | <dbl> | <dbl> | <dbl> | <dbl> | <dbl> |
| ## | 1 qsmk | 3.46 | 0.438 | 7.90 | 5.36e-15 | 2.60 |

```
## # ... with 1 more variable: conf.high <dbl>
```

model your assumptions

counterfactual: what if everyone
quit smoking vs. what if no one
quit smoking

Fit propensity score model

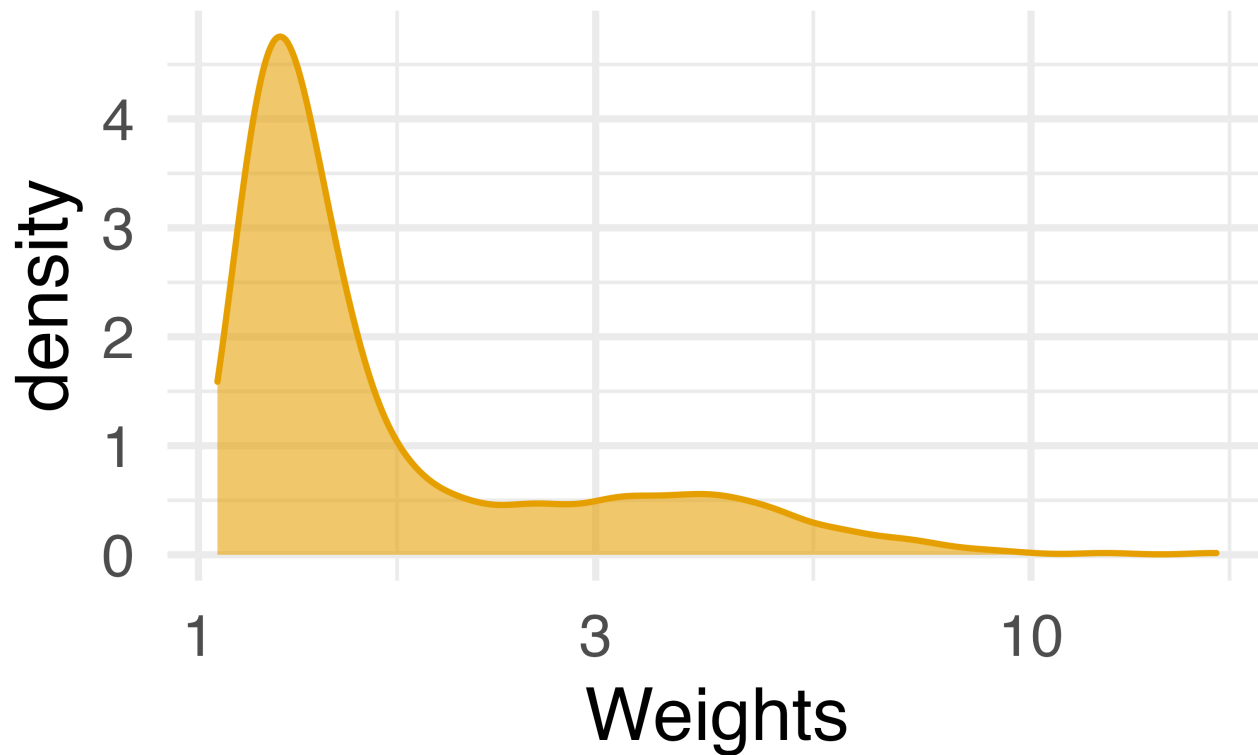
```
propensity_model <- glm(  
  qsmk ~ sex +  
    race + age + I(age^2) + education +  
    smokeintensity + I(smokeintensity^2) +  
    smokeyrs + I(smokeyrs^2) + exercise + active +  
    wt71 + I(wt71^2),  
  family = binomial(),  
  data = nhefs_complete_uc  
)
```

