

Using Propensity Scores

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Propensity scores

Matching

Weighting

Stratification

Direct Adjustment

...



Ingredients

150g unsalted butter, plus extra for greasing
150g plain chocolate, broken into pieces
150g plain flour
½ tsp baking powder
½ tsp bicarbonate of soda
200g light muscovado sugar
2 large eggs

Method

1. Heat the oven to 160C/140C fan/gas 3. Grease and base line a 1 litre heatproof glass pudding basin and a 450g loaf tin with baking parchment.
2. Put the butter and chocolate into a saucepan and melt over a low heat, stirring. When the chocolate has all melted remove from the heat.



estimand

estimator

estimate

Propensity scores

Matching

Weighting

Stratification

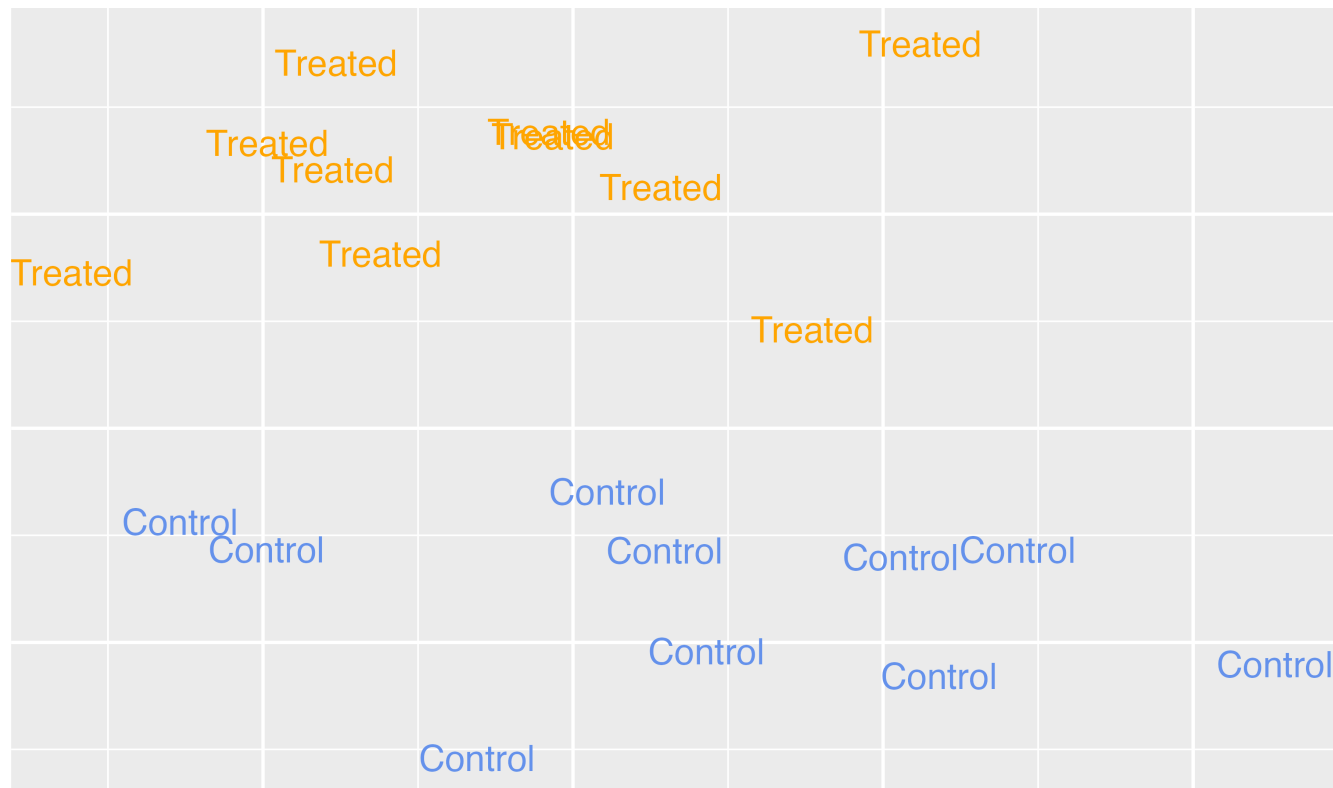
Direct Adjustment

...

