Simulation Study in Thesis

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```
require(dplyr)
require(Rlab)
require(ggplot2)
require(plotly)
require(grf)
require(forcats)
require(tidyr)
require(gridExtra)

set.seed(101)

setwd("C:/Users/juhol/OneDrive/Documents/Tyokansio/Gradu/Koodit")
```

1 Abstract

Simulation study consists nine different SCMs (and the responding DAGs). Let's define the sample size to equal N = 10 000.

```
n <- 10000
```

In the first part of this report, the simulation functions will be defined.In the second part the *causal forest* algorithm will be ran.

2 Functions

2.1 Randomized Controlled Trial with Constant Treatment Effect

```
#New exogeneous parameters and variables

w_1 <- rbern(n, 1/2)

u_y <- rnorm(n, mean = 100, sd = 10)

tau <- 10

# Variables X_1, ..., X_10

X <- matrix(0, nrow = n, ncol = 10)

for (k in 1:10) {


  if(k%%2 != 0){    #if k is odd
```

4.1.2 Randomized Controlled Trial with Constant Treatment Effect, Including Covariates Affecting to Output

$$
\begin{array}{ccccc}
 & & U_Y & & \\
 & & \downarrow & & \\
U_W & \longrightarrow W \xrightarrow[\tau]{} & Y & & \\
 & & \uparrow & & \\
 & & X_1, \ldots, X_{10} & &
\end{array}
\tag{4.4}
$$

$$
f_W(U_W) = \text{Bern}\left(\frac{1}{2}\right) \tag{4.5}
$$

$$
f_Y(W, X_1, \ldots, X_{10}, U_Y) = \tau \cdot W + \sum_{k=1}^{10} \beta_{X_k} X_k + U_Y \tag{4.6}
$$

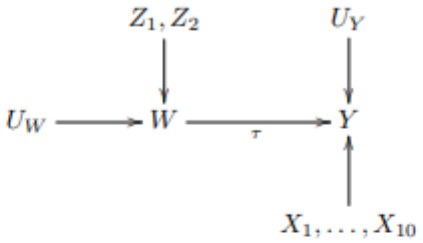
, where

$$
\begin{cases}
U_Y & \sim \text{Norm}(\mu_Y(0), \sigma_Y^2) \\
X_K & \sim \text{Norm}(\mu_K, \sigma_K^2) \text{ when } k \text{ is odd and} \\
X_K & \sim \text{Bern}\left(\frac{1}{2}\right) \text{ when } k \text{ is even}
\end{cases}
$$

Figure 1: Simulation 1

```
    for (i in 1:n) {

      X[i, k] <- rnorm(1, mean = 0, sd = 1)
    }

  } else {         #if k is even

      for (i in 1:n) {

        X[i, k] <- rbern(1, 1/2)

    }

  }
}

beta_X_k <- runif(10, min = -3, max = 3)

#SCM

y_1 <- tau*w_1 + X%*%beta_X_k + u_y  #Output
```

4.1.3 Constant Treatment Effect with Unconfounded Assignment, Including Covariates Affecting to Output



(4.7)

$$f_W(Z_1, Z_2, U_W) = \frac{1}{1 + \exp\left\{-\left(\sum_{j=1}^{2} \gamma_{Z_j} Z_j + U_W\right)\right\}} \tag{4.8}$$

$$f_Y(W, X_1, \ldots, X_{10}, U_Y) = \tau \cdot W + \sum_{k=1}^{10} \beta_{X_k} X_k + U_Y \tag{4.9}$$

, where

$$\begin{cases} U_W & \sim \text{Norm}(0, \sigma_W^2) \\ U_Y & \sim \text{Norm}(\mu_Y(0), \sigma_Y^2) \\ Z_1, Z_2 & \sim \text{Bern}\left(\frac{1}{2}\right) \\ X_K & \sim \text{Norm}(\mu_K, \sigma_K^2) \text{ when } k \text{ is odd and} \\ X_K & \sim \text{Bern}\left(\frac{1}{2}\right) \text{ when } k \text{ is even} \end{cases}$$

Figure 2: Simulation 2

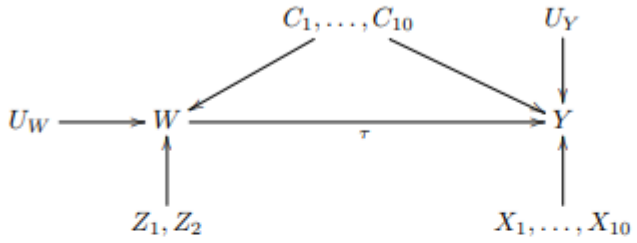
2.2 Constant Treatment Effect with Unconfounded Assignment, Including Covariates Affecting to Output

```
#New exogeneous parameters and variables

# Variables Z_1, Z_2

z_1 <- rbern(n, 1/2)

z_2 <- rbern(n, 1/2)

Z <- cbind(z_1, z_2)

u_w <- rnorm(n = n, mean = 0, sd = 1)

gamma_z <- runif(2, min = -1, max =  1)


#SCMs

w_2_propensity <- 1/(1 + exp(-(Z%*%gamma_z + u_w))) #Underlying propensity scores

w_2 <- rep.int(0, n)

for (i in 1:n) {                      # Treatment assignment
  w_2[i] <- rbern(1, w_2_propensity[i])
}

y_2 <-  tau*w_2 + X%*%beta_X_k + u_y  #Output
```

2.3 Constant Treatment Effect with Confounded Assignment, Including Covariates Affecting to Output

```
#New exogeneous parameters and variables

#Confounders C_1, ..., C_10

C <- matrix(0, nrow = n, ncol = 10)

for (l in 1:10) {


  if(l%%2 != 0){    #if k is odd

    for (i in 1:n) {

      C[i,l] <- rnorm(1, mean = 0, sd = 1)
    }

  } else {        #if k is even
```

4.1.4 Constant Treatment Effect with Confounded Assignment, Including Covariates Affecting to Output



(4.10)

$$f_W(Z_1, Z_2, C_1, \ldots, C_{10}, U_W) = \frac{1}{1 + \exp\left\{-\left(\sum_{j=1}^{2} \gamma_{Z_j} Z_j + \sum_{l=1}^{10} \gamma_{C_l} C_l + U_Y\right)\right\}} \tag{4.11}$$

$$f_Y(W, X_1, \ldots, X_{10}, C_1, \ldots, C_{10}, U_Y) = \tau \cdot W + \sum_{k=1}^{10} \beta_{X_k} X_k + \sum_{l=1}^{10} \beta_{C_l} C_l + U_Y \tag{4.12}$$

Figure 3: Simulation 3-1

, where

$$\begin{cases} U_Y & \sim \text{Norm}(\mu_Y(0), \sigma_Y^2) \\ U_W & \sim \text{Norm}(0, \sigma_W^2) \\ Z_1, Z_2 & \sim \text{Bern}\left(\frac{1}{2}\right) \\ X_K & \sim \text{Norm}(\mu_K, \sigma_K^2) \text{ when } k \text{ is odd and} \\ X_K & \sim \text{Bern}\left(\frac{1}{2}\right) \text{ when } k \text{ is even} \\ C_L & \sim \text{Norm}(\mu_L, \sigma_L^2) \text{ when } l \text{ is odd and} \\ C_L & \sim \text{Bern}\left(\frac{1}{2}\right) \text{ when } l \text{ is even} \end{cases}$$

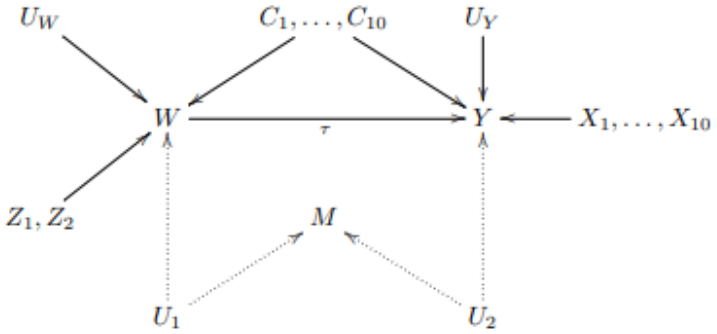
Figure 4: Simulation 3-2

```
      for (i in 1:n) {

        C[i, l] <- rbern(1, 1/2)

    }

  }
}


gamma_C_l <- runif(10, min = -0.5, max = 0.5)    #Coefficients for confounders for W

beta_C_l <- runif(10, min = -3, max = 3)    #Coefficients for confounders for Y


#SCMs

w_3_propensity <- 1/(1 + exp(-(Z%*%gamma_z + C%*%gamma_C_l + u_w))) #Underlying propensity scores

w_3 <- rep.int(0, n)

for (i in 1:n) {                        # Treatment assignment
  w_3[i] <- rbern(1, w_2_propensity[i])
}

y_3 <-  tau*w_3 + X%*%beta_X_k + C%*%beta_C_l + u_y  #Output
```

2.4 Constant Treatment Effect with Confounded Assignment, Including Covariates Affecting to Output and a Pure Local M-Structure

```
#New exogeneous parameters and variables

# Unobserved covariates U_1 and U_2
u_1 <- rbern(n, 1/2)
u_2 <- rbern(n, 1/2)

#Coefficients
gamma_U_1 <- 0.5
beta_U_2 <- 5

delta_1 <- 5
delta_2 <- 5

#SCMs

w_4_propensity <- 1/(1 + exp(-(Z%*%gamma_z + C%*%gamma_C_l + gamma_U_1*u_1 + u_w))) #Underlying propens

w_4 <- rep.int(0, n)

for (i in 1:n) {                        # Treatment assignment
  w_4[i] <- rbern(1, w_2_propensity[i])
```

4.1.6 Constant Treatment Effect with Confounded Assignment, Including Covariates Affecting to Output and a Pure Local M-Structure



(4.17)

$$f_W(Z_1, Z_2, C_1, \ldots, C_{10}, U_1, U_W) = \frac{1}{1 + \exp\left\{-\left(\sum_{j=1}^{2} \gamma_{Z_j} Z_j + \sum_{l=1}^{10} \gamma_{C_l} C_l + \gamma_{U_1} U_1 + U_Y\right)\right\}} \tag{4.18}$$

$$f_M = \delta_1 U_1 + \delta_2 U_2 \tag{4.19}$$

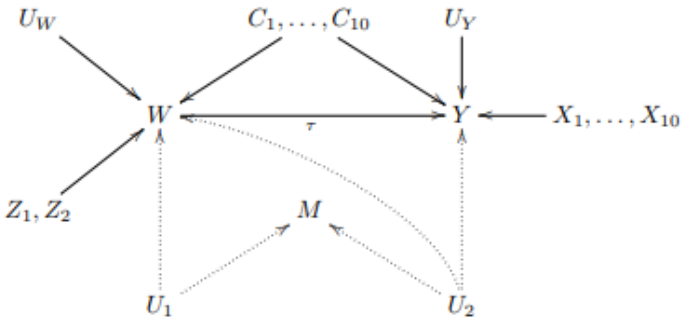
$$f_Y(W, X_1, \ldots, X_{10}, C_1, \ldots, C_{10}, I, U_2, U_Y) = \tau \cdot W + \sum_{k=1}^{10} \beta_{X_k} X_k + \sum_{l=1}^{10} \beta_{C_l} C_l + \beta_{U_2} U_2 + U_Y \tag{4.20}$$

, where

$$\begin{cases} U_Y & \sim \text{Norm}(\mu_Y(0), \sigma_Y^2) \\ U_W & \sim \text{Norm}(0, \sigma_W^2) \\ Z_1, Z_2 & \sim \text{Bern}\left(\frac{1}{2}\right) \\ X_K & \sim \text{Norm}(\mu_K, \sigma_K^2) \text{ when } k \text{ is odd and} \\ X_K & \sim \text{Bern}\left(\frac{1}{2}\right) \text{ when } k \text{ is even} \\ C_L & \sim \text{Norm}(\mu_L, \sigma_L^2) \text{ when } l \text{ is odd and} \\ C_L & \sim \text{Bern}\left(\frac{1}{2}\right) \text{ when } l \text{ is even} \\ U_1, U_2 & \sim \text{Bern}\left(\frac{1}{2}\right) \end{cases}$$

Figure 5: Simulation 4

4.1.7 Constant Treatment Effect with Confounded Assignment, Including Covariates Affecting to Output and a Impure Local M-Structure



(4.21)

$$f_W(Z_1, Z_2, C_1, \ldots, C_{10}, U_1, U_2, U_W) = \frac{1}{1 + \exp\left\{-\left(\sum_{j=1}^{2} \gamma_{Z_j} Z_j + \sum_{l=1}^{10} \gamma_{C_l} C_l + \sum_{m=1}^{2} \gamma_{U_m} U_m + U_Y\right)\right\}} \tag{4.22}$$

$$f_M = \delta_1 U_1 + \delta_2 U_2 \tag{4.23}$$

$$f_Y(W, X_1, \ldots, X_{10}, C_1, \ldots, C_{10}, U_2, U_Y) = \tau \cdot W + \sum_{k=1}^{10} \beta_{X_k} X_k + \sum_{l=1}^{10} \beta_{C_l} C_l + \beta_{U_2} U_2 + U_Y \tag{4.24}$$

, where

$$\begin{cases} U_Y & \sim \text{Norm}(\mu_Y(0), \sigma_Y^2) \\ U_W & \sim \text{Norm}(0, \sigma_W^2) \\ Z_1, Z_2 & \sim \text{Bern}\left(\frac{1}{2}\right) \\ X_K & \sim \text{Norm}(\mu_K, \sigma_K^2) \text{ when } k \text{ is odd and} \\ X_K & \sim \text{Bern}\left(\frac{1}{2}\right) \text{ when } k \text{ is even} \\ C_L & \sim \text{Norm}(\mu_L, \sigma_L^2) \text{ when } l \text{ is odd and} \\ C_L & \sim \text{Bern}\left(\frac{1}{2}\right) \text{ when } l \text{ is even} \\ U_1, U_2 & \sim \text{Bern}\left(\frac{1}{2}\right) \end{cases}$$

Figure 6: Simulation 5

```
}

m <- delta_1*u_1 + delta_2*u_2          # Observed collider M


y_4 <-  tau*w_4 + X%*%beta_X_k + C%*%beta_C_l + beta_U_2*u_2 + u_y  #Output
```

2.5 Constant Treatment Effect with Confounded Assignment, Including Covariates Affecting to Output and a Impure Local M-Structure

```
#New coefficient

gamma_U_2 <- 0.2
```

4.1.8 Randomized Controlled Trial with Heterogeneous Treatment Effect, Including Covariates Affecting to Output

$$U_Y \tag{4.25}$$

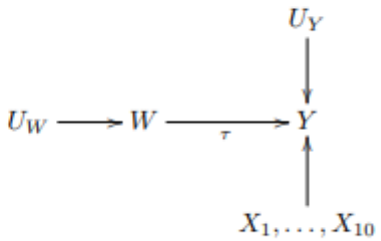


Figure 7: Simulation 6-1

$$f_W(U_W) = \text{Bern}\left(\frac{1}{2}\right) \tag{4.26}$$

$$f_Y(W, X_1, \ldots, X_{10}, U_Y) = \tau(x_1, x_2, x_3) \cdot W + \sum_{k=1}^{10} \beta_{X_k} X_k + U_Y \tag{4.27}$$

, where

$$\begin{cases} U_Y & \sim \text{Norm}(\mu_Y(0), \sigma_Y^2) \\ X_K & \sim \text{Norm}(\mu_K, \sigma_K^2) \text{ when } k \text{ is odd and} \\ X_K & \sim \text{Bern}\left(\frac{1}{2}\right) \text{ when } k \text{ is even} \end{cases}$$

and $\tau(x_1, x_2, x_3) = \alpha_0 + \alpha_1 x_1 + \alpha_2 x_2 x_3$.

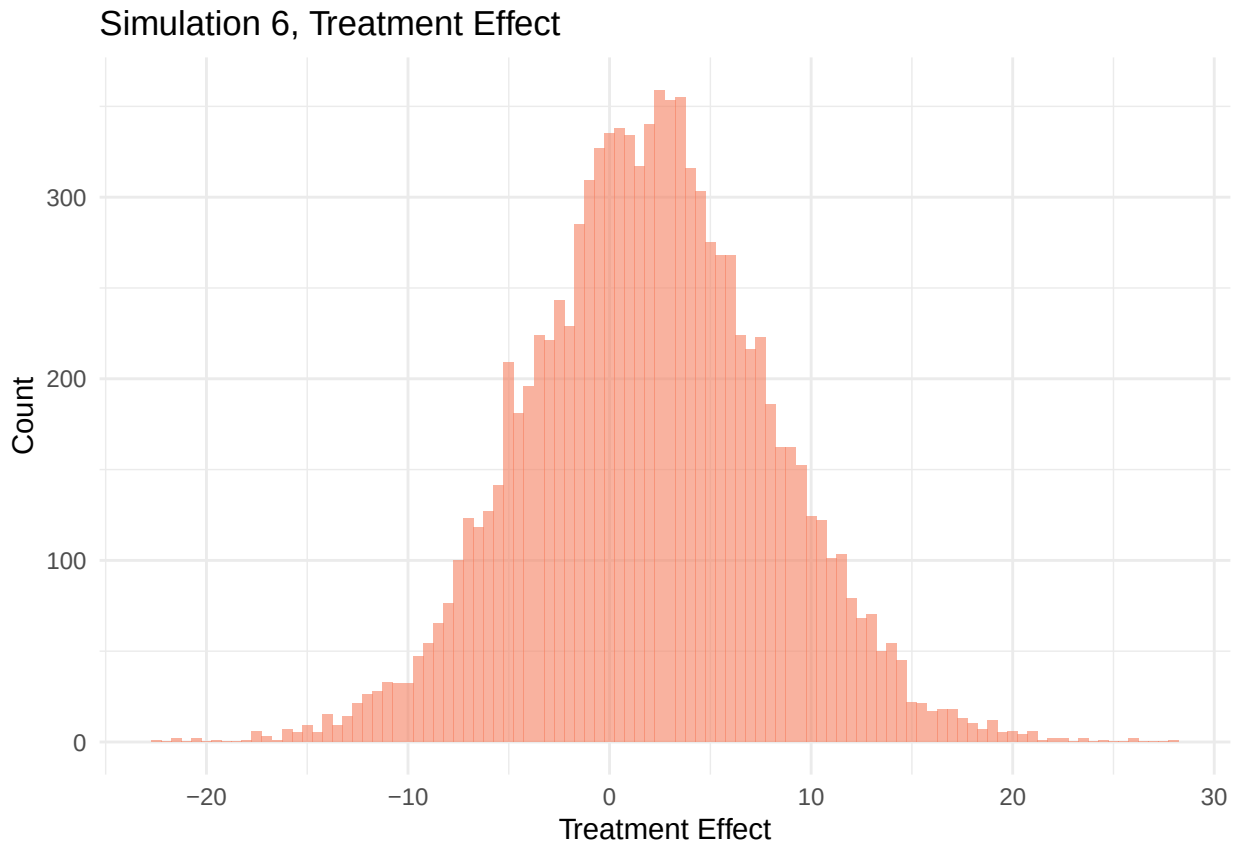
Figure 8: Simulation 6-2

