

# Propensity Score Weighting

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# Propensity scores

Weighting

Matching

Stratification

Direct Adjustment

...

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**Weighting**

Matching

Stratification

Direct Adjustment

...

# Target estimands

## Average Treatment Effect (ATE)

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

# Target estimands

## Average Treatment Effect Among the Treated (ATT)

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

## Average Treatment Effect Among the Controls (ATC)

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

# Target estimands

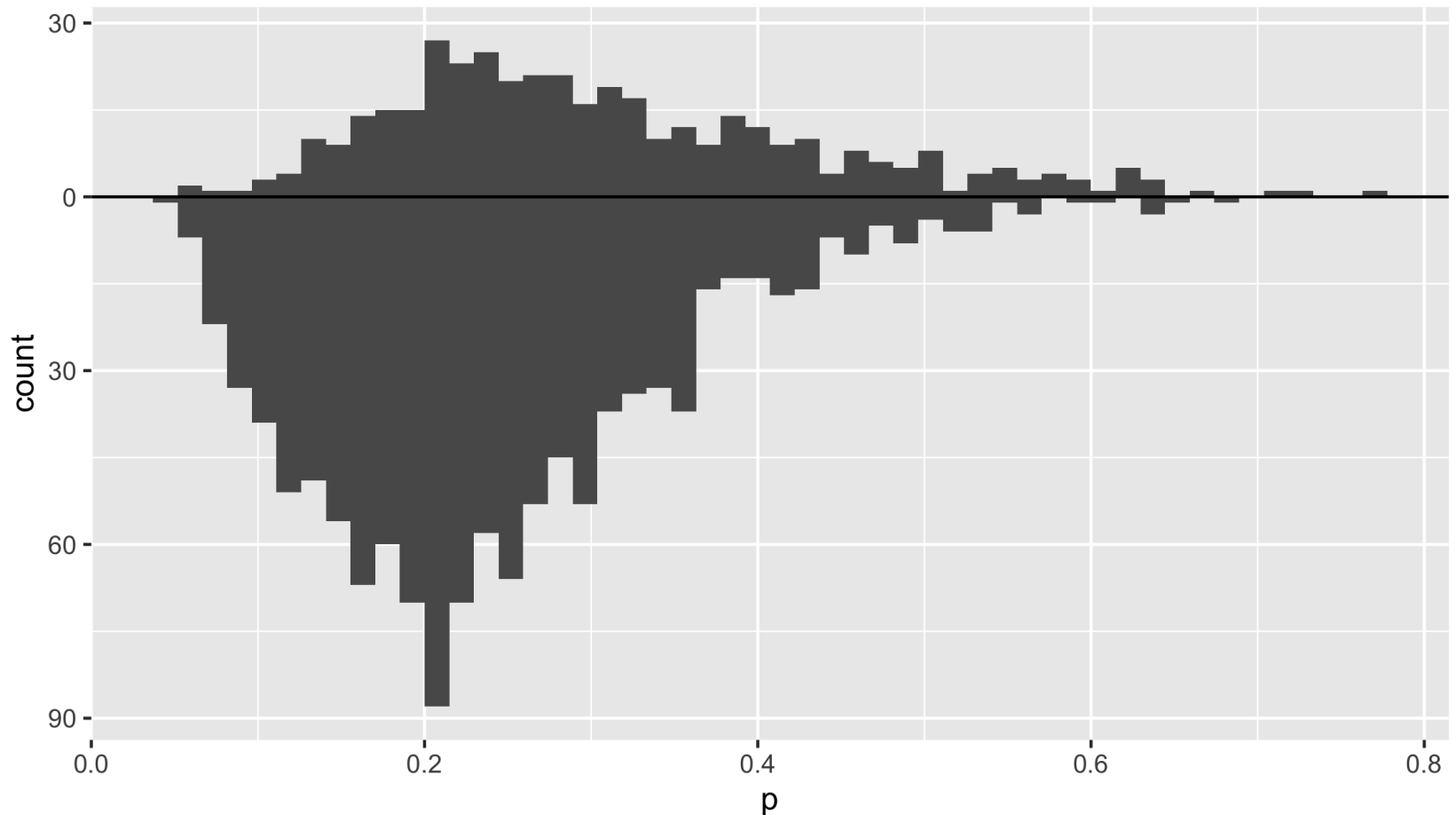
## Average Treatment Effect Among the Evenly Matchable (ATM)