Target estimands

Average Treatment Effect (ATE)

$$\tau = E[Y(1) - Y(0)]$$



Target estimands

Estimand	Target population	Example Research Question
ATE	Full population	<i>Should we decide whether to have extra magic hours all mornings to change the wait time for Seven Dwarfs Mine Train between 9-10 AM?</i> <i>Should a specific policy be applied to all eligible observations?</i>

Target estimands

Average Treatment Effect among the Treated (ATT)

$$\tau = E[Y(1) - Y(0) | Z = 1]$$

Target estimands

Estimand	Target population	Example Research Question
ATT	Exposed (treated) observations	<i>Should we stop extra magic hours to change the wait time for Seven Dwarfs Mine Train between 9-10 AMpm?</i> <i>Should we stop our marketing campaign to those currently receiving it?</i> <i>Should medical providers stop recommending treatment for those currently receiving it?</i>

Matching in R (ATT)

```
1 library(MatchIt)
2 m <- matchit(
3   qsmk ~ sex +
4     race + age + I(age^2) + education +
5     smokeintensity + I(smokeintensity^2) +
6     smokeyrs + I(smokeyrs^2) + exercise +
7     active + wt71 + I(wt71^2),
8   data = nhfs_complete
9 )
10 m
```

A 'matchit' object

- method: 1:1 nearest neighbor matching without replacement
- distance: Propensity score
 - estimated with logistic regression
- number of obs.: 1566 (original), 806 (matched)
- target estimand: ATT
- covariates: sex, race, age, I(age^2), education, smokeintensity, I(smokeintensity^2), smokeyrs, I(smokeyrs^2), exercise, active, wt71, I(wt71^2)

Matching in R (ATT)

```
1 matched_data <- get_matches(m, id = "i")
2 as_tibble(matched_data)
```

```
# A tibble: 806 × 71
```

	i	subclass	weights	seqn	qsmk	death	yrdth	modth
	<chr>	<fct>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	11	1	1	428	1	0	NA	NA
2	1220	1	1	23045	0	0	NA	NA
3	15	2	1	446	1	1	88	1
4	1082	2	1	22294	0	0	NA	NA
5	18	3	1	596	1	0	NA	NA
6	534	3	1	14088	0	0	NA	NA
7	23	4	1	618	1	0	NA	NA
8	697	4	1	18085	0	0	NA	NA
9	27	5	1	806	1	0	NA	NA
10	879	5	1	21128	0	0	NA	NA

```
" - 706 - - - - -
```

Target estimands

*Average Treatment Effect among the Controls
(ATC)*

$$\tau = E[Y(1) - Y(0)|Z = 0]$$

Target estimands

Estimand	Target population	Example Research Question
ATU	Unexposed (control) observations	<i>Should we add extra magic hours for all days to change the wait time for Seven Dwarfs Mine Train between 9-10 AMpm?</i> <i>Should we extend our marketing campaign to those not receiving it?</i> <i>Should medical providers extend treatment to those not currently receiving it?</i>

Matching in R (ATC)

```
1 m <- matchit(  
2   qsmk ~ sex +  
3     race + age + I(age^2) + education +  
4     smokeintensity + I(smokeintensity^2) +  
5     smokeyrs + I(smokeyrs^2) + exercise +  
6     active + wt71 + I(wt71^2),  
7   data = nhefs_complete,  
8   estimand = "ATC"  
9 )  
10 m
```

A `matchit` object

- method: 1:1 nearest neighbor matching without replacement
- distance: Propensity score
 - estimated with logistic regression
- number of obs.: 1566 (original), 806 (matched)
- target estimand: ATC
- covariates: sex, race, age, I(age^2), education, smokeintensity, I(smokeintensity^2), smokeyrs, I(smokeyrs^2), exercise, active, wt71, I(wt71^2)

Target estimands

Average Treatment Effect among the Matched (ATM)

Target estimands

Estimand	Target population	Example Research Question
ATM	Evenly matchable	<i>Are there some days we should change whether we are offering extra magic hours in order to change the wait time for Seven Dwarfs Mine Train between 9-10 AMpm?</i> <i>Is there an effect of the exposure for some observations?</i> <i>Should those at clinical equipoise receive treatment?</i>

Matching in R (ATM)

```
1 m <- matchit(  
2   qsmk ~ sex +  
3     race + age + I(age^2) + education +  
4     smokeintensity + I(smokeintensity^2) +  
5     smokeyrs + I(smokeyrs^2) + exercise +  
6     active + wt71 + I(wt71^2),  
7   data = nhefs_complete,  
8   link = "linear.logit",  
9   caliper = 0.1  
10 )  
11 m
```

Observations with propensity scores (on the linear logit scale) within 0.1 standard errors (the caliper) will be discarded