```
#SCMs

w_5_propensity <- 1/(1 + exp(-(Z%*%gamma_z + C%*%gamma_C_l + gamma_U_1*u_1 + gamma_U_2*u_2 + u_w))) #Un

w_5 <- rep.int(0, n)

for (i in 1:n) {                        # Treatment assignment
  w_5[i] <- rbern(1, w_2_propensity[i])
}

y_5 <-  tau*w_5 + X%*%beta_X_k + C%*%beta_C_l + beta_U_2*u_2 + u_y      #Output
```

2.6 Randomized Controlled Trial with Heterogeneous Treatment Effect, Including Covariates Affecting to Output

```
#Heterogeneous treatment effect

#Alphas
```

```r
alp_0 <- 2
alp_1 <- 5
alp_2 <- -5

tau_1 <- rep.int(alp_0,n) + alp_1*X[,1] + alp_2*X[,2]*X[,3]  #Treatment effect

ggplot(data = as.data.frame(tau_1), aes(x = tau_1)) +
  geom_histogram(fill="#f68060", alpha=.6, binwidth = 0.5) +
  labs(title ="Simulation 6, Treatment Effect", x = "Treatment Effect", y = "Count") +
  theme_minimal()
```

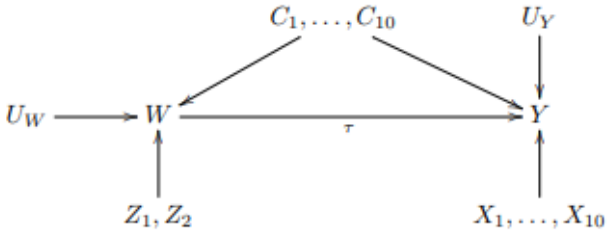



```r
#SCM

y_6 <- tau_1*w_1 + X%*%beta_X_k + u_y  #Output
```

2.7 Heterogeneous Treatment Effect with the Confounded Assignment, Including Covariates Affecting to Output

```r
#New alpha

alp_3 <- 3

tau_2 <- rep.int(alp_0,n) + alp_1*X[,1] + alp_2*X[,2]*X[,3] + alp_3*C[,1]   #Treatment effect
```

4.1.9 Heterogeneous Treatment Effect with Confounded Assignment, Including Covariates Affecting to Output



(4.28)

$$f_W(Z_1, Z_2, C_1, \ldots, C_{10}, U_W) = \frac{1}{1 + \exp\left\{-\left(\sum_{j=1}^{2} \gamma_{Z_j} Z_j + \sum_{l=1}^{10} \gamma_{C_l} C_l + U_Y\right)\right\}} \tag{4.29}$$

$$f_Y(W, X_1, \ldots, X_{10}, C_1, \ldots, C_{10}, U_Y) = \tau(x_1, x_2, x_3, c_1) \cdot W + \sum_{k=1}^{10} \beta_{X_k} X_k + \sum_{l=1}^{10} \beta_{C_l} C_l + U_Y \tag{4.30}$$

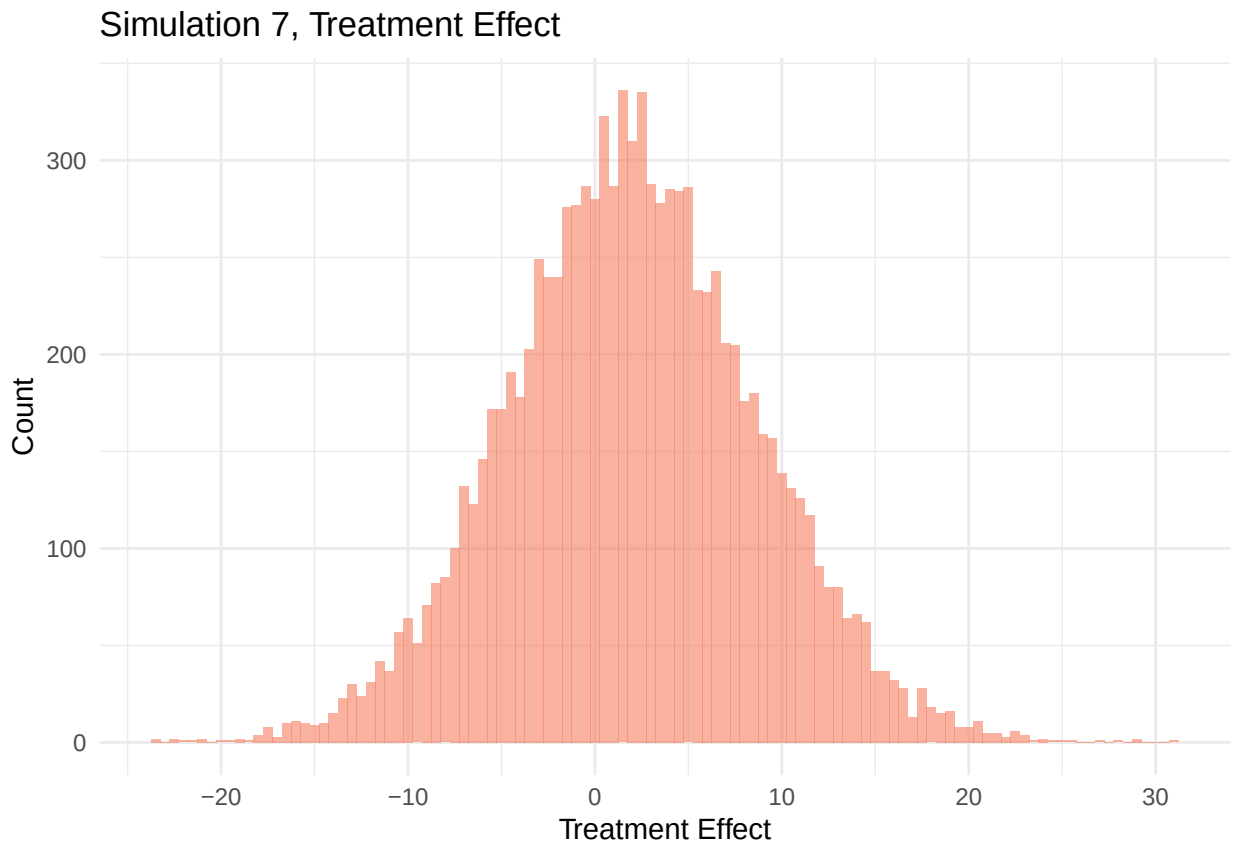
, where

$$\begin{cases} U_Y & \sim \text{Norm}(\mu_Y(0), \sigma_Y^2) \\ U_W & \sim \text{Norm}(0, \sigma_W^2) \\ Z_1, Z_2 & \sim \text{Bern}\left(\frac{1}{2}\right) \\ X_K & \sim \text{Norm}(\mu_K, \sigma_K^2) \text{ when } k \text{ is odd and} \\ X_K & \sim \text{Bern}\left(\frac{1}{2}\right) \text{ when } k \text{ is even} \\ C_L & \sim \text{Norm}(\mu_L, \sigma_L^2) \text{ when } l \text{ is odd and} \\ C_L & \sim \text{Bern}\left(\frac{1}{2}\right) \text{ when } l \text{ is even} \end{cases}$$

and $\tau(x_1, x_2, x_3, c_1) = \alpha_0 + \alpha_1 x_1 + \alpha_2 x_2 x_3 + \alpha_3 c_1$.

Figure 9: Simulation 7

```r
ggplot(data = as.data.frame(tau_2), aes(x = tau_2)) +
  geom_histogram(fill="#f68060", alpha=.6,binwidth = 0.5) +
  labs(title ="Simulation 7, Treatment Effect", x = "Treatment Effect", y = "Count") +
  theme_minimal()
```



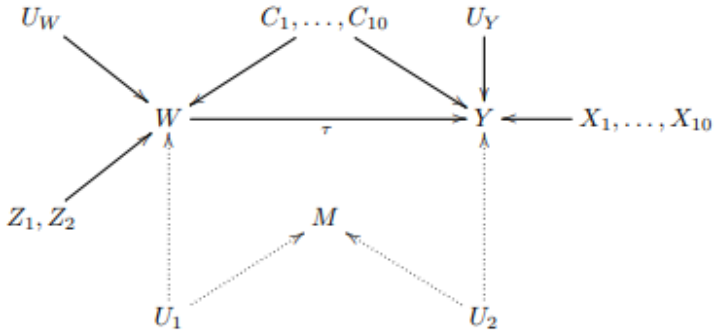

```r
#SCM

y_7 <-  tau_2*w_3 + X%*%beta_X_k + C%*%beta_C_l + u_y  #Output
```

2.8 Heterogeneous Treatment Effect with Confounded Assignment, Including Covariates Affecting to Output and a Pure Local M-Structure

```r
#SCM

y_8 <-  tau_2*w_4 + X%*%beta_X_k + C%*%beta_C_l + beta_U_2*u_2 + u_y  #Output
```

2.9 Heterogeneous Treatment Effect with Confounded Assignment, Including Covariates Affecting to Output and a Impure Local M-Structure

4.1.11 Heterogeneous Treatment Effect with Confounded Assignment, Including Covariates Affecting to Output and a Pure Local M-Structure



(4.35)

$$f_W(Z_1, Z_2, C_1, \ldots, C_{10}, U_1, U_W) = \frac{1}{1 + \exp\left\{-\left(\sum_{j=1}^{2} \gamma_{Z_j} Z_j + \sum_{l=1}^{10} \gamma_{C_l} C_l + \gamma_{U_1} U_1 + U_Y\right)\right\}} \tag{4.36}$$

$$f_M = \delta_1 U_1 + \delta_2 U_2 \tag{4.37}$$

$$f_Y(W, X_1, \ldots, X_{10}, C_1, \ldots, C_{10}, U_2, U_Y) = \tau(x_1, x_2, x_3, c_1) \cdot W + \sum_{k=1}^{10} \beta_{X_k} X_k + \sum_{l=1}^{10} \beta_{C_l} C_l + \beta_{U_2} U_2 + U_Y \tag{4.38}$$

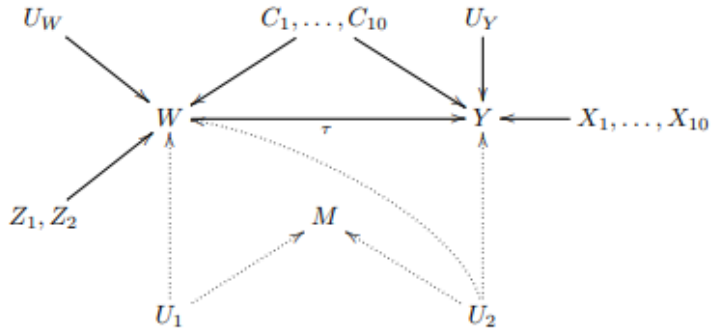
, where

$$\begin{cases} U_Y & \sim \text{Norm}(\mu_Y(0), \sigma_Y^2) \\ U_W & \sim \text{Norm}(0, \sigma_W^2) \\ Z_1, Z_2 & \sim \text{Bern}\left(\frac{1}{2}\right) \\ X_K & \sim \text{Norm}(\mu_K, \sigma_K^2) \text{ when } k \text{ is odd and} \\ X_K & \sim \text{Bern}\left(\frac{1}{2}\right) \text{ when } k \text{ is even} \\ C_L & \sim \text{Norm}(\mu_L, \sigma_L^2) \text{ when } l \text{ is odd and} \\ C_L & \sim \text{Bern}\left(\frac{1}{2}\right) \text{ when } l \text{ is even} \\ U_1, U_2 & \sim \text{Bern}\left(\frac{1}{2}\right) \end{cases}$$

and $\tau(x_1, x_2, x_3, c_1) = \alpha_0 + \alpha_1 x_1 + \alpha_2 x_2 x_3 + \alpha_3 c_1$.

Figure 10: Simulation 8

4.1.12 Heterogeneous Treatment Effect with Confounded Assignment, Including Covariates Affecting to Output and a Impure Local M-Structure



(4.39)

$$f_W(Z_1, Z_2, C_1, \ldots, C_{10}, U_1, U_2, U_W) = \frac{1}{1 + \exp\left\{-\left(\sum_{j=1}^{2} \gamma_{Z_j} Z_j + \sum_{l=1}^{10} \gamma_{C_l} C_l + \sum_{m=1}^{2} \gamma_{U_m} U_m + U_Y\right)\right\}} \tag{4.40}$$

$$f_M = \delta_1 U_1 + \delta_2 U_2 \tag{4.41}$$

$$f_Y(W, X_1, \ldots, X_{10}, C_1, \ldots, C_{10}, U_2, U_Y) = \tau(x_1, x_2, x_3, c_1) \cdot W + \sum_{k=1}^{10} \beta_{X_k} X_k + \sum_{l=1}^{10} \beta_{C_l} C_l + \beta_{U_2} U_2 + U_Y \tag{4.42}$$

, where

$$\begin{cases} U_Y & \sim \text{Norm}(\mu_Y(0), \sigma_Y^2) \\ U_W & \sim \text{Norm}(0, \sigma_W^2) \\ Z_1, Z_2 & \sim \text{Bern}\left(\frac{1}{2}\right) \\ X_K & \sim \text{Norm}(\mu_K, \sigma_K^2) \text{ when } k \text{ is odd and} \\ X_K & \sim \text{Bern}\left(\frac{1}{2}\right) \text{ when } k \text{ is even} \\ C_L & \sim \text{Norm}(\mu_L, \sigma_L^2) \text{ when } l \text{ is odd and} \\ C_L & \sim \text{Bern}\left(\frac{1}{2}\right) \text{ when } l \text{ is even} \\ U_1, U_2 & \sim \text{Bern}\left(\frac{1}{2}\right) \end{cases}$$

and $\tau(x_1, x_2, x_3, c_1) = \alpha_0 + \alpha_1 x_1 + \alpha_2 x_2 x_3 + \alpha_3 c_1$.

Figure 11: Simulation 9

```
#SCM

y_9 <- tau_2*w_5 + X%*%beta_X_k + C%*%beta_C_l + beta_U_2*u_2 + u_y      #Output
```

All the parameters, table:

```
#Betas

betas <- as.data.frame(c(beta_X_k, beta_C_l, beta_U_2))

rownames(betas) <- c("$\\beta_{X_1}$",
                     "$\\beta_{X_2}$",
                     "$\\beta_{X_3}$",
                     "$\\beta_{X_4}$",
                     "$\\beta_{X_5}$",
                     "$\\beta_{X_6}$",
                     "$\\beta_{X_7}$",
                     "$\\beta_{X_8}$",
                     "$\\beta_{X_9}$",
                     "$\\beta_{X_10}$",
                     "$\\beta_{C_1}$",
                     "$\\beta_{C_2}$",
                     "$\\beta_{C_3}$",
                     "$\\beta_{C_4}$",
                     "$\\beta_{C_5}$",
                     "$\\beta_{C_6}$",
                     "$\\beta_{C_7}$",
                     "$\\beta_{C_8}$",
                     "$\\beta_{C_9}$",
                     "$\\beta_{C_10}$",
                     "$\\beta_{U_2}$")

colnames(betas) <- c("Value")

knitr::kable(betas, escape = FALSE)
```

	Value
β_{X_1}	1.1846881
β_{X_2}	1.6731552
β_{X_3}	2.9565855
β_{X_4}	-1.8355449
β_{X_5}	2.8452661
β_{X_6}	-1.1567457
β_{X_7}	-1.5805033
β_{X_8}	1.4988092
β_{X_9}	1.3516565
β_{X_10}	2.8661819
β_{C_1}	2.9628036
β_{C_2}	0.8623509
β_{C_3}	-0.0993400
β_{C_4}	-1.1987373
β_{C_5}	-2.5123647

	Value
β_{C_6}	-1.7654443
β_{C_7}	0.2969675
β_{C_8}	0.9698760
β_{C_9}	0.9790413
β_{C_10}	0.3159898
β_{U_2}	5.0000000