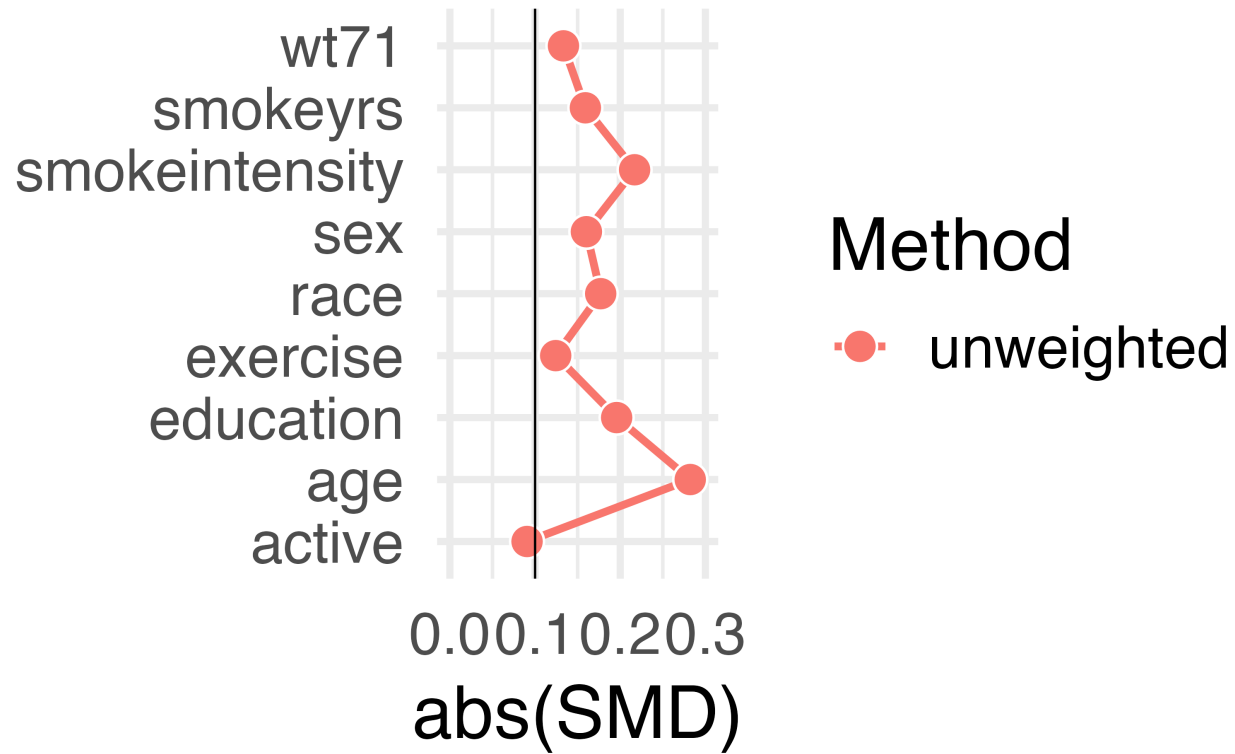

Calculate inverse probability weights

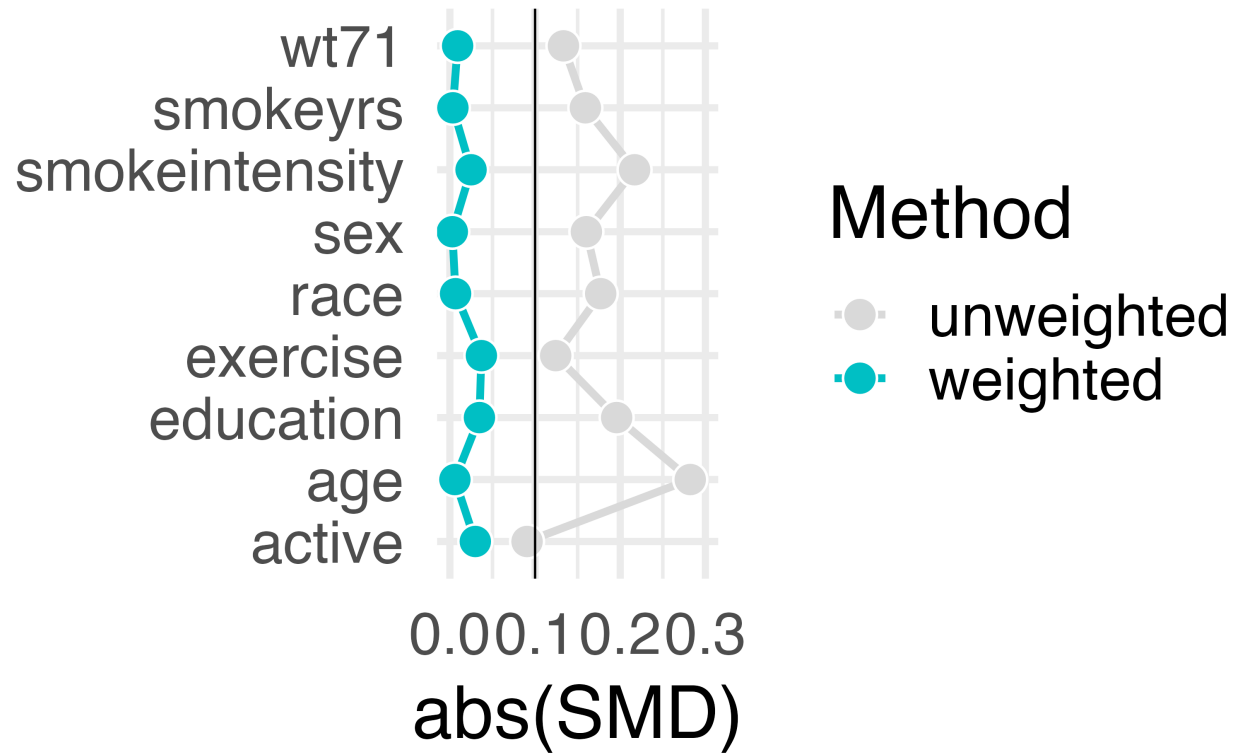
```
nhefs_complete_uc <- propensity_model %>%  
  # predict whether quit smoking  
  augment(type.predict = "response", data = nehs_complete_uc) %>%  
  # calculate inverse probability  
  mutate(wts = 1 / ifelse(qsmk == 0, 1 - .fitted, .fitted))
```