Matching in R (ATM)

A `'matchit'` object

- method: 1:1 nearest neighbor matching without replacement
- distance: Propensity score [caliper]
 - estimated with logistic regression and linearized
- caliper: <distance> (0.063)
- number of obs.: 1566 (original), 780 (matched)
- target estimand: ATT
- covariates: sex, race, age, I(age^2), education, smokeintensity, I(smokeintensity^2), smokeyrs, I(smokeyrs^2), exercise, active, wt71, I(wt71^2)

Matching in R (ATM)

```
1 matched_data <- get_matches(m, id = "i")
2 as_tibble(matched_data)
```

A tibble: 780 × 71

	i	subclass	weights	seqn	qsmk	death	yrdth	modth
	<chr>	<fct>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	11	1	1	428	1	0	NA	NA
2	1220	1	1	23045	0	0	NA	NA
3	15	2	1	446	1	1	88	1
4	1082	2	1	22294	0	0	NA	NA
5	18	3	1	596	1	0	NA	NA
6	534	3	1	14088	0	0	NA	NA
7	23	4	1	618	1	0	NA	NA
8	697	4	1	18085	0	0	NA	NA
9	27	5	1	806	1	0	NA	NA
10	879	5	1	21128	0	0	NA	NA

" ... 770 ...

Your Turn 1

Using the propensity scores you created in the previous exercise, create a “matched” data set using the ATM method with a caliper of 0.2.