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

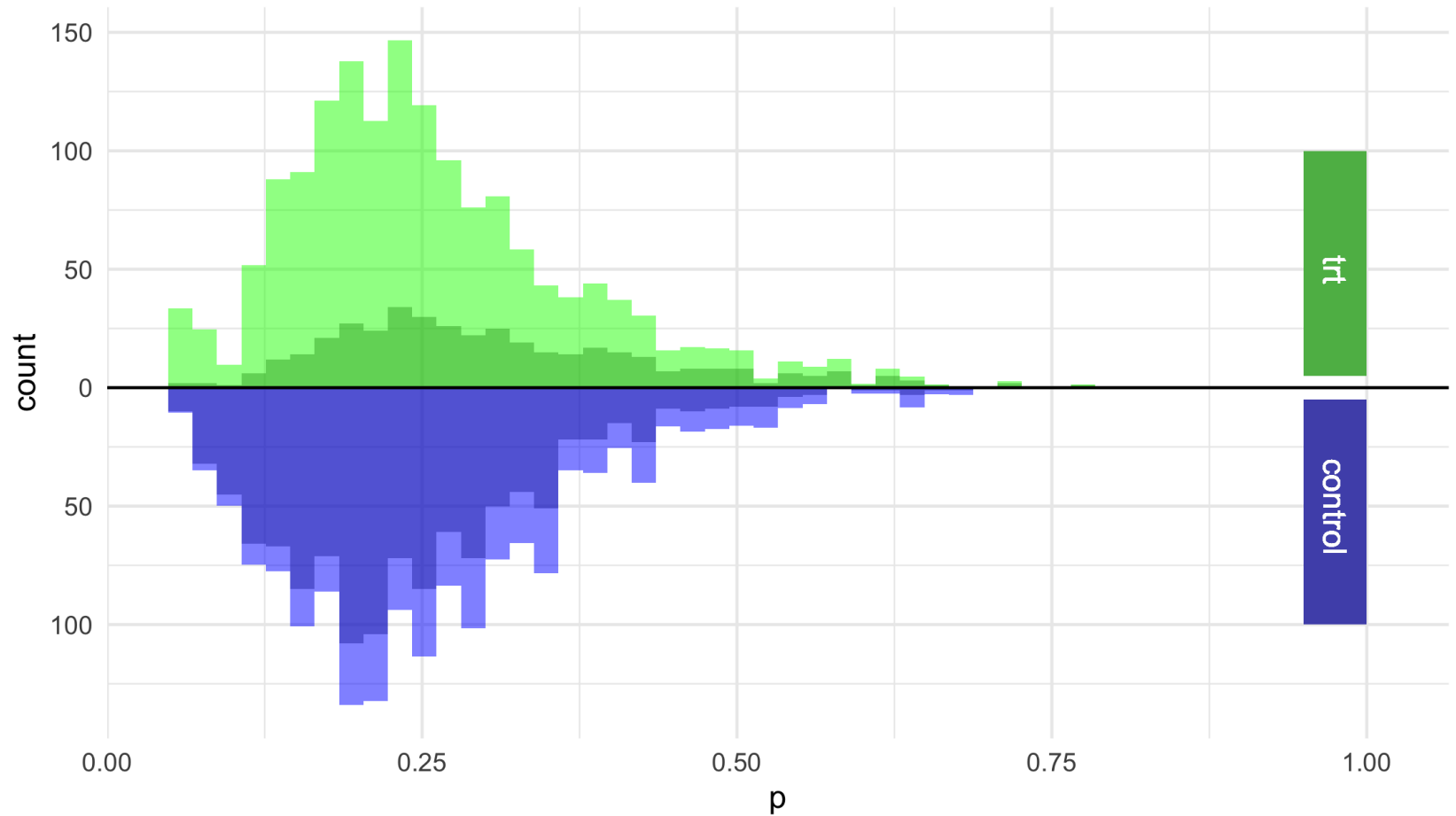
## Average Treatment Effect Among the Overlap Population