**diagnose your model
assumptions**

What's the distribution of weights?







estimate the causal effects

Estimate causal effect with IPW

```
ipw_model <- lm(  
  wt82_71 ~ qsmk,  
  data = nhfs_complete_uc,  
  weights = wts  
)  
  
ipw_estimate <- ipw_model %>%  
  tidy(conf.int = TRUE) %>%  
  filter(term == "qsmk")
```

Estimate causal effect with IPW

```
ipw_estimate
```

```
## # A tibble: 1 × 7
##   term      estimate std.error statistic  p.value conf.low
##   <chr>      <dbl>      <dbl>      <dbl>    <dbl>    <dbl>
## 1 qsmk        3.44        0.408        8.43 7.47e-17    2.64
## # ... with 1 more variable: conf.high <dbl>
```


Let's fix our confidence intervals with robust SEs!

```
# also see robustbase, survey, gee, and others
```

```
library(estimatr)
```

```
ipw_model_robust <- lm_robust(
```

```
  wt82_71 ~ qsmk,
```

```
  data = nhfs_complete_uc,
```

```
  weights = wts
```

```
)
```

```
ipw_estimate_robust <- ipw_model_robust %>%
```

```
  tidy(conf.int = TRUE) %>%
```

```
  filter(term == "qsmk")
```

Let's fix our confidence intervals with robust SEs!

```
as_tibble(ipw_estimate_robust)
```

```
## # A tibble: 1 × 9
##   term estimate std.error statistic  p.value conf.low
##   <chr>      <dbl>      <dbl>      <dbl>    <dbl>    <dbl>
## 1 qsmk        3.44        0.526        6.54 8.57e-11    2.41
## # ... with 3 more variables: conf.high <dbl>, df <dbl>,
## #   outcome <chr>
```

Let's fix our confidence intervals with the bootstrap!

```
# fit ipw model for a single bootstrap sample
fit_ipw_not_quite_rightly <- function(split, ...) {
  # get bootstrapped data sample with 'rsample::analysis()'
  .df <- analysis(split)

  # fit ipw model
  lm(wt82_71 ~ qsmk, data = .df, weights = wts) %>%
    tidy()
}
```

```

fit_ipw <- function(split, ...) {
  .df <- analysis(split)

  # fit propensity score model
  propensity_model <- glm(
    qsmk ~ sex +
      race + age + I(age^2) + education +
      smokeintensity + I(smokeintensity^2) +
      smokeyrs + I(smokeyrs^2) + exercise + active +
      wt71 + I(wt71^2),
    family = binomial(),
    data = .df
  )

  # calculate inverse probability weights
  .df <- propensity_model %>%
    augment(type.predict = "response", data = .df) %>%
    mutate(wts = 1 / ifelse(qsmk == 0, 1 - .fitted, .fitted))

  # fit correctly bootstrapped ipw model
  lm(wt82_71 ~ qsmk, data = .df, weights = wts) %>%
    tidy()
}