```
gammas <- as.data.frame(c(gamma_z, gamma_C_l, gamma_U_1))

rownames(gammas) <- c("$\\gamma_{Z_1}$",
                      "$\\gamma_{Z_2}$",
                      "$\\gamma_{C_1}$",
                      "$\\gamma_{C_2}$",
                      "$\\gamma_{C_3}$",
                      "$\\gamma_{C_4}$",
                      "$\\gamma_{C_5}$",
                      "$\\gamma_{C_6}$",
                      "$\\gamma_{C_7}$",
                      "$\\gamma_{C_8}$",
                      "$\\gamma_{C_9}$",
                      "$\\gamma_{C_{10}}$",
                      "$\\gamma_{U_1}$")

colnames(gammas) <- c("Value")

knitr::kable(gammas, escape = FALSE)
```

	Value
γ_{Z_1}	0.3103331
γ_{Z_2}	-0.8675404
γ_{C_1}	0.2809952
γ_{C_2}	0.0842018
γ_{C_3}	-0.2081202
γ_{C_4}	-0.0699206
γ_{C_5}	-0.1153378
γ_{C_6}	-0.3488950
γ_{C_7}	-0.2784899
γ_{C_8}	0.3364730
γ_{C_9}	-0.3641025
$\gamma_{C_{10}}$	-0.1293683
γ_{U_1}	0.5000000

```
deltas <- as.data.frame(c(delta_1, delta_2))

rownames(deltas) <- c("$\\delta_1$", "$\\delta_2$")

colnames(deltas) <- c("Value")

knitr::kable(deltas, escape = FALSE)
```

	Value
δ_1	5
δ_2	5

As LaTeX:

```
knitr::kable(betas, format = "latex", escape = FALSE)
```

	Value
β_{X_1}	1.1846881
β_{X_2}	1.6731552
β_{X_3}	2.9565855
β_{X_4}	-1.8355449
β_{X_5}	2.8452661
β_{X_6}	-1.1567457
β_{X_7}	-1.5805033
β_{X_8}	1.4988092
β_{X_9}	1.3516565
β_{X_10}	2.8661819
β_{C_1}	2.9628036
β_{C_2}	0.8623509
β_{C_3}	-0.0993400
β_{C_4}	-1.1987373
β_{C_5}	-2.5123647
β_{C_6}	-1.7654443
β_{C_7}	0.2969675
β_{C_8}	0.9698760
β_{C_9}	0.9790413
β_{C_10}	0.3159898
β_{U_2}	5.0000000

```
knitr::kable(gammas, format = "latex", escape = FALSE)
```

	Value
γ_{Z_1}	0.3103331
γ_{Z_2}	-0.8675404
γ_{C_1}	0.2809952
γ_{C_2}	0.0842018
γ_{C_3}	-0.2081202
γ_{C_4}	-0.0699206
γ_{C_5}	-0.1153378
γ_{C_6}	-0.3488950
γ_{C_7}	-0.2784899
γ_{C_8}	0.3364730
γ_{C_9}	-0.3641025
$\gamma_{C_{10}}$	-0.1293683
γ_{U_1}	0.5000000

```
knitr::kable(deltas, format = "latex" , escape = FALSE)
```

	Value
δ_1	5
δ_2	5

3 Causal Forest

In the simulation study, we are using the *causal forest* . The function is in *grf* package which can be found from CRAN. See also this.

In each subsection, the causal boosting algorithm will be ran. The performance in each simulations are tested with *root mean squared error*:

$$\widehat{\mathrm{RMSE}} = \sqrt{\frac{1}{n}\sum_{i=1}^{n}\left[(\tau(x) - \hat{\tau}(x)\right]^2}$$

```
fun.rmse <- function(predicted, true){

  rmse <- sqrt(mean((true - predicted)^2))

  rmse
}
```

Also the *proportional difference in the ATE estimates* for the whole population is calcucated (with 95 % confidence interval):

$$\frac{\tau_{\mathrm{ATE}} - \hat{\tau}_{ATE}}{\tau_{ATE}}$$

```
fun.diff_ATE <- function(ATE_est, ATE_true){

  print("Proportional mean of the differences:")

  diff_mean <- (ATE_true - ATE_est[1])/ATE_true

  print(diff_mean)

  print("Proportional mean of the differences, 95 % confidence intervals:")

  print(c((diff_mean - ATE_est[2]/ATE_true), (diff_mean + ATE_est[2]/ATE_true)))

}
```

The 95 % coverage of the CATEs:

```
# Is the real value in the 95% confidence interval

fun.coverage <- function(predicted, true){

  cate <- predicted$predictions

  std_error <- sqrt(predicted$variance.estimates)

  confint <- matrix(c((cate - qnorm(1 - 0.025)*std_error),
                      (cate + qnorm(1 - 0.025)*std_error)), ncol = 2)

  fun.is_in_confint <- function(value, min, max){

    (value >= min)&(value <= max)
```

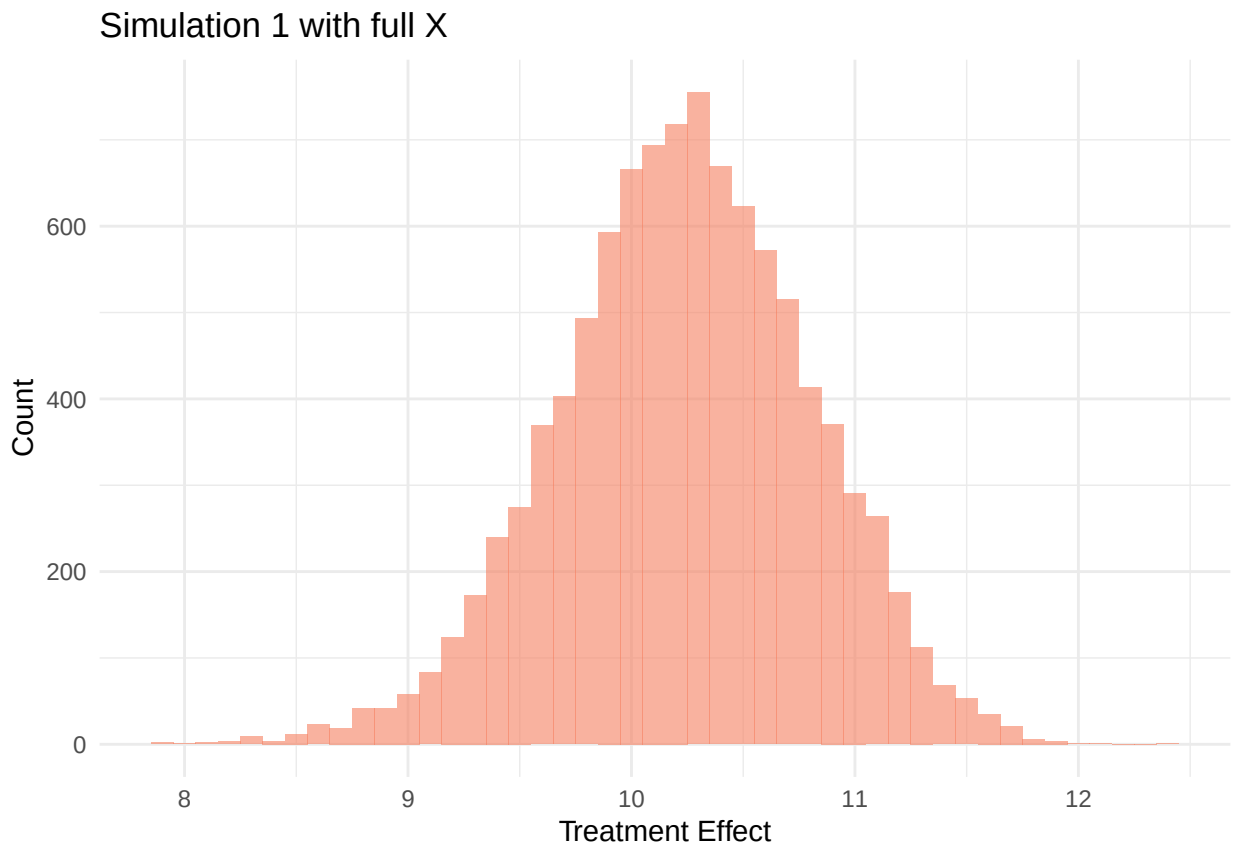
```
  }

  in_confint <- cbind(true, confint) %>%
    as.data.frame()  %>%
    mutate(in_confint = fun.is_in_confint(true, V2, V3)) %>%
    select(in_confint)

  length(which(in_confint$in_confint == TRUE))/length(in_confint$in_confint)

}
```

Also the running times for the algorithm are given for each simulation. Let's remark the adjusted set with $\mathbb{S}$.

3.1 Randomized Controlled Trial with Constant Treatment Effect

$X \in \mathbb{S}$

```
# Estimate causal forest
start_time_1 <- Sys.time() #Recording the running time

#Fitting the model
cf1.full <- grf::causal_forest(X, y_1, w_1)


end_time_1 <- Sys.time()

#Predicted values

pred_tau_1.full <- predict(cf1.full, estimate.variance = TRUE)

plot_pred_tau_1 <- ggplot(data = as.data.frame(pred_tau_1.full$predictions),
                          aes(x = (pred_tau_1.full$predictions))) +
  geom_histogram(fill="#f68060", alpha=.6,binwidth = 0.1) +
  labs(title ="Simulation 1 with full X",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()

plot_pred_tau_1
```



Runing time:

```
start_time_1 - end_time_1
```

```
## Time difference of -35.44318 secs
```

RMSE:

```
rmse_1.full <- fun.rmse(predicted = pred_tau_1.full$predictions, true = tau)

rmse_1.full
```

```
## [1] 0.610858
```

Coverage:

```
coverage_1.full <- fun.coverage(pred_tau_1.full, tau)

coverage_1.full
```

```
## [1] 0.9917
```

Estimated ATE:

```r
ATE_est_1.full <- average_treatment_effect(cf1.full)


ATE_est_1.full
```

```
##  estimate   std.err
## 10.242091  0.203769
```

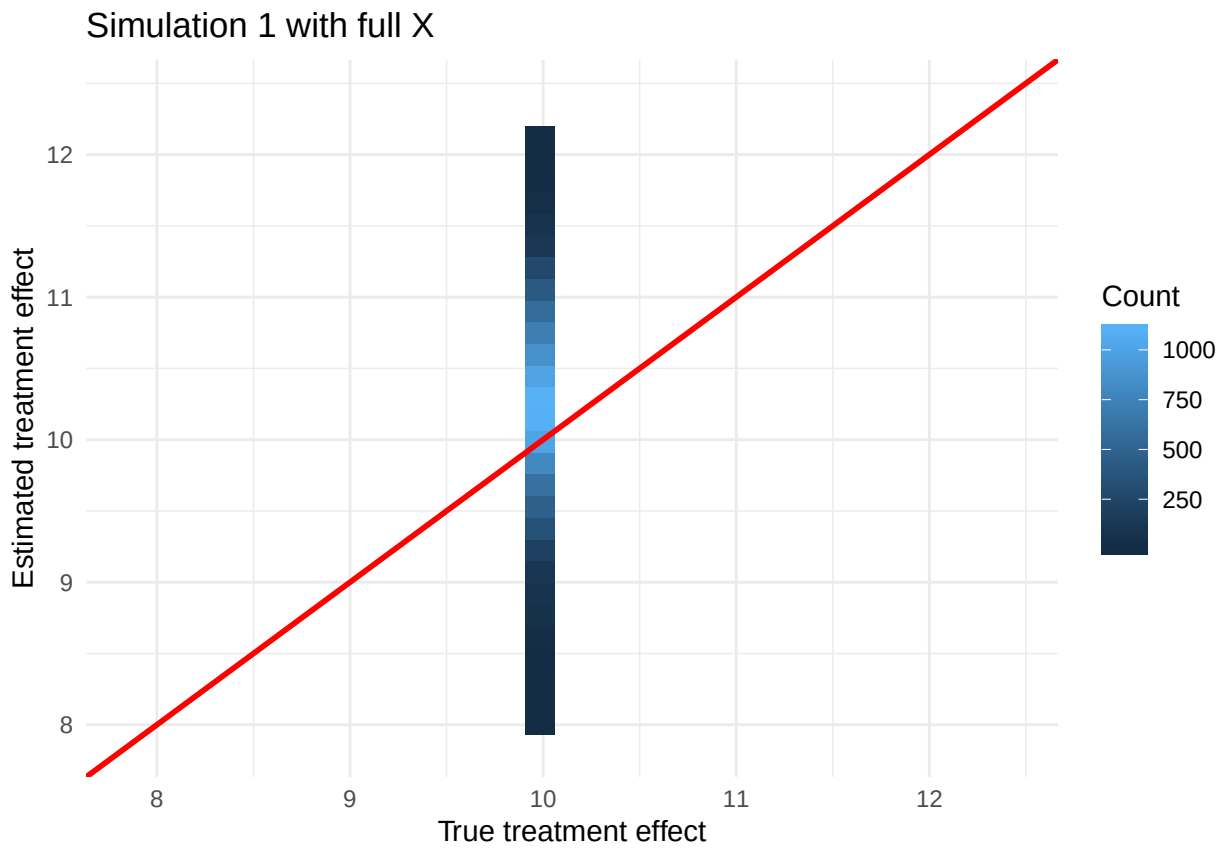
The *proportional difference in the ATE estimates* for the whole population:

```r
fun.diff_ATE(ATE_est = ATE_est_1.full, ATE_true = tau)
```

```
## [1] "Proportional mean of the differences:"
##    estimate
## -0.02420905
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##     estimate     estimate
## -0.044585947 -0.003832155
```

```r
true_vs_pred_1.full <- as.data.frame(cbind(tau, pred_tau_1.full$predictions))

colnames(true_vs_pred_1.full) <- c("tau", "pred_tau")

true_vs_pred_1.full$tau <- true_vs_pred_1.full$tau + rnorm(n, 0 , sd = 0.0001)

plot1 <- ggplot(data = true_vs_pred_1.full, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 1 with full X",
       x = "True treatment effect", y = "Estimated treatment effect",
       fill = "Count") +
  lims(x = c(min(true_vs_pred_1.full$pred_tau),
             max(true_vs_pred_1.full$pred_tau)),
       y = c(min(true_vs_pred_1.full$pred_tau),
             max(true_vs_pred_1.full$pred_tau)))

plot1
```

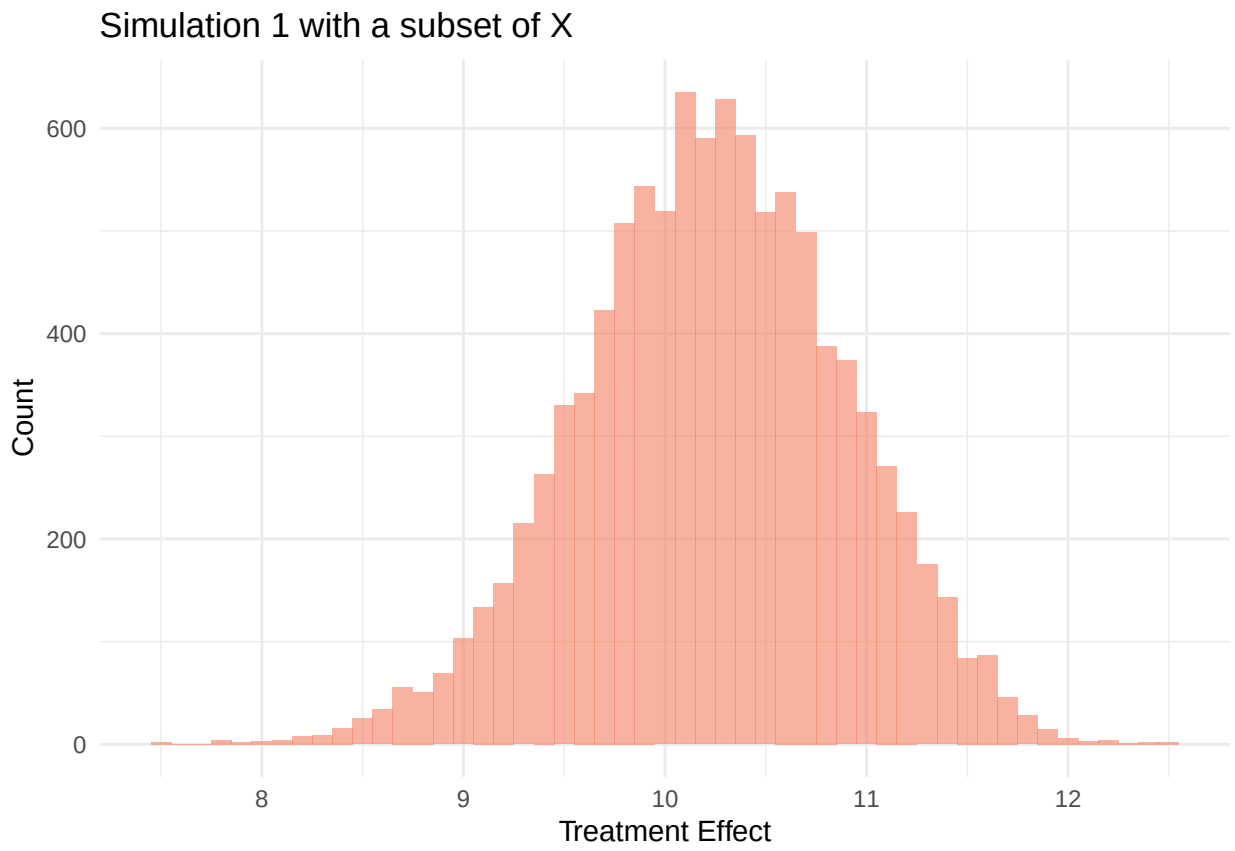
```
## Warning: Removed 1 rows containing missing values (geom_tile).
```



Let's try to use only the most important (*"A simple weighted sum of how many times feature i was split on at each depth in the forest"*) variables (over the median):