Propensity scores

Matching

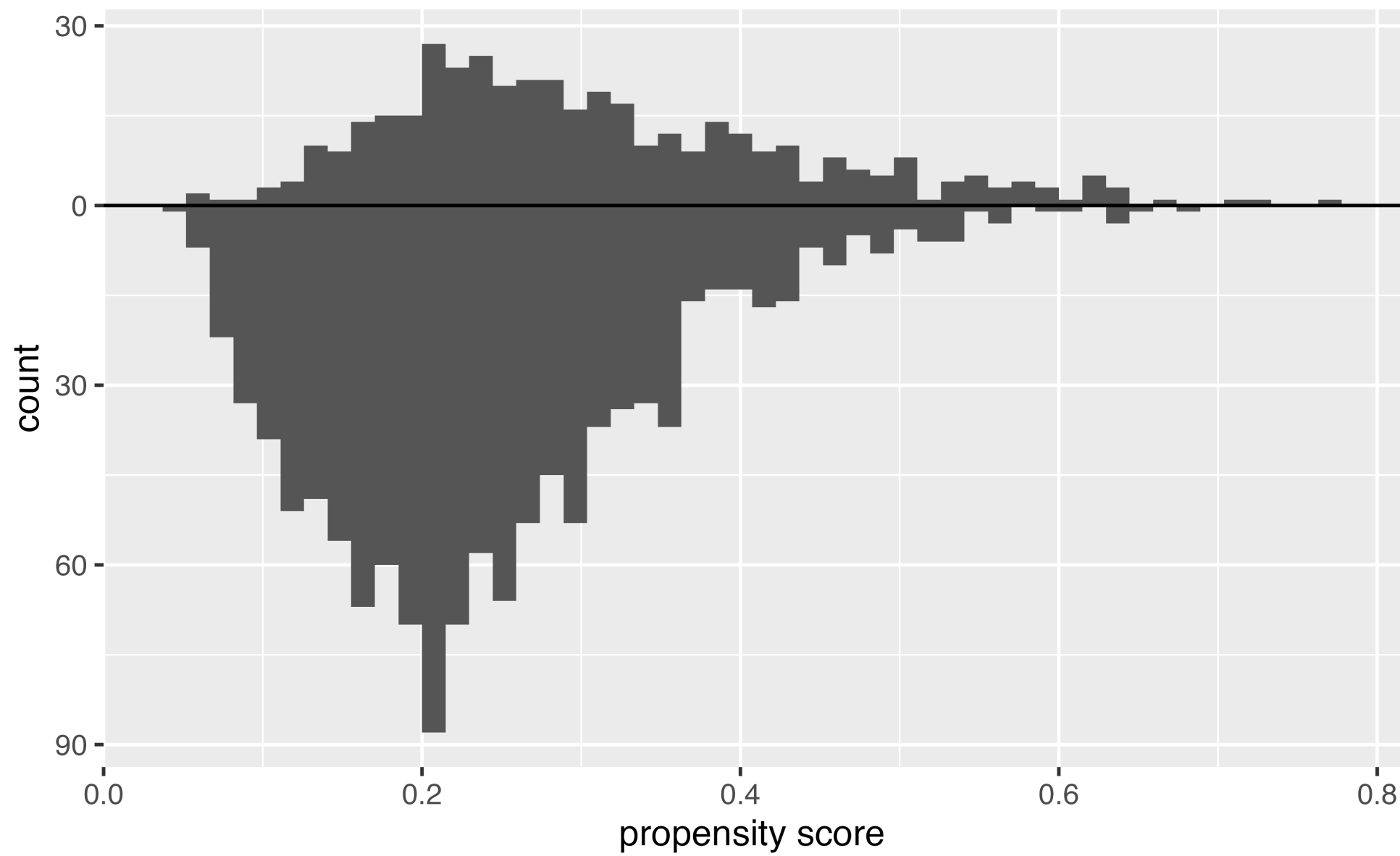
Weighting

Stratification

Direct Adjustment

...

Histogram of propensity scores



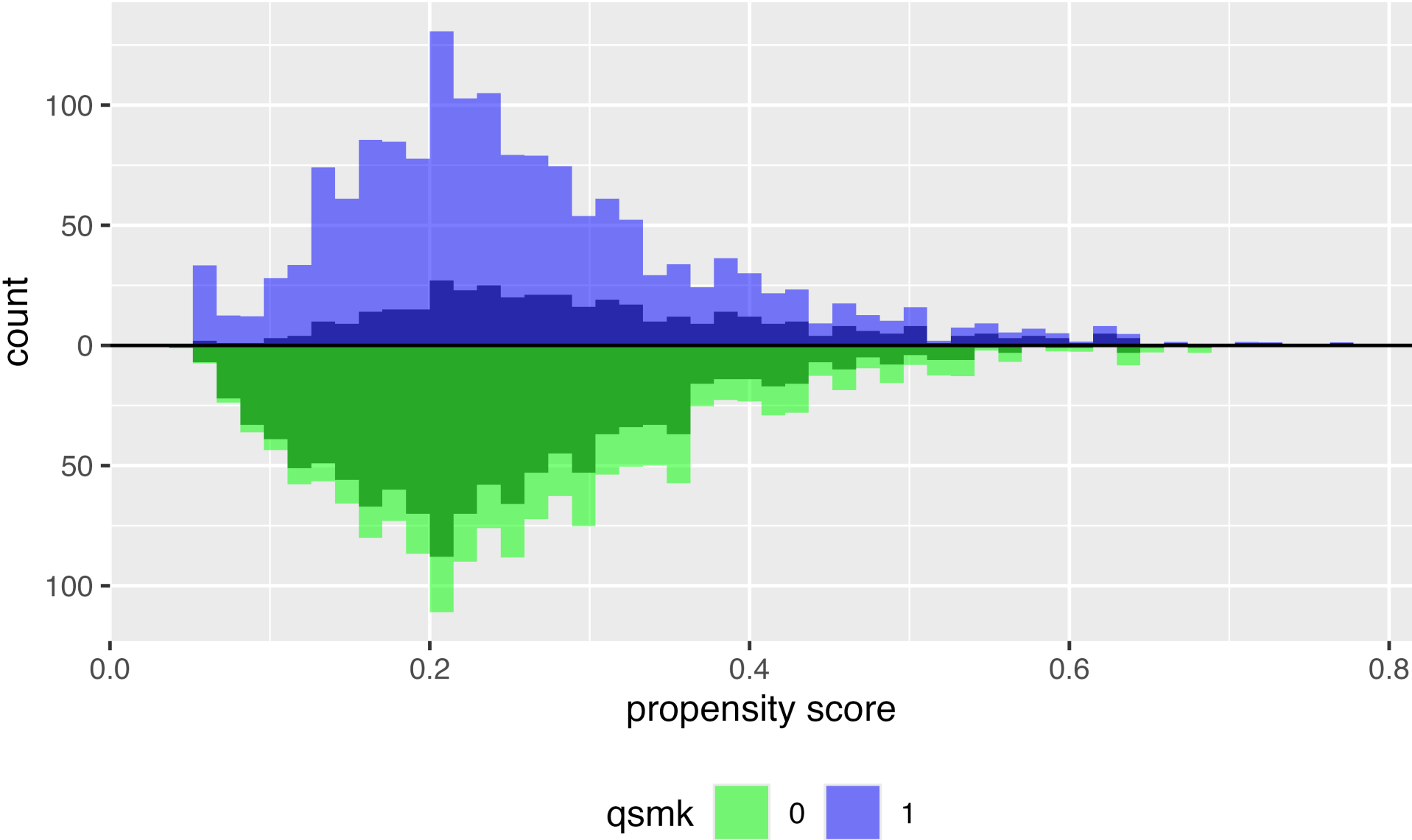
Target estimands: ATE

Average Treatment Effect (ATE)