```

Using {rsample} to bootstrap our causal effect

```
# fit ipw model to bootstrapped samples  
ipw_results <- bootstraps(nhefs_complete, 1000, apparent = TRUE) %>%  
  mutate(results = map(splits, fit_ipw))
```

Using {rsample} to bootstrap our causal effect

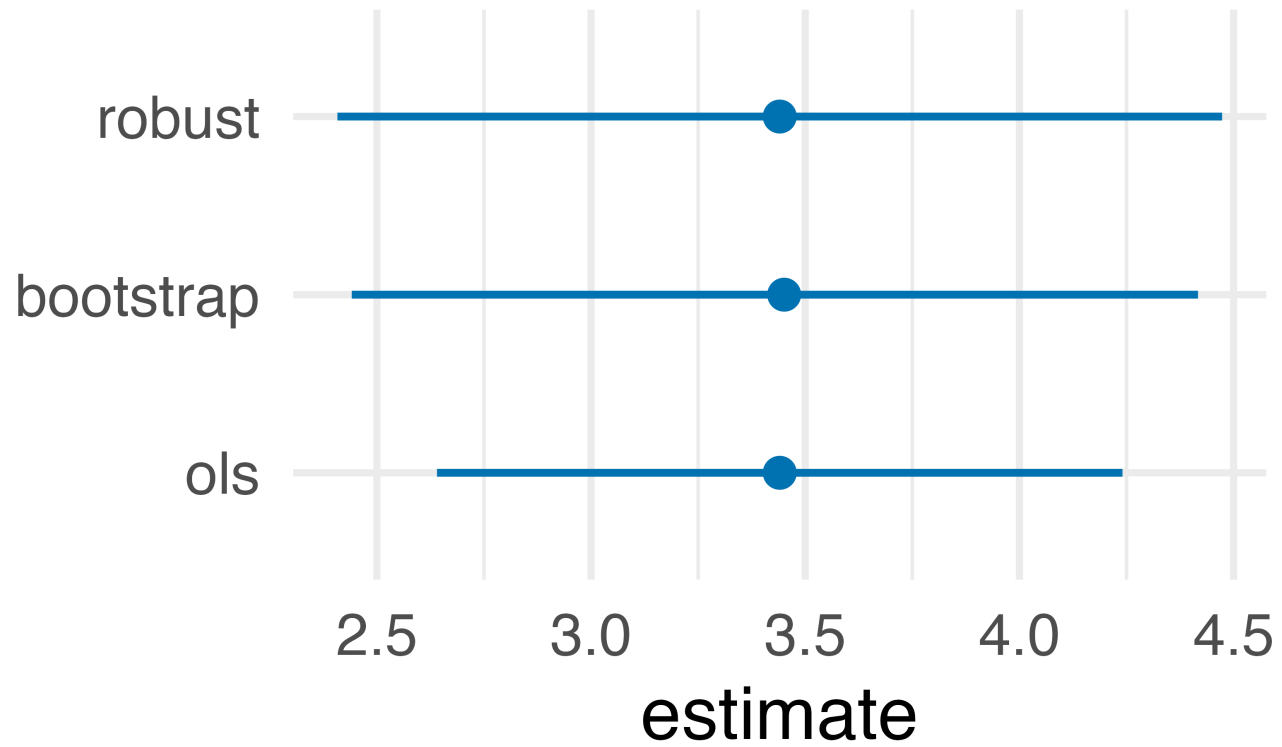
```
# get t-statistic-based CIs  
boot_estimate <- int_t(ipw_results, results) %>%  
  filter(term == "qsmk")  
  
boot_estimate
```

Using {rsample} to bootstrap our causal effect

```
# get t-statistic-based CIs
boot_estimate <- int_t(ipw_results, results) %>%
  filter(term == "qsmk")

boot_estimate
```

```
## # A tibble: 1 × 6
##   term   .lower .estimate .upper .alpha .method
##   <chr> <dbl>      <dbl> <dbl> <dbl> <chr>
## 1 qsmk    2.44      3.45    4.42  0.05 student-t
```



**Our causal effect estimate: 3.5
kg (95% CI 2.4 kg, 4.4 kg)**

**Review the R Markdown file...
later!**

Resources

Causal Inference: Comprehensive text on causal inference. Free online.

Causal Inference Notebook: R code to go along with Causal Inference

Bootstrap confidence intervals with {rsample}