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

# Histogram of propensity scores

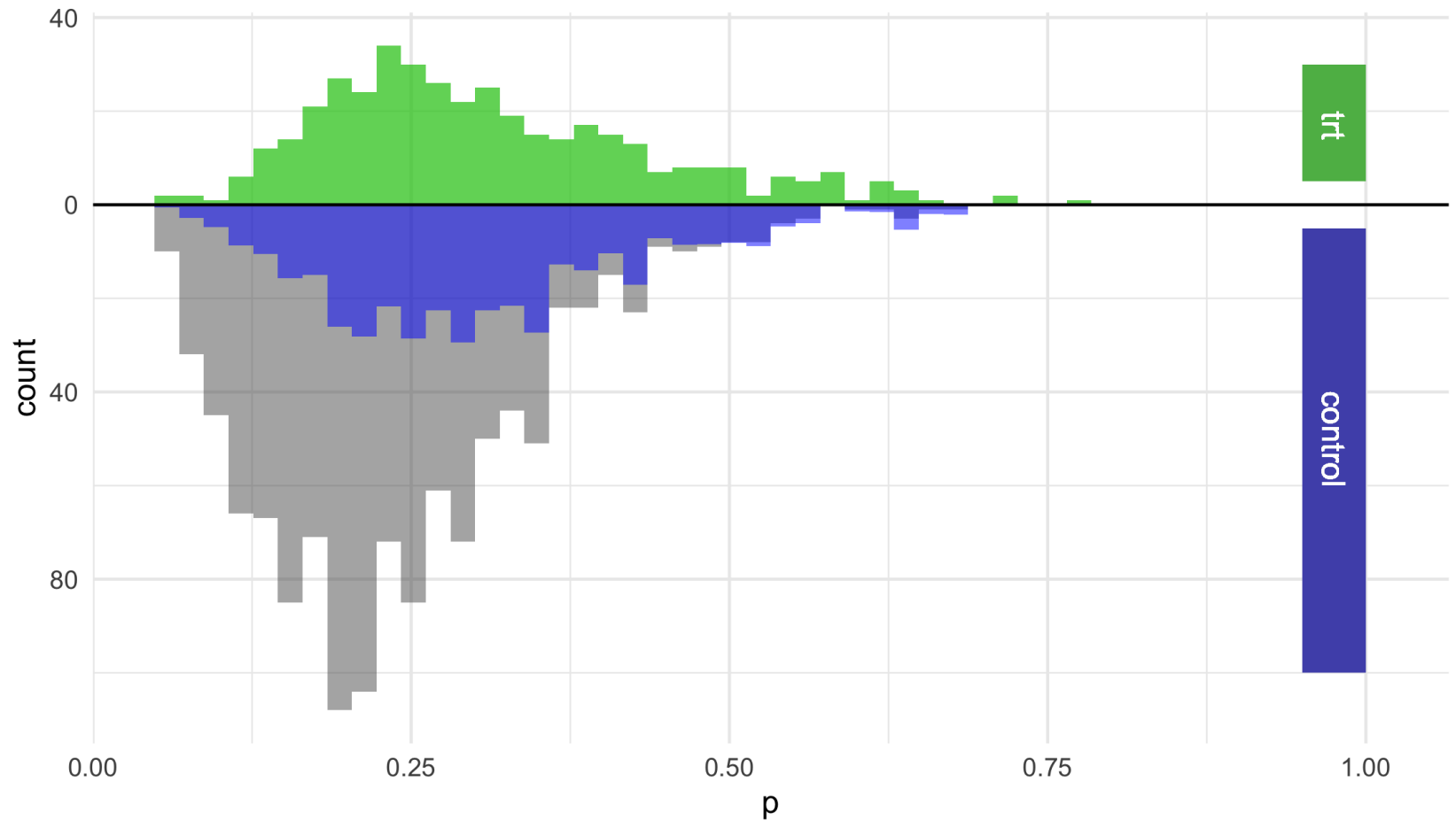


# ATE

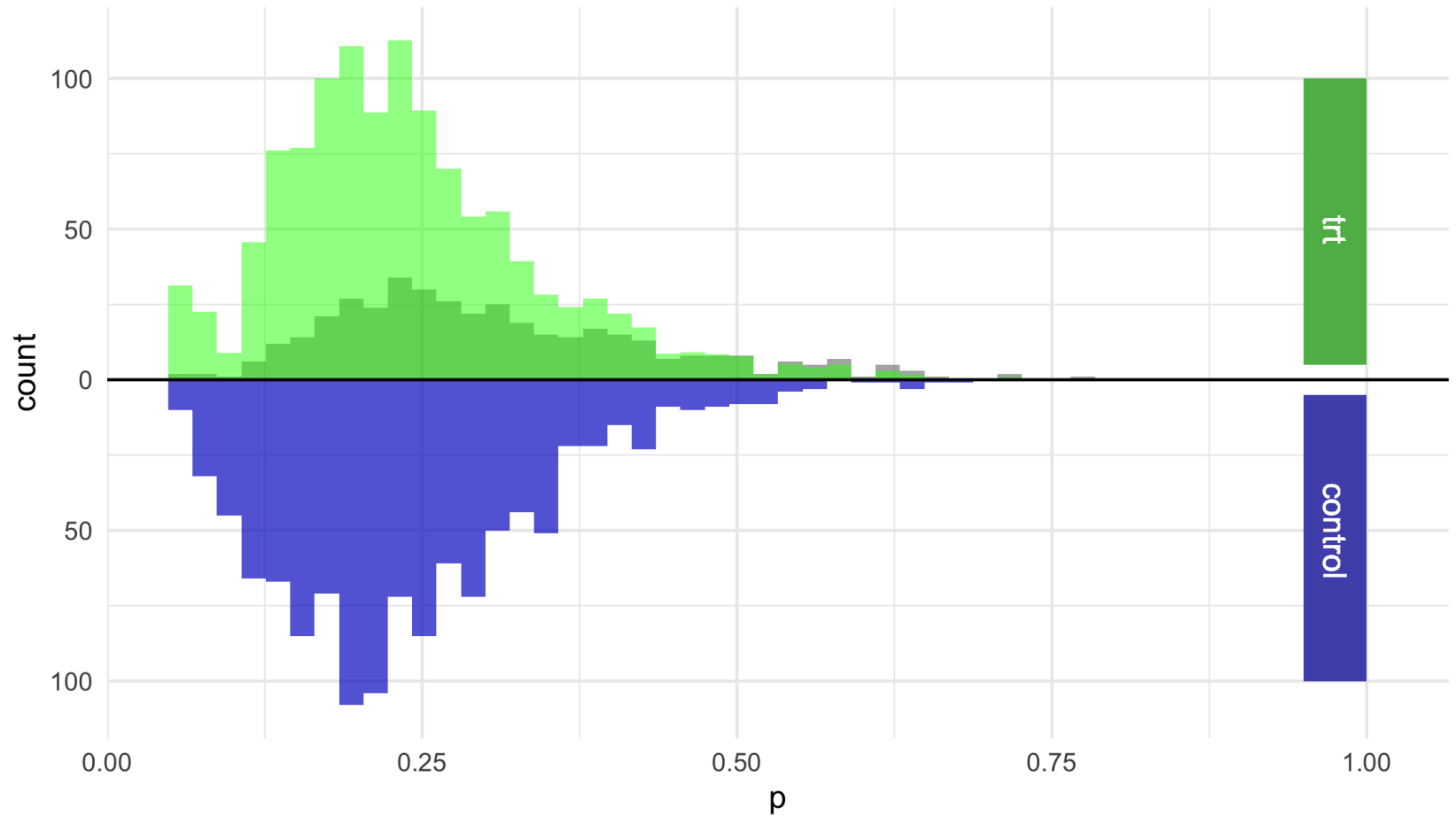