$$w_{ATE} = \frac{Z_i}{p_i} + \frac{1 - Z_i}{1 - p_i}$$

$$1 \cdot (Z / p) + ((1 - Z) / (1 - p))$$

ATE



Target estimands: ATT & ATC

Average Treatment Effect Among the Treated (ATT)

$$w_{ATT} = \frac{p_i Z_i}{p_i} + \frac{p_i(1 - Z_i)}{1 - p_i}$$

$$1 \quad ((p * Z) / p) + ((p * (1 - Z)) / (1 - p))$$

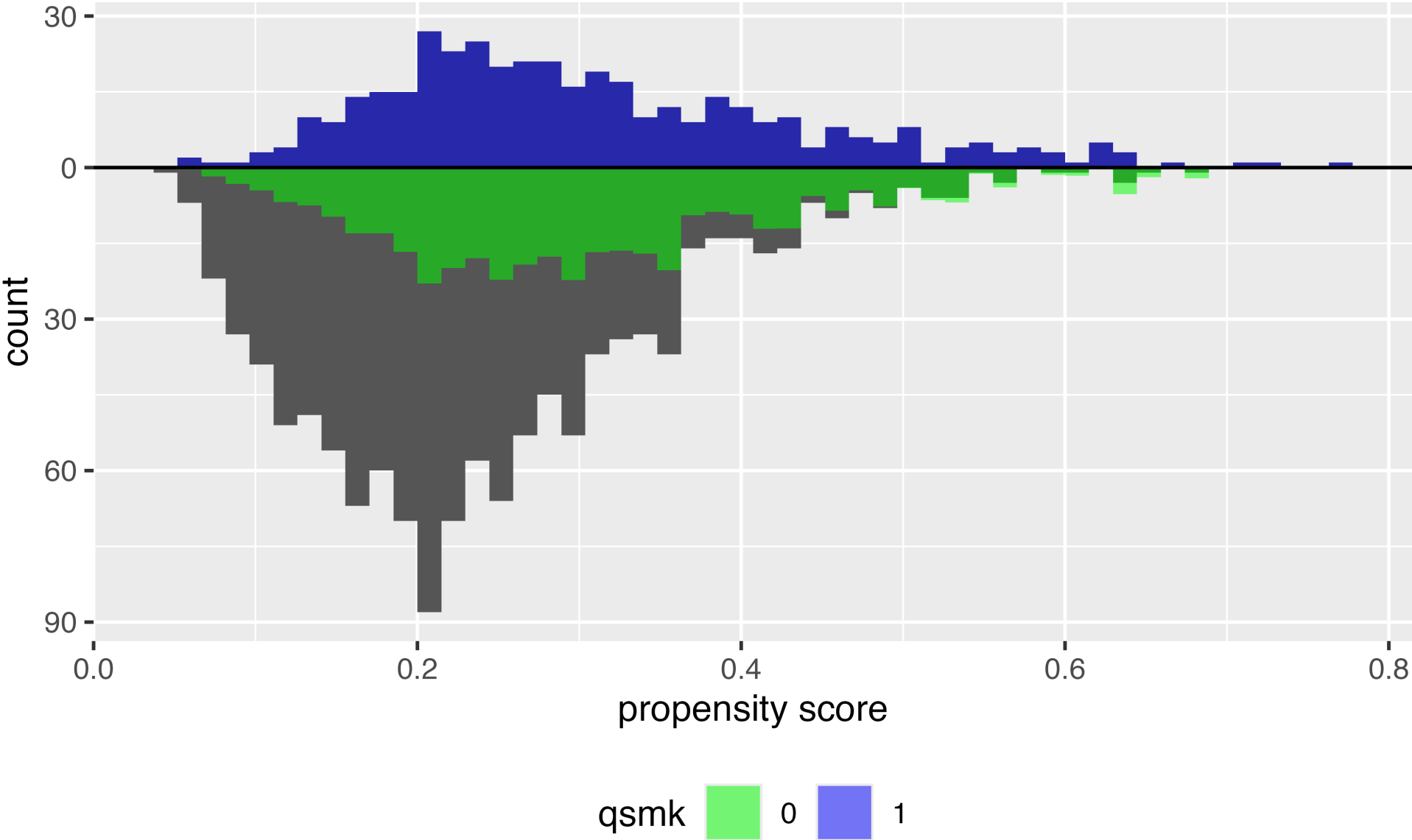
Target estimands: ATT & ATC

Average Treatment Effect Among the Controls (ATC)