```
important_var_1 <- which(variable_importance(cf1.full) >= median(variable_importance(cf1.full))) #Varia
```

```
# Estimate causal forest
start_time_1_2 <- Sys.time() #Recording the running time

#Fitting the model
cf1.important <- grf::causal_forest(X[, important_var_1], y_1, w_1)


end_time_1_2 <- Sys.time()

#Predicted values

pred_tau_1.important <- predict(cf1.important, estimate.variance = TRUE)

plot_pred_tau_1_2 <- ggplot(data = as.data.frame(pred_tau_1.important$predictions),
                      aes(x = (pred_tau_1.important$predictions))) +
  geom_histogram(fill="#f68060", alpha=.6, binwidth = 0.1) +
  labs(title ="Simulation 1 with a subset of X",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()

plot_pred_tau_1_2
```



Runing time:

```
start_time_1_2 - end_time_1_2
```

```
## Time difference of -30.76669 secs
```

RMSE:

```
rmse_1.important <- fun.rmse(predicted = pred_tau_1.important$predictions, true = tau)

rmse_1.important
```

```
## [1] 0.6979229
```

Coverage:

```
coverage_1.important <- fun.coverage(pred_tau_1.important, tau)

coverage_1.important
```

```
## [1] 0.9875
```

Estimated ATE:

```r
ATE_est_1.important <- average_treatment_effect(cf1.important)


ATE_est_1.important
```

```
##   estimate    std.err
## 10.2259539  0.2062475
```

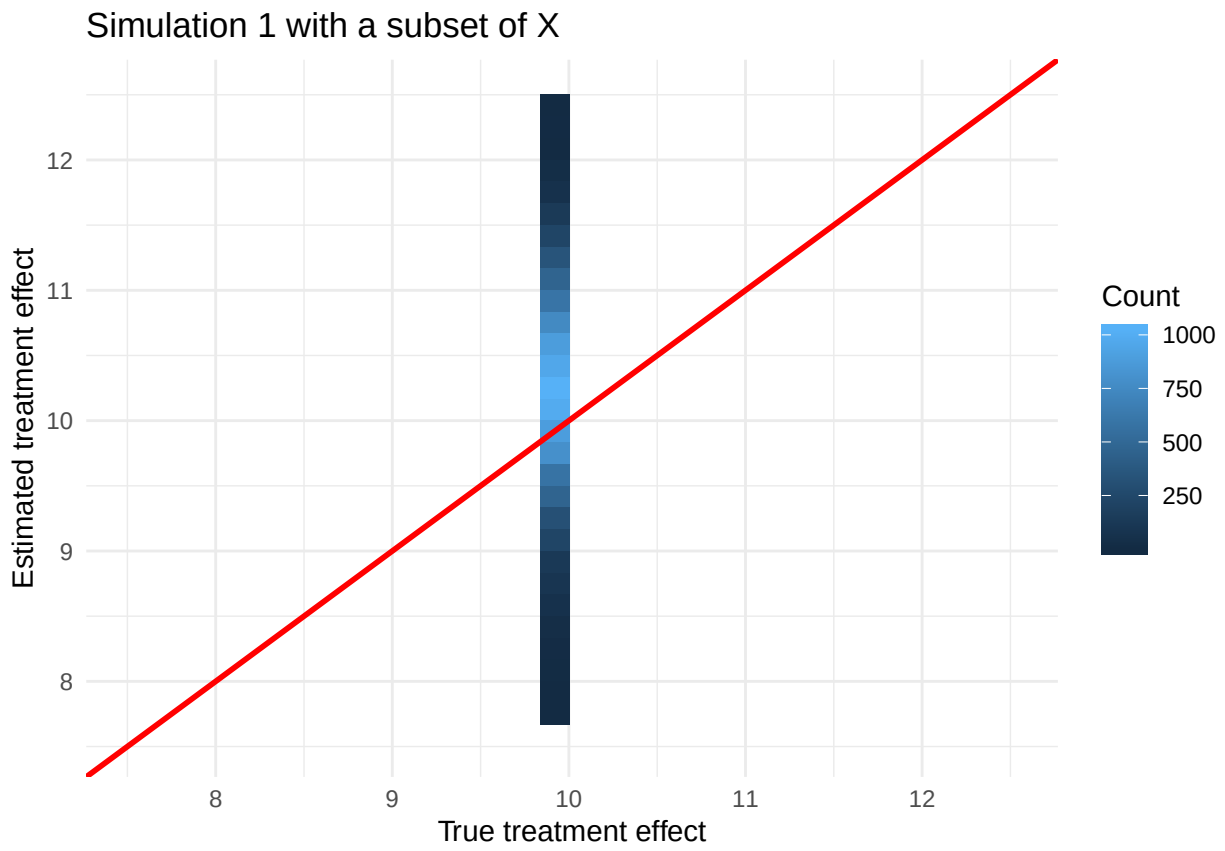
The *proportional difference in the ATE estimates* for the whole population:

```r
fun.diff_ATE(ATE_est = ATE_est_1.important, ATE_true = tau)
```

```
## [1] "Proportional mean of the differences:"
##    estimate
## -0.02259539
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##     estimate     estimate
## -0.043220144 -0.001970645
```

```r
true_vs_pred_1.important <- as.data.frame(cbind(tau, pred_tau_1.important$predictions))

colnames(true_vs_pred_1.important) <- c("tau", "pred_tau")

true_vs_pred_1.important$tau <- true_vs_pred_1.important$tau + rnorm(n, 0 , sd = 0.0001)

plot1_2 <- ggplot(data = true_vs_pred_1.important, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 1 with a subset of X",
       x = "True treatment effect", y = "Estimated treatment effect",
       fill = "Count") +
  lims(x = c(min(true_vs_pred_1.important$pred_tau),
             max(true_vs_pred_1.important$pred_tau)),
       y = c(min(true_vs_pred_1.important$pred_tau),
             max(true_vs_pred_1.important$pred_tau)))

plot1_2
```

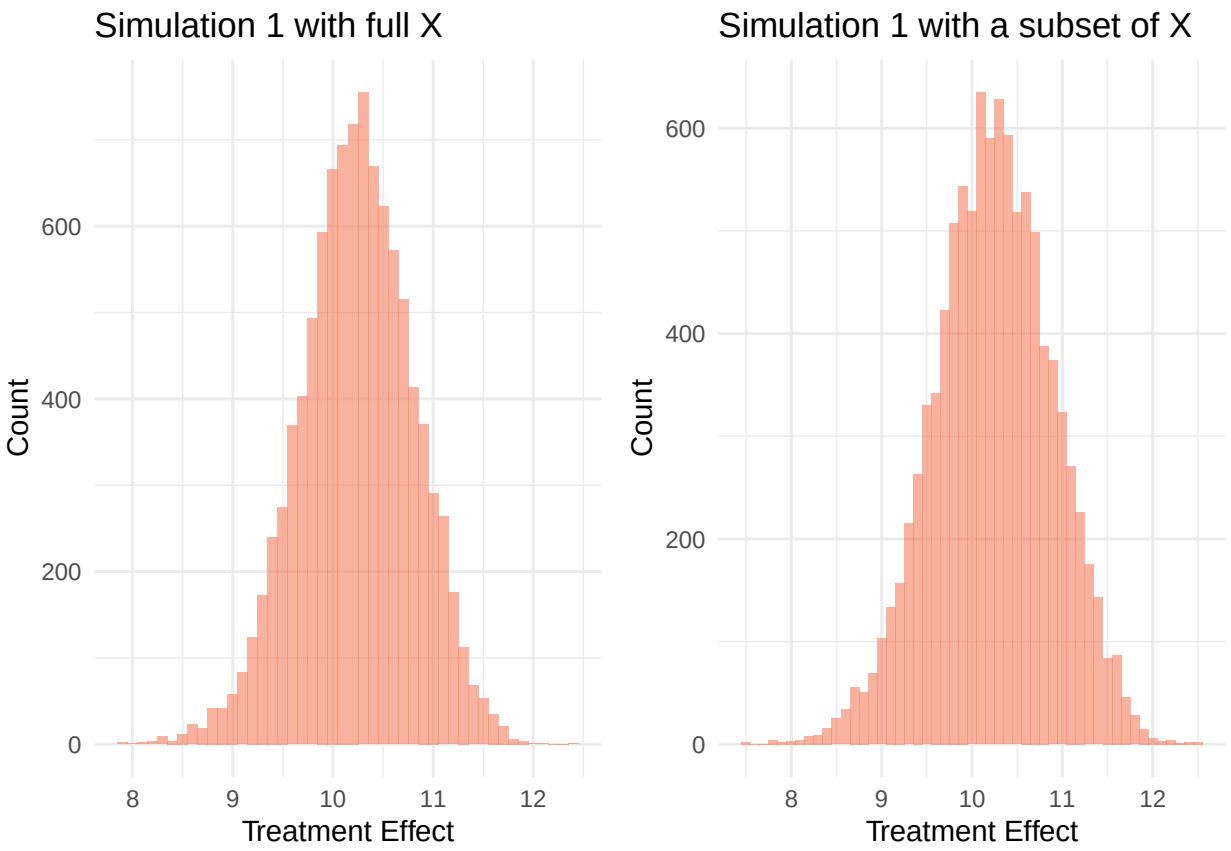
```
## Warning: Removed 1 rows containing missing values (geom_tile).
```



Summary

Predicted $\hat{\tau}s$:

```
grid.arrange(plot_pred_tau_1, plot_pred_tau_1_2, nrow = 1)
```

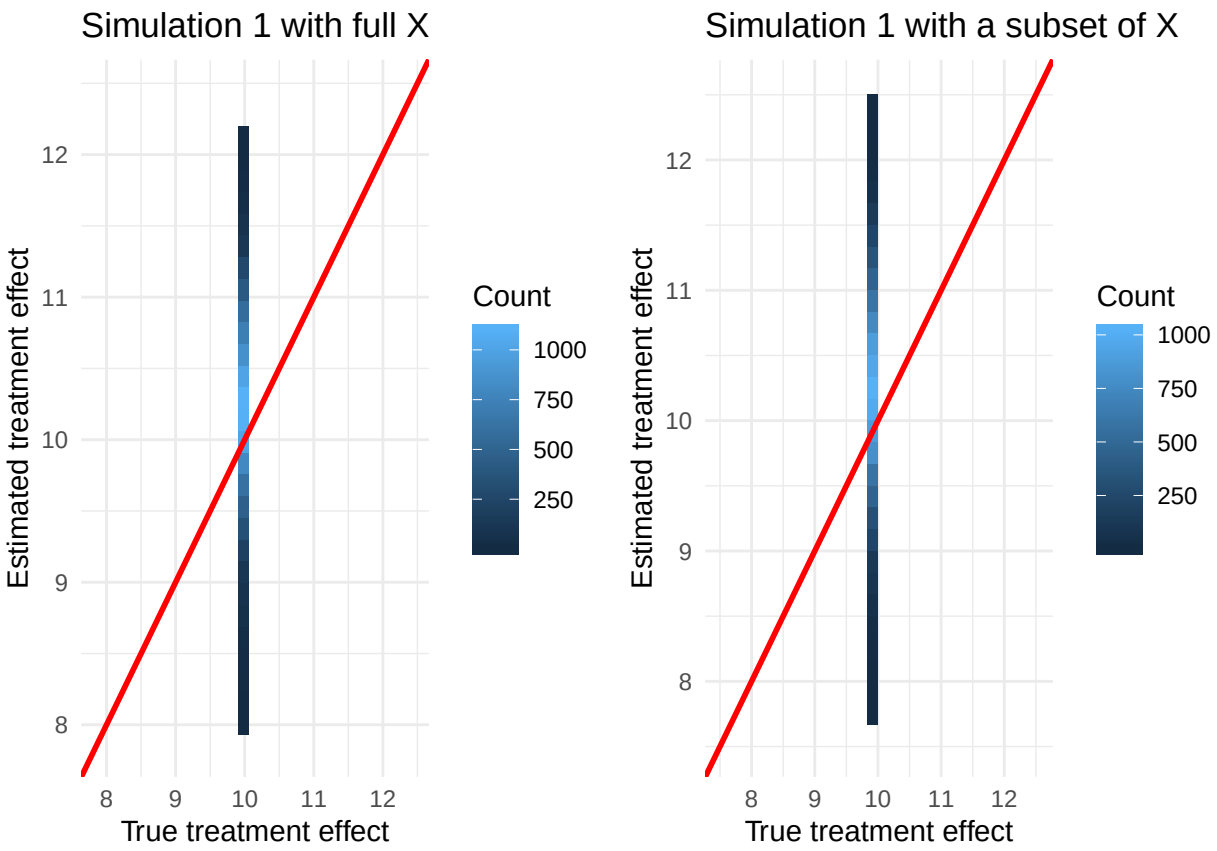


True τ vs. predicted $\hat{\tau}$:

```
grid.arrange(plot1, plot1_2, nrow = 1)
```

```
## Warning: Removed 1 rows containing missing values (geom_tile).
```

```
## Warning: Removed 1 rows containing missing values (geom_tile).
```



RMSEs:

```
rmse_1 <- as.data.frame(c(rmse_1.full, rmse_1.important))

rownames(rmse_1) <- c("Full $X$", "Subset of $X$")

colnames(rmse_1) <- c("RMSE")

knitr::kable(rmse_1, escape = FALSE)
```

	RMSE
Full X	0.6108580
Subset of X	0.6979229

Coverages:

```
coverage_1 <- as.data.frame(c(coverage_1.full, coverage_1.important))

rownames(coverage_1) <- c("Full $X$", "Subset of $X$")

colnames(coverage_1) <- c("Coverage")

knitr::kable(coverage_1, escape = FALSE)
```

	Coverage
Full X	0.9917
Subset of X	0.9875

LaTeX:

```
knitr::kable(rmse_1, format = "latex",escape = FALSE)
```

	RMSE
Full X	0.6108580
Subset of X	0.6979229

```
knitr::kable(coverage_1, format = "latex",escape = FALSE)
```

	Coverage
Full X	0.9917
Subset of X	0.9875

3.2 Constant Treatment Effect with Unconfounded Assignment, Including Covariates Affecting to Output

Let's do the first estimation without the Zs ($X \in \mathbb{S}$):

```
# Estimate causal forest
start_time_2 <- Sys.time() #Recording the running time

#Fitting the model
cf2.no_z <- grf::causal_forest(X, y_2, w_2)


end_time_2 <- Sys.time()

#Predicted values

pred_tau_2.no_z <-predict(cf2.no_z, estimate.variance = TRUE)

plot_pred_tau_2 <- ggplot(data = as.data.frame(pred_tau_2.no_z$predictions),
       aes(x = (pred_tau_2.no_z$predictions))) +
  geom_histogram(fill="#f68060", alpha=.6,binwidth = 0.1) +
  labs(title ="Simulation 2 without Z",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()

plot_pred_tau_2
```

Runing time:

```
start_time_2 - end_time_2
```

```
## Time difference of -38.83714 secs
```

RMSE:

```
rmse_2.no_z <- fun.rmse(predicted = pred_tau_2.no_z$predictions, true = tau)

rmse_2.no_z
```

```
## [1] 0.6930577
```

Coverage:

```
coverage_2.no_z <- fun.coverage(pred_tau_2.no_z, tau)

coverage_2.no_z
```

```
## [1] 0.9842
```

Estimated ATE:

```r
ATE_est_2.no_z <- average_treatment_effect(cf2.no_z)