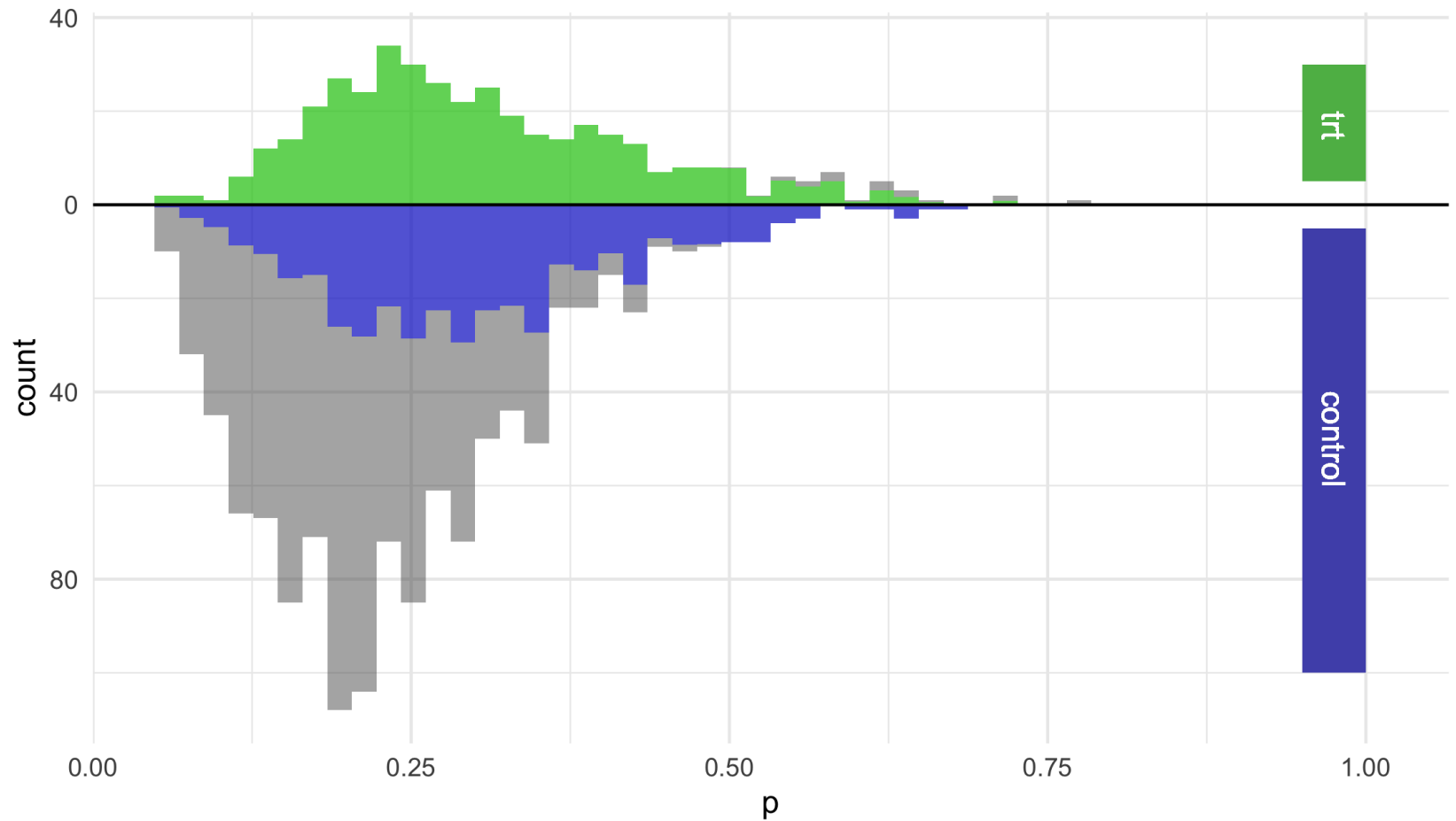
# ATT



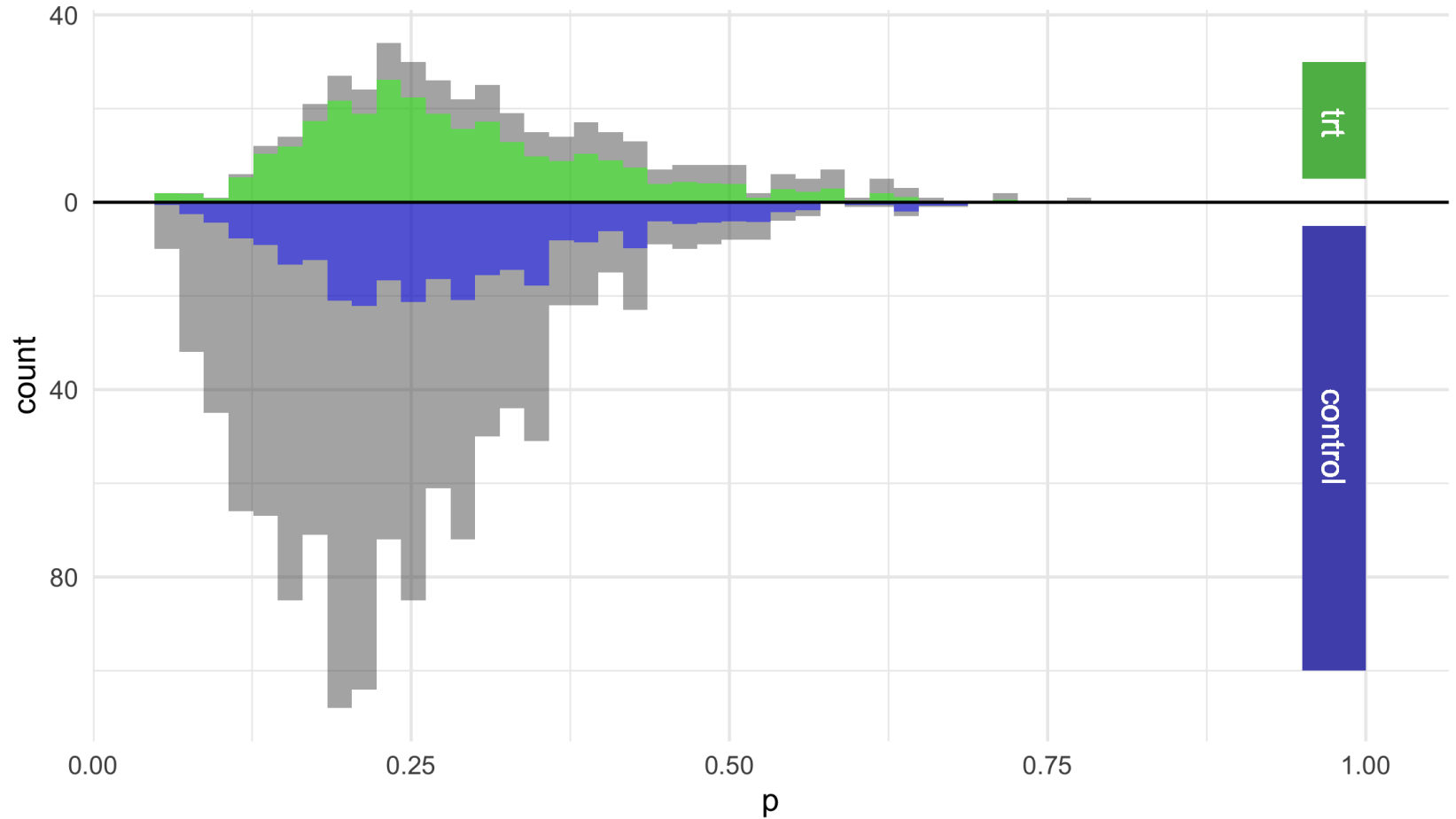
# ATC



# ATM



# ATO



# ATE in R

## Average Treatment Effect (ATE)

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

```
df <- propensity_model %>%  
  augment(type.predict = "response", data = nhfs_complete) %>%  
  mutate(w_ate = (qsmk / .fitted) + ((1 - qsmk) / (1 - .fitted)))
```

# Your Turn

- 1 Using the propensity scores you created in the previous exercise, add the ATE weights to your data frame df**
- 2 Stretch: Using the same propensity scores, create ATT weights**

05:00