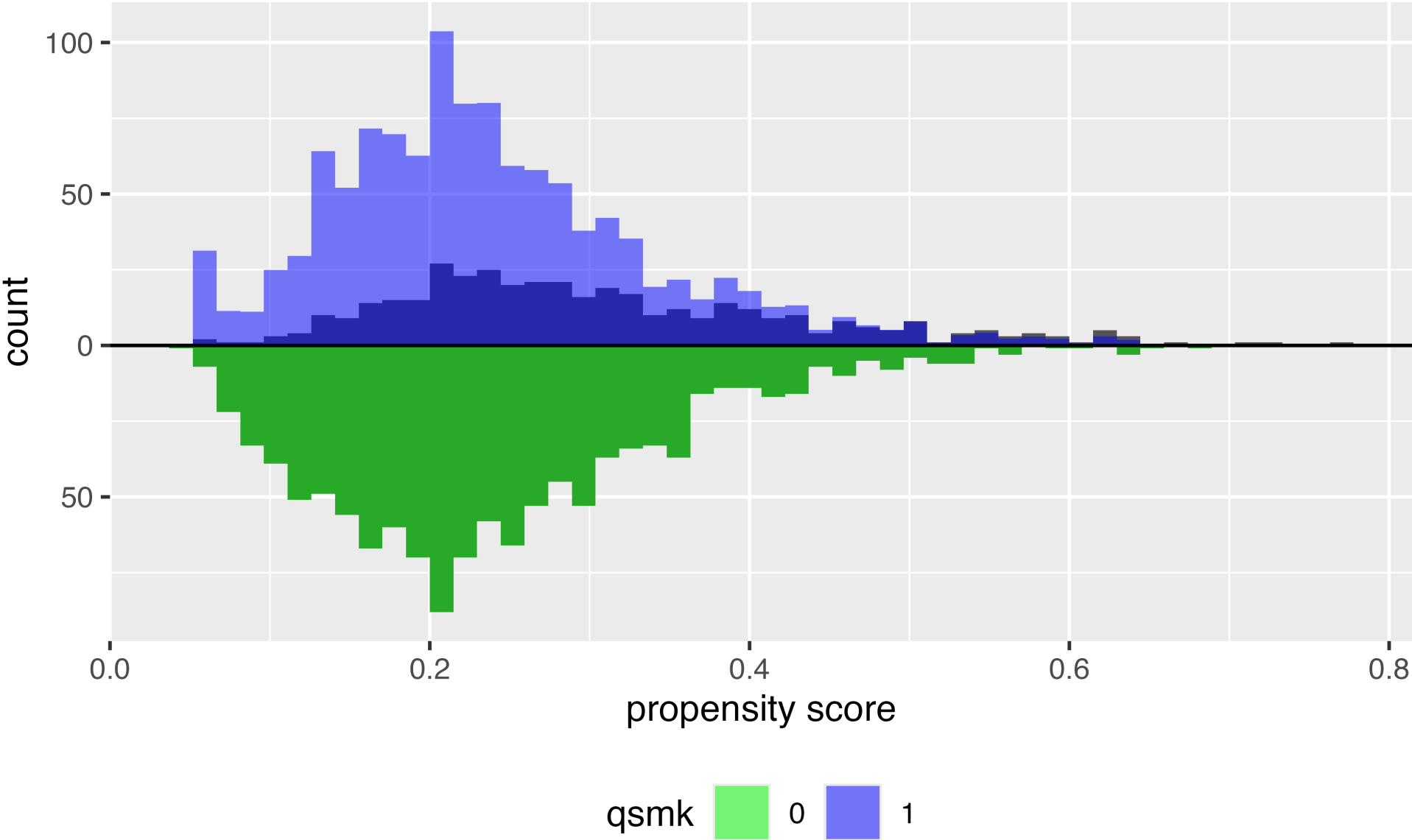
$$w_{ATC} = \frac{(1 - p_i)Z_i}{p_i} + \frac{(1 - p_i)(1 - Z_i)}{(1 - p_i)}$$

$$1 \left(\frac{((1 - p) * Z)}{p} + \frac{((1 - p) * (1 - Z))}{(1 - p)} \right)$$