ATE_est_2.no_z
```

```
##  estimate   std.err
## 9.9265084 0.2053532
```

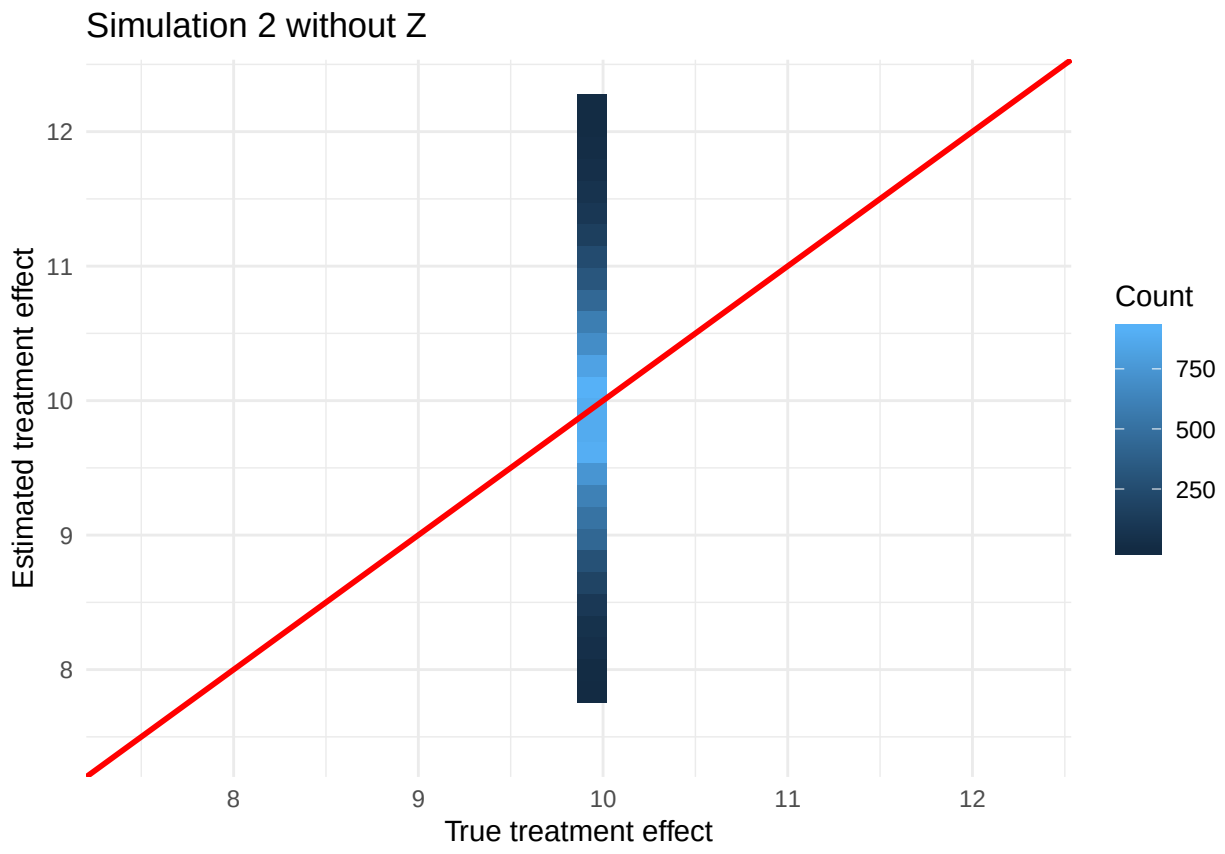
The *proportional difference in the ATE estimates* for the whole population:

```r
fun.diff_ATE(ATE_est = ATE_est_2.no_z, ATE_true = tau)
```

```
## [1] "Proportional mean of the differences:"
##    estimate
## 0.007349159
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##    estimate    estimate
## -0.01318616  0.02788447
```

```r
true_vs_pred_2.no_z <- as.data.frame(cbind(tau, pred_tau_2.no_z$predictions))

colnames(true_vs_pred_2.no_z) <- c("tau", "pred_tau")

true_vs_pred_2.no_z$tau <- true_vs_pred_2.no_z$tau + rnorm(n, 0 , sd = 0.0001)

plot2 <- ggplot(data = true_vs_pred_2.no_z, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 2 without Z",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_2.no_z$pred_tau), max(true_vs_pred_2.no_z$pred_tau)),
       y = c(min(true_vs_pred_2.no_z$pred_tau), max(true_vs_pred_2.no_z$pred_tau)))

plot2
```

```
## Warning: Removed 1 rows containing missing values (geom_tile).
```



$X \cup Z \in \mathbb{S}$s.

```
# Estimate causal forest
start_time_3 <- Sys.time() #Recording the running time

#Fitting the model
cf2.with_z <- grf::causal_forest(cbind(X, Z), y_2, w_2, orthog.boosting = FALSE)


end_time_3 <- Sys.time()

#Predicted values

pred_tau_2.with_z <-predict(cf2.with_z, estimate.variance = TRUE)

plot_pred_tau_3 <- ggplot(data = as.data.frame(pred_tau_2.with_z$predictions),
       aes(x = (pred_tau_2.with_z$predictions))) +
  geom_histogram(fill="#f68060", alpha=.6, binwidth = 0.1) +
  labs(title ="Simulation 2 with Z",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()

plot_pred_tau_3
```

Runing time:

```
start_time_3 - end_time_3
```

```
## Time difference of -36.1214 secs
```

RMSE:

```
rmse_2.with_z <- fun.rmse(predicted = pred_tau_2.with_z$predictions, true = tau)

rmse_2.with_z
```

```
## [1] 0.6742028
```

Coverage:

```
coverage_2.with_z <- fun.coverage(pred_tau_2.with_z, tau)

coverage_2.with_z
```

```
## [1] 0.9877
```

Estimated ATE:

```r
ATE_est_2.with_z <- average_treatment_effect(cf2.with_z)

ATE_est_2.with_z
```

```
##  estimate   std.err
## 9.9278134 0.2096408
```

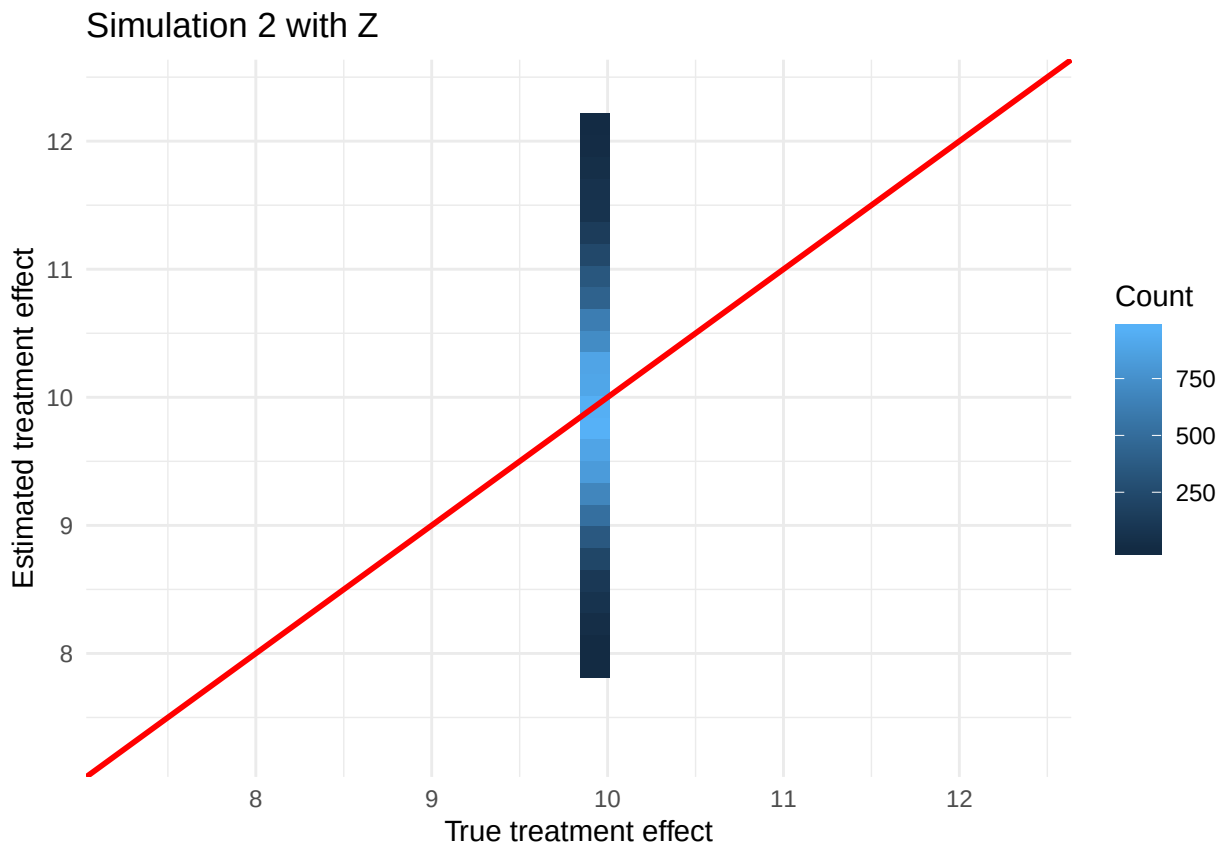
The *proportional difference in the ATE estimates* for the whole population:

```r
fun.diff_ATE(ATE_est = ATE_est_2.with_z, ATE_true = tau)
```

```
## [1] "Proportional mean of the differences:"
##    estimate
## 0.007218663
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##    estimate    estimate
## -0.01374542  0.02818274
```

```r
true_vs_pred_2.with_z <- as.data.frame(cbind(tau, pred_tau_2.with_z$predictions))

colnames(true_vs_pred_2.with_z) <- c("tau", "pred_tau")

true_vs_pred_2.with_z$tau <- true_vs_pred_2.with_z$tau + rnorm(n, 0 , sd = 0.0001)

plot3 <- ggplot(data = true_vs_pred_2.with_z, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 2 with Z",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_2.with_z$pred_tau),
             max(true_vs_pred_2.with_z$pred_tau)),
       y = c(min(true_vs_pred_2.with_z$pred_tau),
             max(true_vs_pred_2.with_z$pred_tau)))

plot3
```

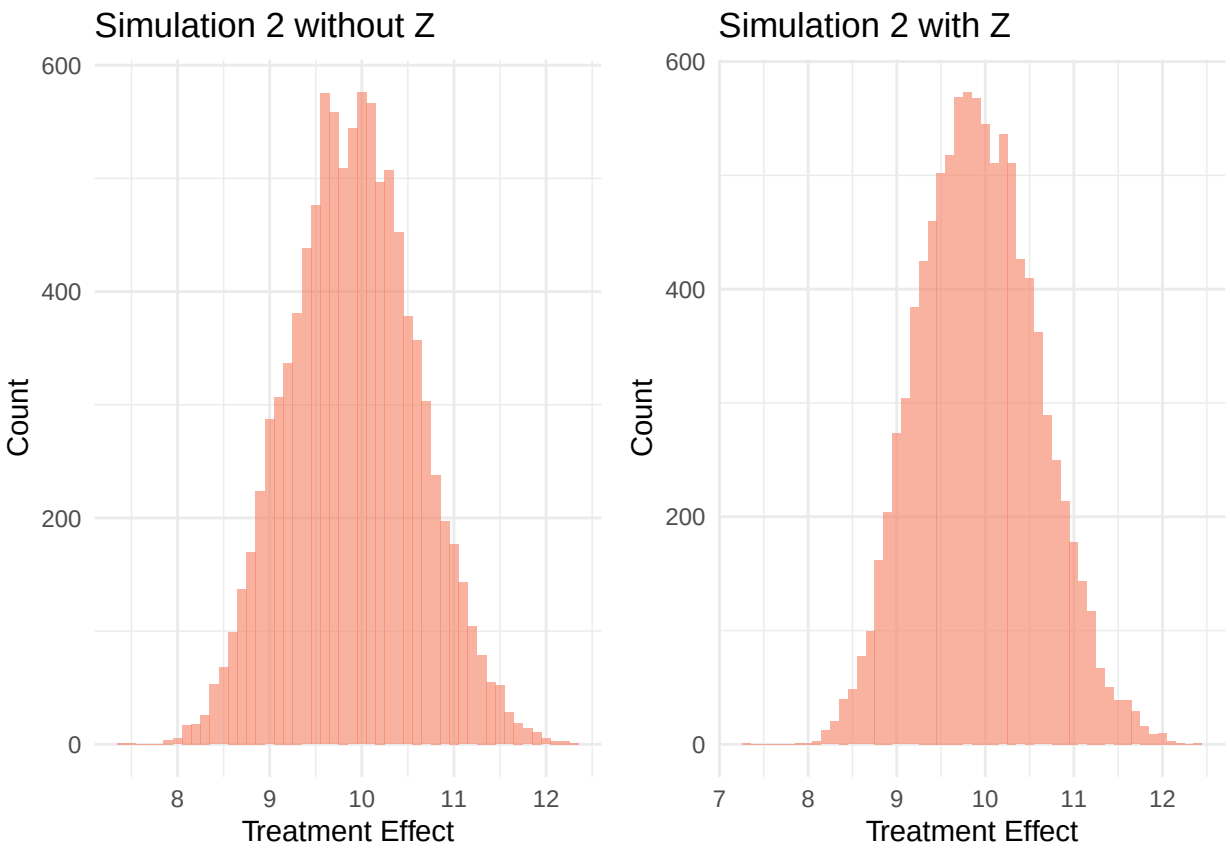
```
## Warning: Removed 1 rows containing missing values (geom_tile).
```



Summary

Predicted $\hat{\tau}s$:

```
grid.arrange(plot_pred_tau_2, plot_pred_tau_3, nrow = 1)
```

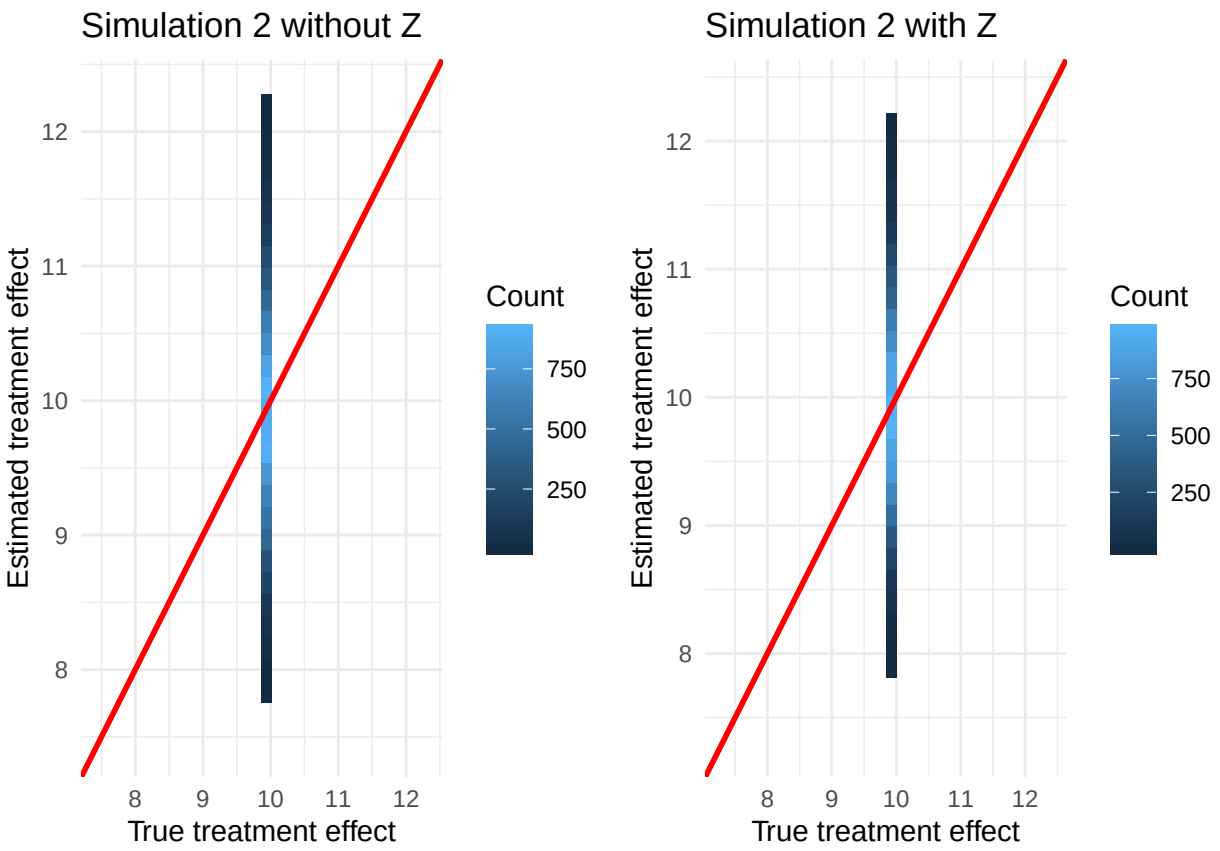


True τ vs. predicted $\hat{\tau}$:

```
grid.arrange(plot2, plot3, nrow = 1)
```

```
## Warning: Removed 1 rows containing missing values (geom_tile).
```

```
## Warning: Removed 1 rows containing missing values (geom_tile).
```



RMSEs:

```
rmse_2 <- as.data.frame(c(rmse_2.no_z, rmse_2.with_z))

rownames(rmse_2) <- c("Without $Z$", "With $Z$")

colnames(rmse_2) <- c("RMSE")

knitr::kable(rmse_2, escape = FALSE)
```

	RMSE
Without Z	0.6930577
With Z	0.6742028

Coverages:

```
coverage_2 <- as.data.frame(c(coverage_2.no_z, coverage_2.with_z))

rownames(coverage_2) <- c("Without $Z$", "With $Z$")

colnames(coverage_2) <- c("Coverage")

knitr::kable(coverage_2, escape = FALSE)
```

	Coverage
Without Z	0.9842
With Z	0.9877

LaTeX:

```
knitr::kable(rmse_2, format = "latex",escape = FALSE)
```

	RMSE
Without Z	0.6930577
With Z	0.6742028

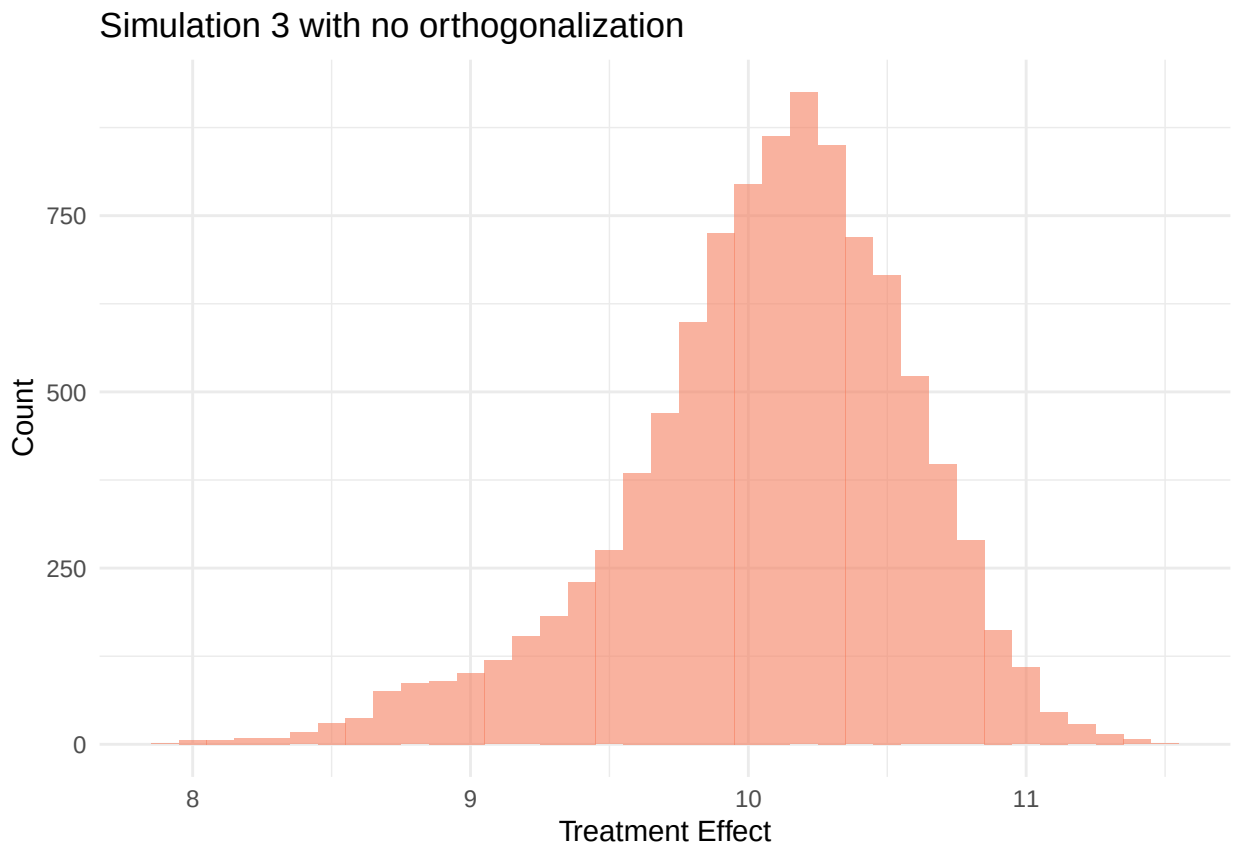
```
knitr::kable(coverage_2, format = "latex",escape = FALSE)
```

	Coverage
Without Z	0.9842
With Z	0.9877

3.3 Constant Treatment Effect with Confounded Assignment, Including Covariates Affecting to Output

Let's do the first estimation with all the observed variables $X \cup Z \cup C \in \mathbb{S}$. orthogonalization is not used in the first test:

```
# Estimate causal forest
start_time_4 <- Sys.time() #Recording the running time

#Fitting the model
cf3.no_ort <- grf::causal_forest(cbind(X, Z, C), y_3, w_3, orthog.boosting = FALSE)


end_time_4 <- Sys.time()

#Predicted values

pred_tau_3.no_ort <-predict(cf3.no_ort, estimate.variance = TRUE)

plot_pred_tau_4 <- ggplot(data = as.data.frame(pred_tau_3.no_ort$predictions),
       aes(x = (pred_tau_3.no_ort$predictions))) +
  geom_histogram(fill="#f68060", alpha=.6, binwidth = 0.1) +
  labs(title ="Simulation 3 with no orthogonalization",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()

plot_pred_tau_4
```



Runing time:

```
start_time_4 - end_time_4
```

```
## Time difference of -1.07855 mins
```

RMSE:

```
rmse_3.no_ort <- fun.rmse(predicted = pred_tau_3.no_ort$predictions, true = tau)

rmse_3.no_ort
```

```
## [1] 0.5160037
```

Coverage:

```
coverage_3.no_ort <- fun.coverage(pred_tau_3.no_ort, tau)

coverage_3.no_ort
```

```
## [1] 0.9976
```

Estimated ATE:

```r
ATE_est_3.no_ort <- average_treatment_effect(cf3.no_ort)

ATE_est_3.no_ort
```

```
##   estimate    std.err
## 10.0475465  0.2168458
```

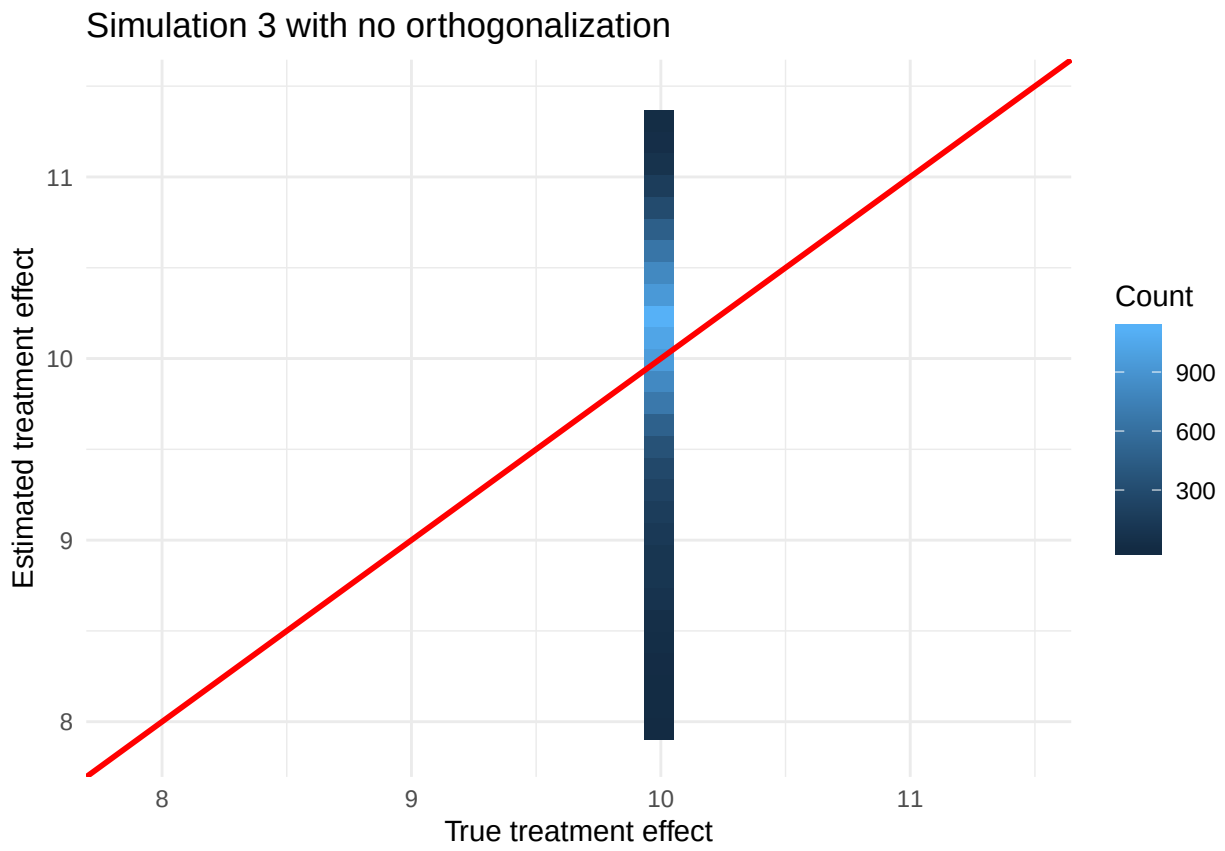
The *proportional difference in the ATE estimates* for the whole population:

```r
fun.diff_ATE(ATE_est = ATE_est_3.no_ort, ATE_true = tau)
```

```
## [1] "Proportional mean of the differences:"
##     estimate
## -0.004754651
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##    estimate    estimate
## -0.02643923  0.01692993
```

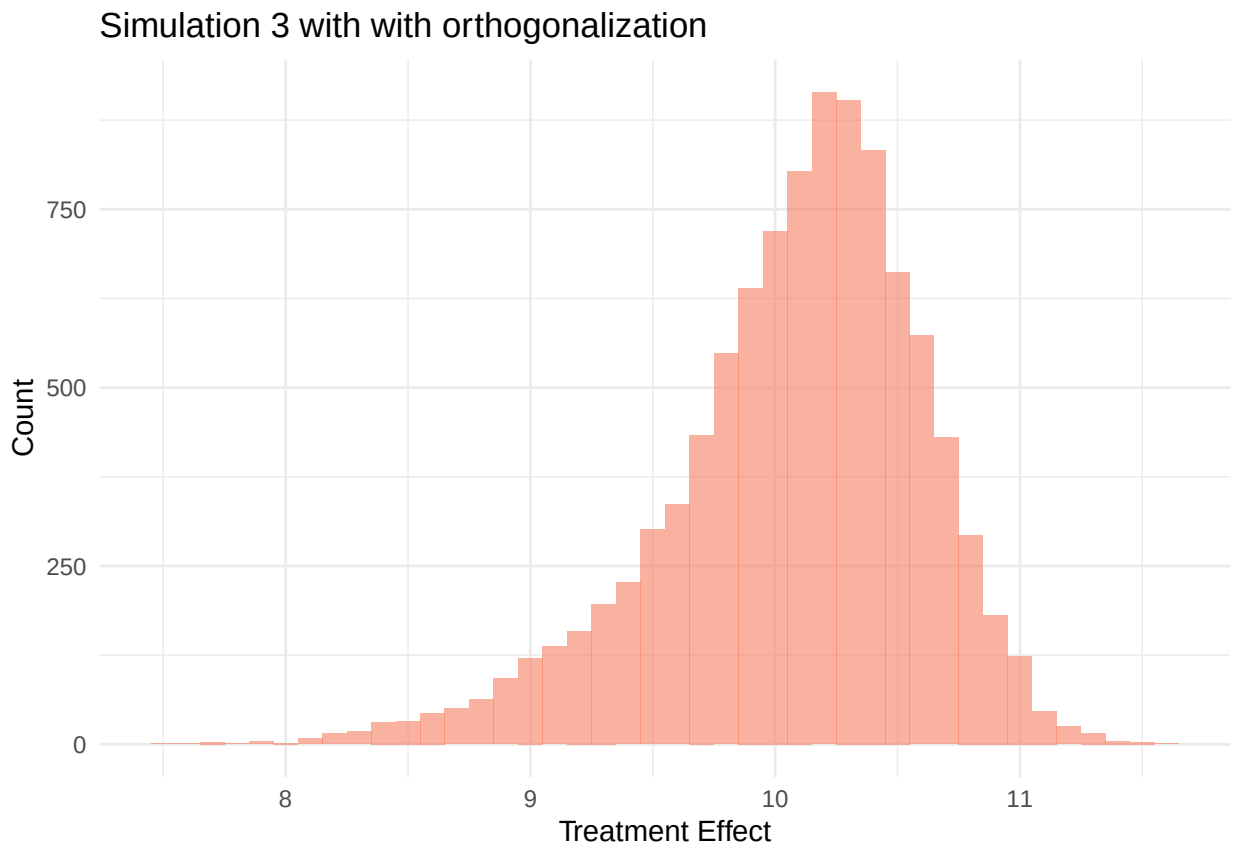
```r
true_vs_pred_3.no_ort <- as.data.frame(cbind(tau, pred_tau_3.no_ort$predictions))

colnames(true_vs_pred_3.no_ort) <- c("tau", "pred_tau")

true_vs_pred_3.no_ort$tau <- true_vs_pred_3.no_ort$tau + rnorm(n, 0 , sd = 0.0001)

plot4 <- ggplot(data = true_vs_pred_3.no_ort, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 3 with no orthogonalization",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_3.no_ort$pred_tau), max(true_vs_pred_3.no_ort$pred_tau)),
       y = c(min(true_vs_pred_3.no_ort$pred_tau), max(true_vs_pred_3.no_ort$pred_tau)))

plot4
```

```
## Warning: Removed 1 rows containing missing values (geom_tile).
```



$X \cup Z \cup C \in \mathbb{S}$. Orthogonalizarion is used in the second test:

```
# Estimate causal forest
start_time_5 <- Sys.time() #Recording the running time

#Fitting the model
cf3.with_ort <- grf::causal_forest(cbind(X, Z, C), y_3, w_3, orthog.boosting = TRUE)


end_time_5 <- Sys.time()

#Predicted values

pred_tau_3.with_ort <-predict(cf3.with_ort, estimate.variance = TRUE)

plot_pred_tau_5 <- ggplot(data = as.data.frame(pred_tau_3.with_ort$predictions)
                          , aes(x = (pred_tau_3.with_ort$predictions))) +
  geom_histogram(fill="#f68060", alpha=.6, binwidth = 0.1) +
  labs(title ="Simulation 3 with with orthogonalization",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()

plot_pred_tau_5
```



Runing time:

```
start_time_5 - end_time_5
```

```
## Time difference of -1.204727 mins
```

RMSE:

```
rmse_3.with_ort <- fun.rmse(predicted = pred_tau_3.with_ort$predictions, true = tau)

rmse_3.with_ort
```

```
## [1] 0.534276
```

Coverage:

```
coverage_3.with_ort <- fun.coverage(pred_tau_3.with_ort, tau)

coverage_3.with_ort
```

```
## [1] 0.9966
```

Estimated ATE:

```
ATE_est_3.with_ort <- average_treatment_effect(cf3.with_ort)

ATE_est_3.with_ort
```

```
##   estimate    std.err
## 10.0927628  0.2105682
```

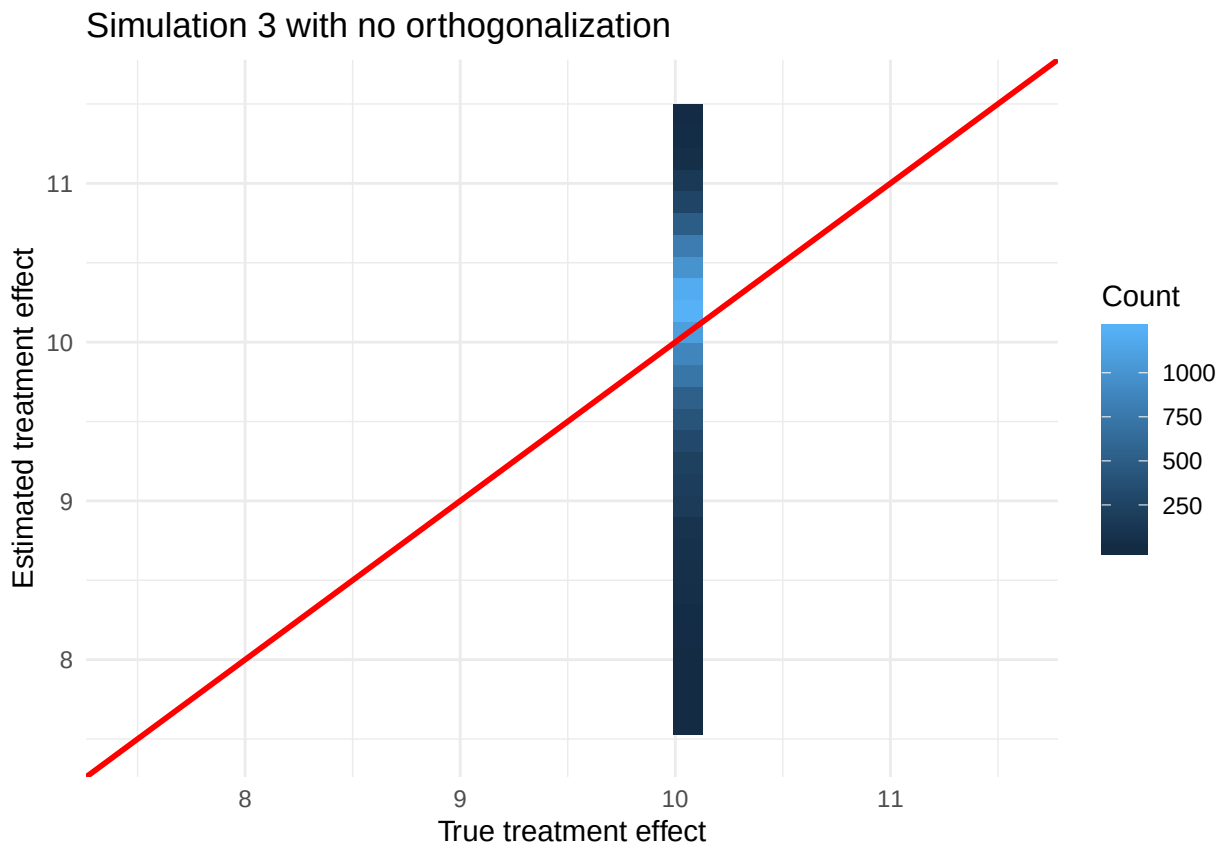
The *proportional difference in the ATE estimates* for the whole population:

```
fun.diff_ATE(ATE_est = ATE_est_3.with_ort, ATE_true = tau)
```

```
## [1] "Proportional mean of the differences:"
##     estimate
## -0.009276278
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##    estimate    estimate
## -0.03033310  0.01178054
```

```
true_vs_pred_3.with_ort <- as.data.frame(cbind(tau, pred_tau_3.with_ort$predictions))

colnames(true_vs_pred_3.with_ort) <- c("tau", "pred_tau")

true_vs_pred_3.with_ort$tau <- true_vs_pred_3.with_ort$tau + rnorm(n, 0 , sd = 0.0001)

plot5 <- ggplot(data = true_vs_pred_3.with_ort, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 3 with no orthogonalization",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_3.with_ort$pred_tau), max(true_vs_pred_3.with_ort$pred_tau)),
       y = c(min(true_vs_pred_3.with_ort$pred_tau), max(true_vs_pred_3.with_ort$pred_tau)))

plot5
```

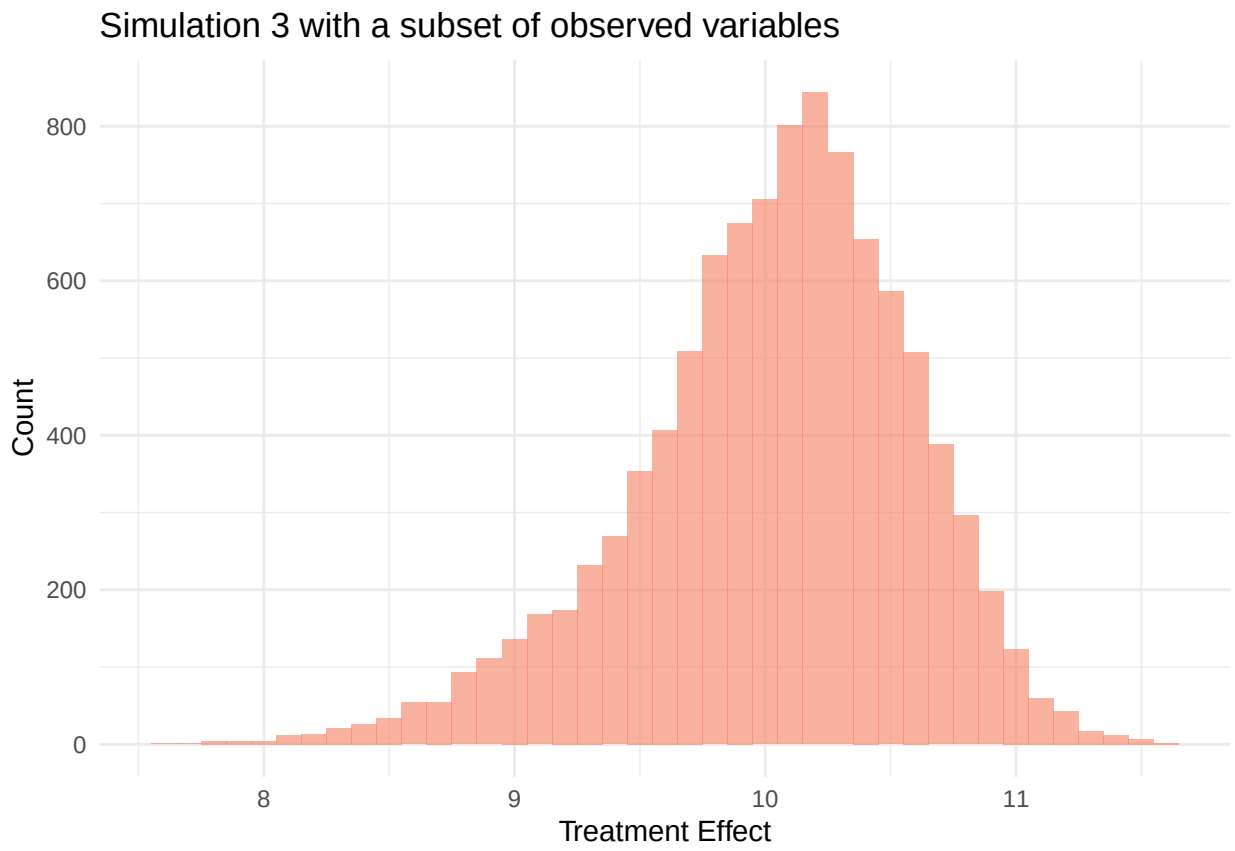
```
## Warning: Removed 1 rows containing missing values (geom_tile).
```



As the third test, let's try to use only the most important variables (over the median):

```
important_var_3 <- which(variable_importance(cf3.with_ort) >= median(variable_importance(cf3.with_ort)))
```

```
# Estimate causal forest
start_time_6 <- Sys.time() #Recording the running time

#Fitting the model
cf3.important <- grf::causal_forest(cbind(X, Z, C)[, important_var_3], y_3, w_3, orthog.boosting = TRUE)


end_time_6 <- Sys.time()

#Predicted values

pred_tau_3.important <- predict(cf3.important, estimate.variance = TRUE)

plot_pred_tau_6 <- ggplot(data = as.data.frame(pred_tau_3.important$predictions),
       aes(x = (pred_tau_3.important$predictions))) +
  geom_histogram(fill="#f68060", alpha=.6, binwidth = 0.1) +
  labs(title ="Simulation 3 with a subset of observed variables",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()

plot_pred_tau_6
```



Runing time:

```
start_time_6 - end_time_6
```

```
## Time difference of -51.46338 secs
```

RMSE:

```
rmse_3.important <- fun.rmse(predicted = pred_tau_3.important$predictions, true = tau)

rmse_3.important
```

```
## [1] 0.5526428
```

Coverage:

```
coverage_3.important <- fun.coverage(pred_tau_3.important, tau)

coverage_3.important
```

```
## [1] 0.9972
```

Estimated ATE:

```r
ATE_est_3.important <- average_treatment_effect(cf3.important)

ATE_est_3.important
```

```
##   estimate    std.err
## 10.0280011  0.2138981
```

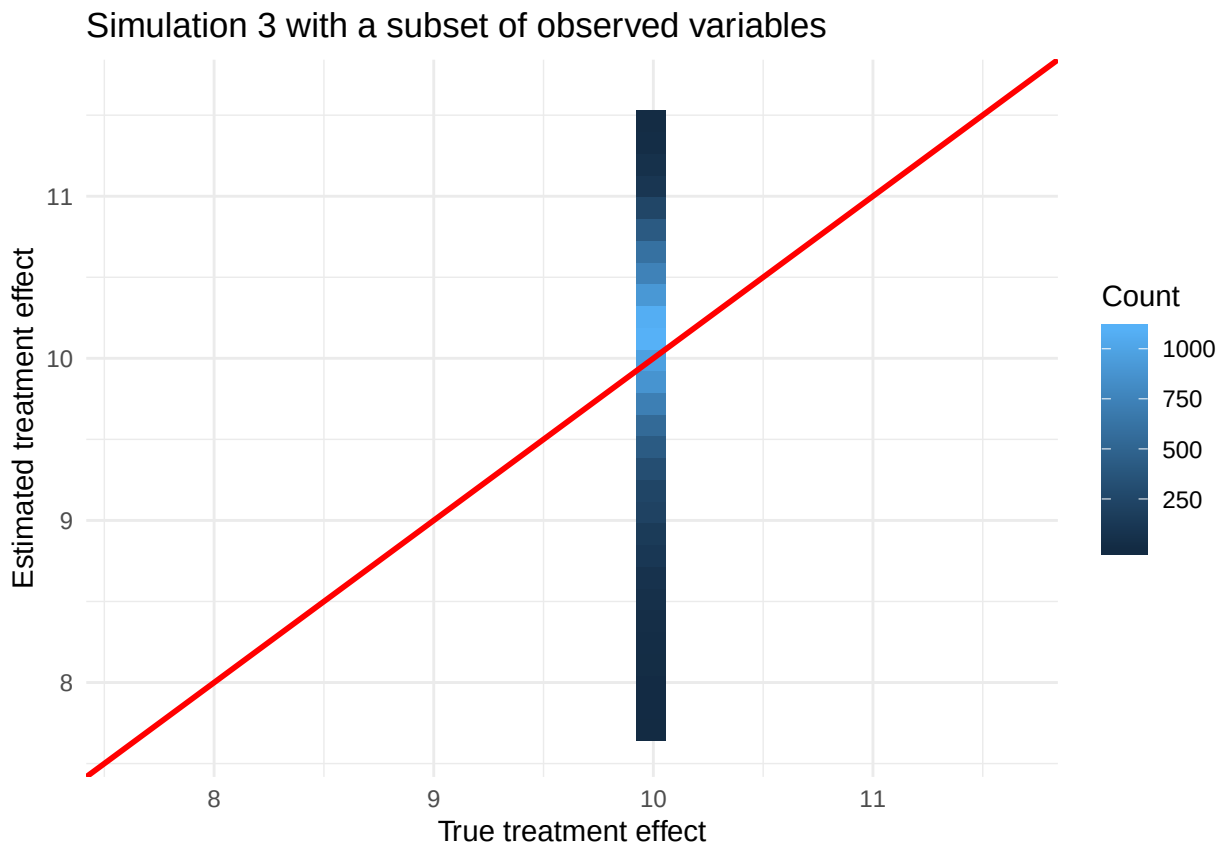
The *proportional difference in the ATE estimates* for the whole population:

```r
fun.diff_ATE(ATE_est = ATE_est_3.important, ATE_true = tau)
```

```
## [1] "Proportional mean of the differences:"
##     estimate
## -0.002800106
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##    estimate    estimate
## -0.02418992  0.01858971
```

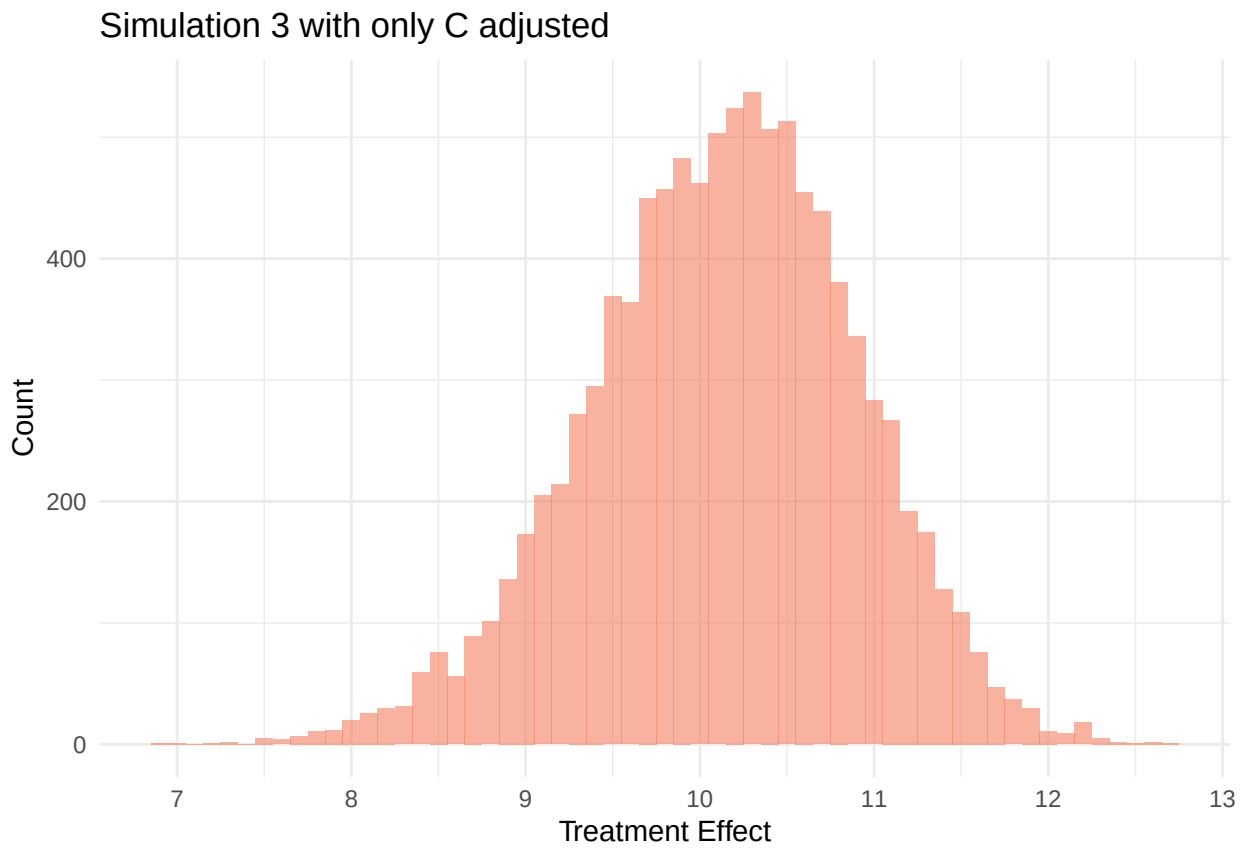
```r
true_vs_pred_3.important <- as.data.frame(cbind(tau, pred_tau_3.important$predictions))

colnames(true_vs_pred_3.important) <- c("tau", "pred_tau")

true_vs_pred_3.important$tau <- true_vs_pred_3.important$tau + rnorm(n, 0 , sd = 0.0001)

plot6 <- ggplot(data = true_vs_pred_3.important, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 3 with a subset of observed variables",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_3.important$pred_tau), max(true_vs_pred_3.important$pred_tau)),
       y = c(min(true_vs_pred_3.important$pred_tau), max(true_vs_pred_3.important$pred_tau)))

plot6
```

```
## Warning: Removed 1 rows containing missing values (geom_tile).
```



As the last test, let's test the backdoor criterion (adjusting only for $C \in \mathbb{S}$):

```
# Estimate causal forest
start_time_7 <- Sys.time() #Recording the running time

#Fitting the model
cf3.bd <- grf::causal_forest(C, y_3, w_3, orthog.boosting = TRUE)


end_time_7 <- Sys.time()

#Predicted values

pred_tau_3.bd <- predict(cf3.bd, estimate.variance = TRUE)

plot_pred_tau_7 <- ggplot(data = as.data.frame(pred_tau_3.bd$predictions),
       aes(x = (pred_tau_3.bd$predictions))) +
  geom_histogram(fill="#f68060", alpha=.6, binwidth = 0.1) +
  labs(title ="Simulation 3 with only C adjusted",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()

plot_pred_tau_7
```



Runing time:

```
start_time_7 - end_time_7
```

```
## Time difference of -39.08847 secs
```

RMSE:

```
rmse_3.bd <- fun.rmse(predicted = pred_tau_3.bd$predictions, true = tau)

rmse_3.bd
```

```
## [1] 0.7784988
```

Coverage:

```
coverage_3.bd <- fun.coverage(pred_tau_3.bd, tau)

coverage_3.bd
```

```
## [1] 0.9815
```

Estimated ATE:

```r
ATE_est_3.bd <- average_treatment_effect(cf3.bd)