ATT



ATC



Target estimands: ATM & ATO

Average Treatment Effect Among the Evenly Matchable (ATM)

$$w_{ATM} = \frac{\min\{p_i, 1 - p_i\}}{Z_i p_i + (1 - Z_i)(1 - p_i)}$$

```
1 pmin(p, 1 - p) / (Z * p + (1 - Z) * (1 - p))
```

Target estimands: ATM & ATO

Average Treatment Effect Among the Overlap Population

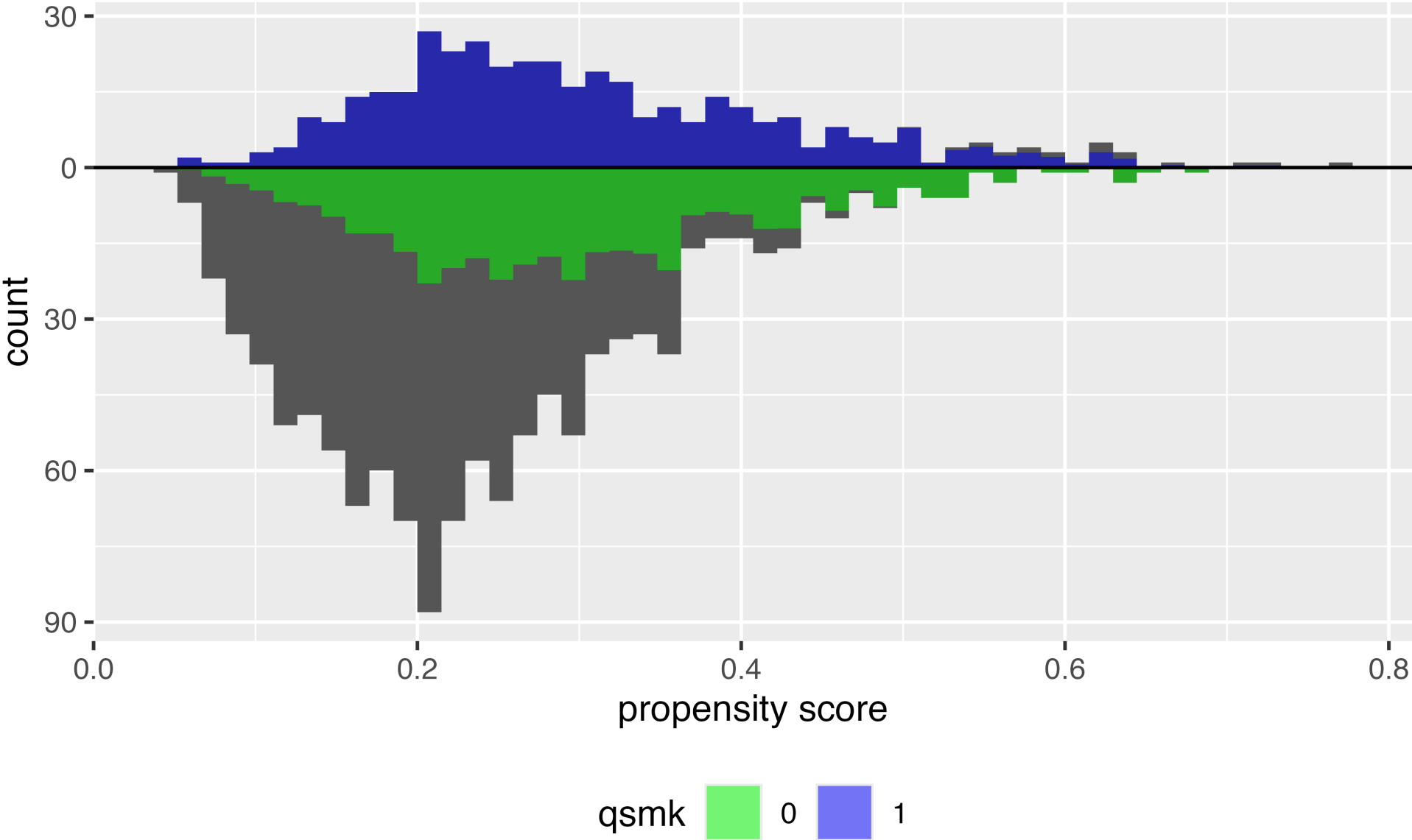
$$w_{ATO} = (1 - p_i)Z_i + p_i(1 - Z_i)$$

$$1 \quad (1 - p) * Z + p * (1 - Z)$$

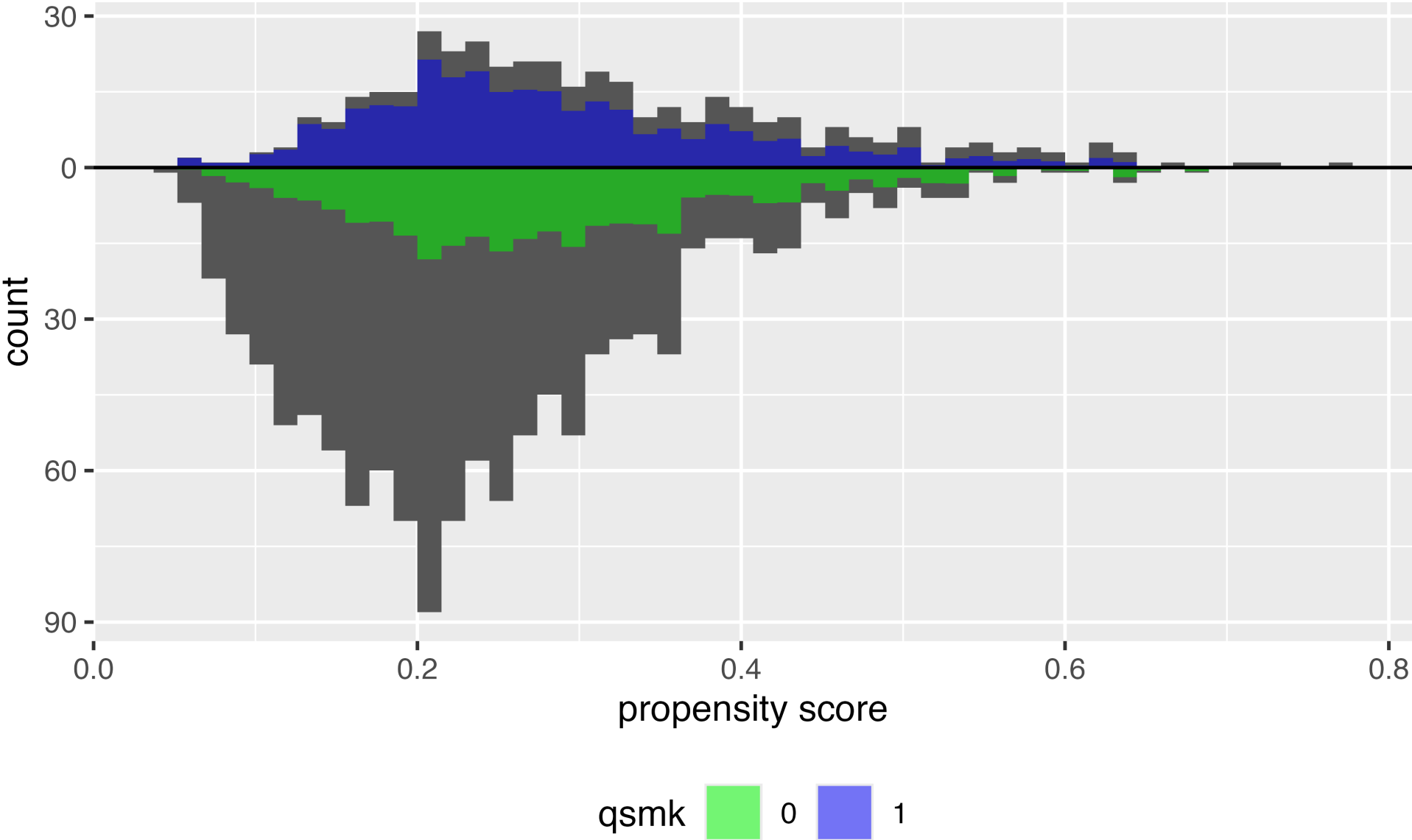
Target estimands

Estimand	Target population	Example Research Question
ATO	Overlap population	<i>Same as ATM</i>

ATM



ATO



ATE in R



Average Treatment Effect (ATE) $w_{ATE} = \frac{Z_i}{p_i} + \frac{1-Z_i}{1-p_i}$

```
1 library(propensity)
2 df <- propensity_model |>
3   augment(type.predict = "response", data = nhefs_complete) |>
4   mutate(w_ate = wt_ate(.fitted, qsmk))
```

Your Turn 2

Using the propensity scores you created in the previous exercise, add the ATE weights to your data frame

Stretch: Using the same propensity scores, create ATM weights