ATE_est_3.bd
```

```
##   estimate    std.err
## 10.1332955  0.2297555
```

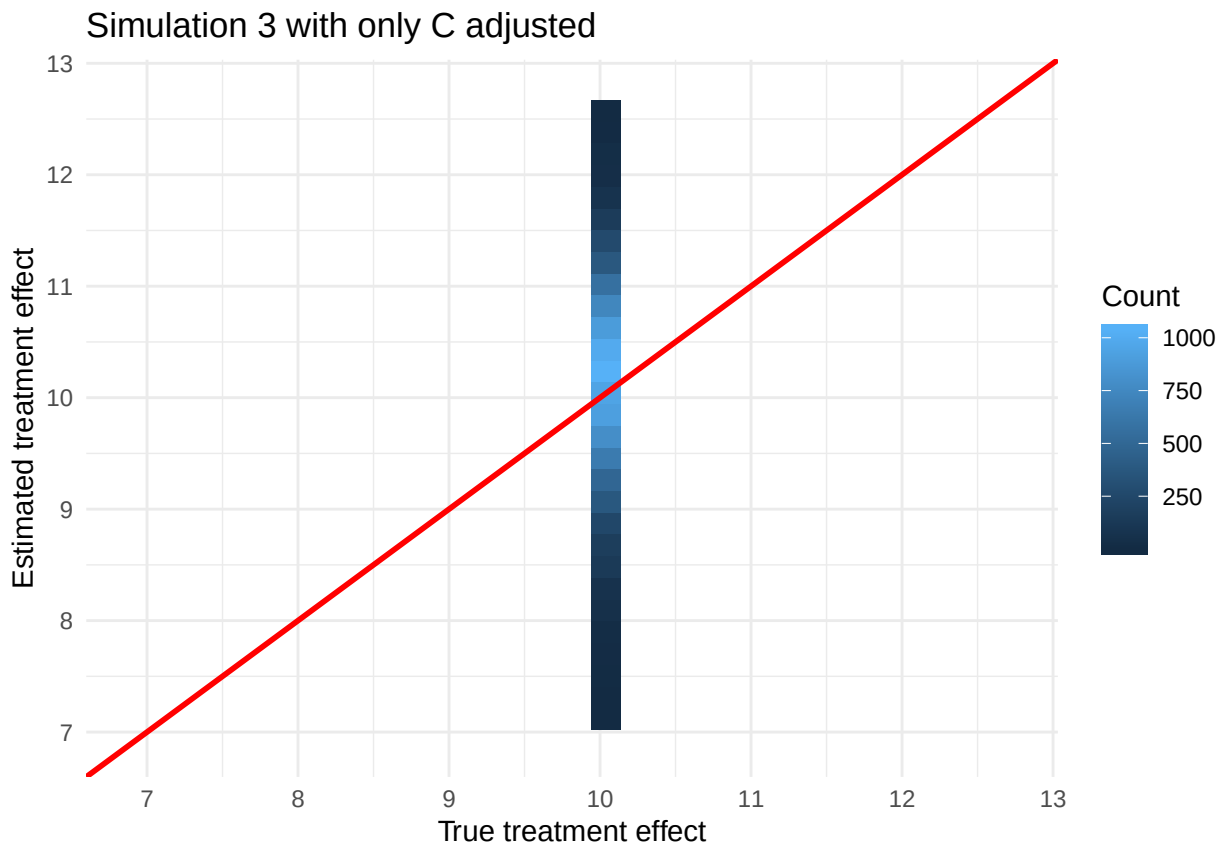
The *proportional difference in the ATE estimates* for the whole population:

```r
fun.diff_ATE(ATE_est = ATE_est_3.bd, ATE_true = tau)
```

```
## [1] "Proportional mean of the differences:"
##    estimate
## -0.01332955
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##     estimate     estimate
## -0.036305105  0.009646001
```

```r
true_vs_pred_3.bd <- as.data.frame(cbind(tau, pred_tau_3.bd$predictions))

colnames(true_vs_pred_3.bd) <- c("tau", "pred_tau")

true_vs_pred_3.bd$tau <- true_vs_pred_3.bd$tau + rnorm(n, 0 , sd = 0.0001)

plot7 <- ggplot(data = true_vs_pred_3.bd, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 3 with only C adjusted",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_3.bd$pred_tau), max(true_vs_pred_3.bd$pred_tau)),
       y = c(min(true_vs_pred_3.bd$pred_tau), max(true_vs_pred_3.bd$pred_tau)))

plot7
```

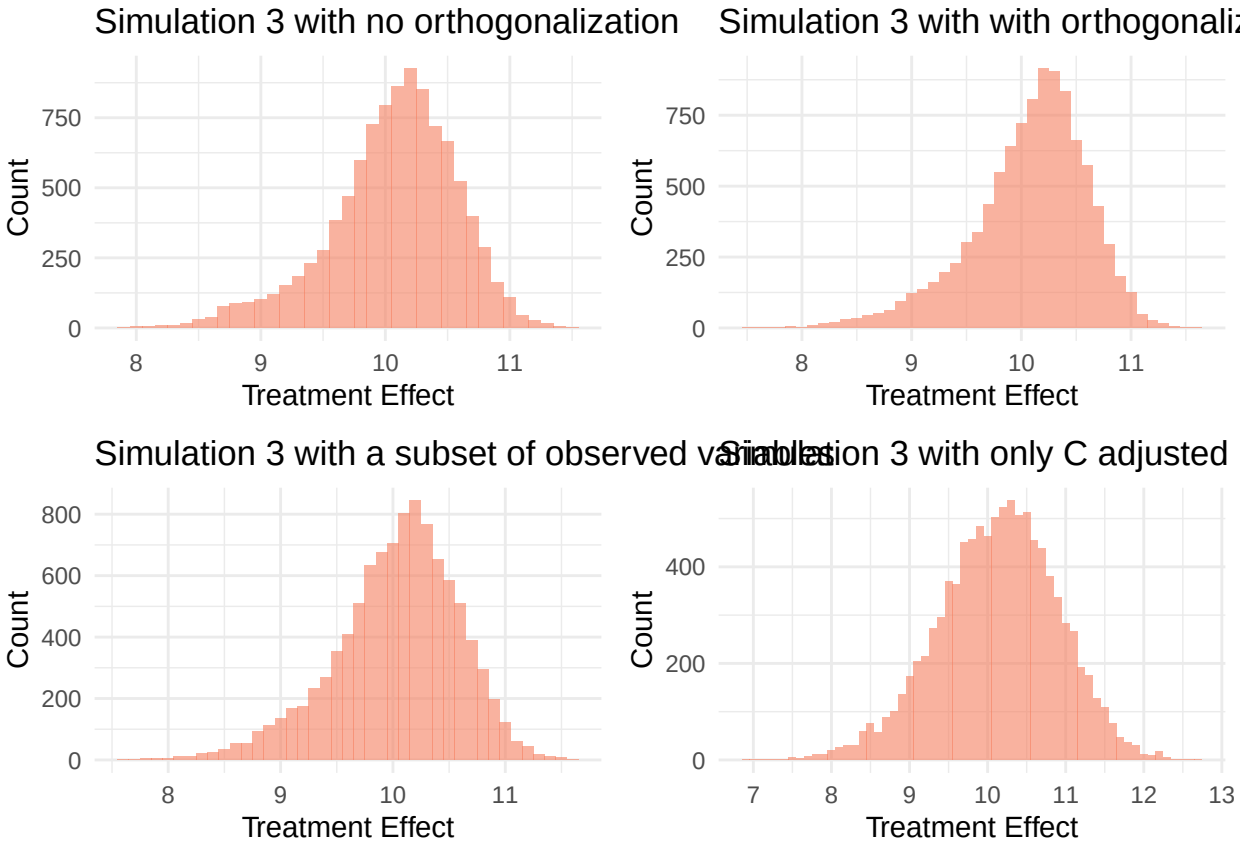
```
## Warning: Removed 1 rows containing missing values (geom_tile).
```



Summary

Predicted $\hat{\tau}s$:

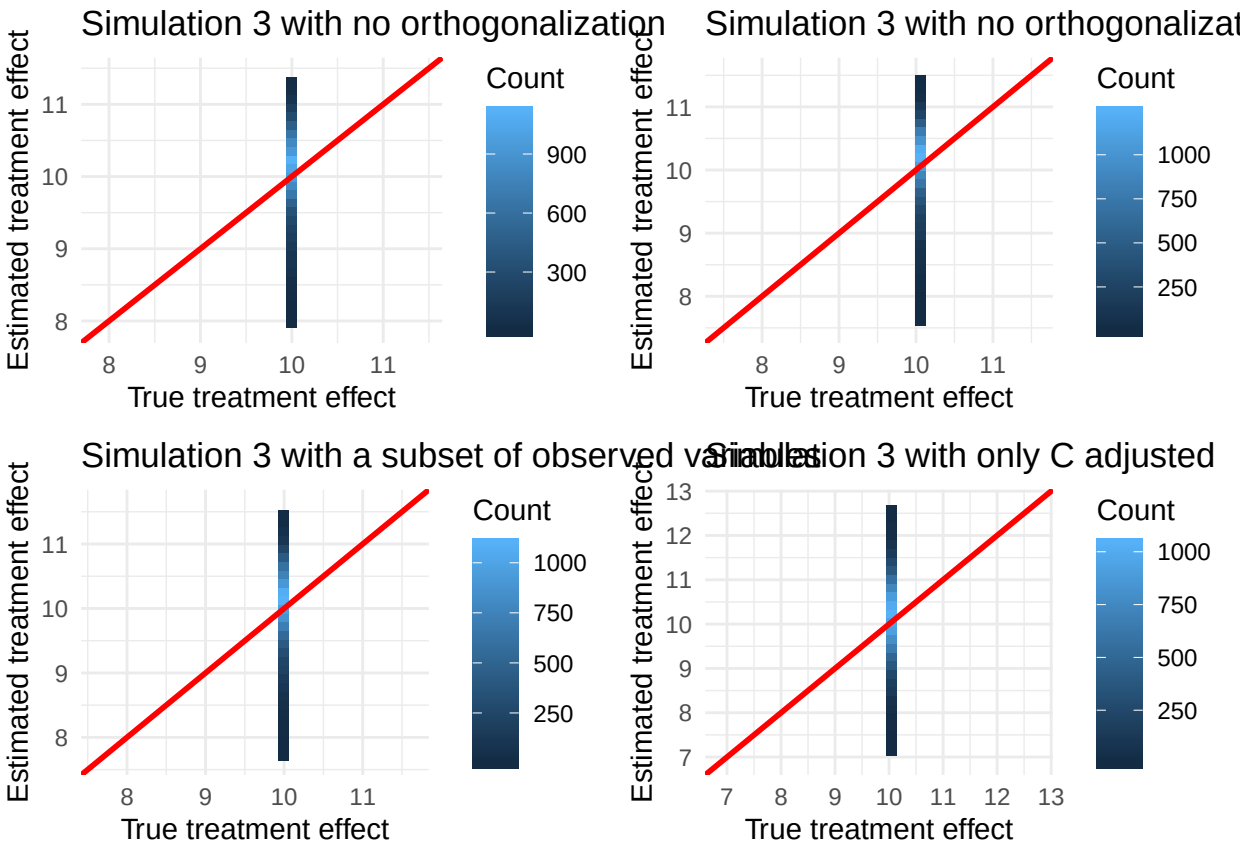
```
grid.arrange(plot_pred_tau_4, plot_pred_tau_5, plot_pred_tau_6, plot_pred_tau_7, nrow = 2)
```



True τ vs. predicted $\hat{\tau}$:

```
grid.arrange(plot4, plot5, plot6, plot7, nrow = 2)
```

```
## Warning: Removed 1 rows containing missing values (geom_tile).

## Warning: Removed 1 rows containing missing values (geom_tile).

## Warning: Removed 1 rows containing missing values (geom_tile).

## Warning: Removed 1 rows containing missing values (geom_tile).
```



RMSEs:

```
rmse_3 <- as.data.frame(c(rmse_3.no_ort, rmse_3.with_ort, rmse_3.important, rmse_3.bd))

rownames(rmse_3) <- c("No orthogonalization", "With orthogonalization",
                      "Subset of observed variables", "Only confounders adjusted")

colnames(rmse_3) <- c("RMSE")

knitr::kable(rmse_3, escape = FALSE)
```

	RMSE
No orthogonalization	0.5160037
With orthogonalization	0.5342760
Subset of observed variables	0.5526428
Only confounders adjusted	0.7784988

Coverages:

```
coverage_3 <- as.data.frame(c(coverage_3.no_ort, coverage_3.with_ort,
                              coverage_3.important, coverage_3.bd))

rownames(coverage_3) <- c("No orthogonalization", "With orthogonalization",
                      "Subset of observed variables", "Only confounders adjusted")
```

```r
colnames(coverage_3) <- c("Coverage")

knitr::kable(coverage_3, escape = FALSE)
```

	Coverage
No orthogonalization	0.9976
With orthogonalization	0.9966
Subset of observed variables	0.9972
Only confounders adjusted	0.9815

LaTeX:

```r
knitr::kable(rmse_3, format = "latex",escape = FALSE)
```

	RMSE
No orthogonalization	0.5160037
With orthogonalization	0.5342760
Subset of observed variables	0.5526428
Only confounders adjusted	0.7784988

```r
knitr::kable(coverage_3, format = "latex",escape = FALSE)
```

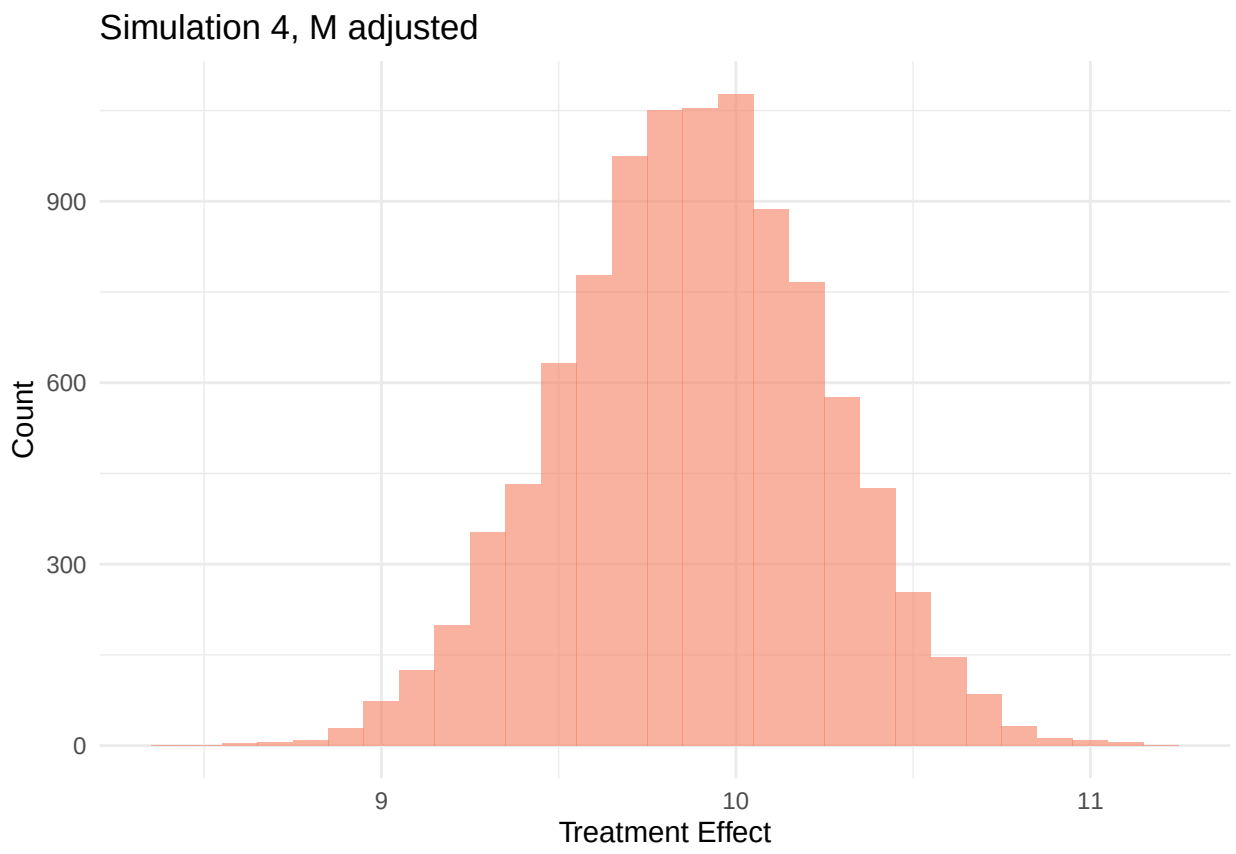
	Coverage
No orthogonalization	0.9976
With orthogonalization	0.9966
Subset of observed variables	0.9972
Only confounders adjusted	0.9815

3.4 Constant Treatment Effect with Confounded Assignment, Including Covariates Affecting to Output and a Pure Local M-Structure

Let's adjust the collider M (incorrectly) and then leave it out from the adjusted set $\mathbb{S}$ ($X \cup Z \cup C \cup M \in \mathbb{S}$).

```r
# Estimate causal forest
start_time_8 <- Sys.time() #Recording the running time

#Fitting the model
cf4.with_M <- grf::causal_forest(cbind(X, Z, C, m), y_4, w_4, orthog.boosting = TRUE)


end_time_8 <- Sys.time()

#Predicted values

pred_tau_4.with_M <- predict(cf4.with_M, estimate.variance = TRUE)

plot_pred_tau_8 <- ggplot(data = as.data.frame(pred_tau_4.with_M$predictions),
       aes(x = (pred_tau_4.with_M$predictions))) +
  geom_histogram(fill="#f68060", alpha=.6, binwidth = 0.1) +
```

```
  labs(title ="Simulation 4, M adjusted",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()

plot_pred_tau_8
```



Runing time:

```
start_time_8 - end_time_8
```

```
## Time difference of -1.218691 mins
```

RMSE:

```
rmse_4.with_M <- fun.rmse(predicted = pred_tau_4.with_M$predictions, true = tau)

rmse_4.with_M
```

```
## [1] 0.3844006
```

Coverage:

```r
coverage_4.with_M <- fun.coverage(pred_tau_4.with_M, tau)

coverage_4.with_M
```

```
## [1] 0.9998
```

Estimated ATE:

```r
ATE_est_4.with_M <- average_treatment_effect(cf4.with_M)

ATE_est_4.with_M
```

```
##  estimate   std.err
## 9.8655052 0.2150415
```

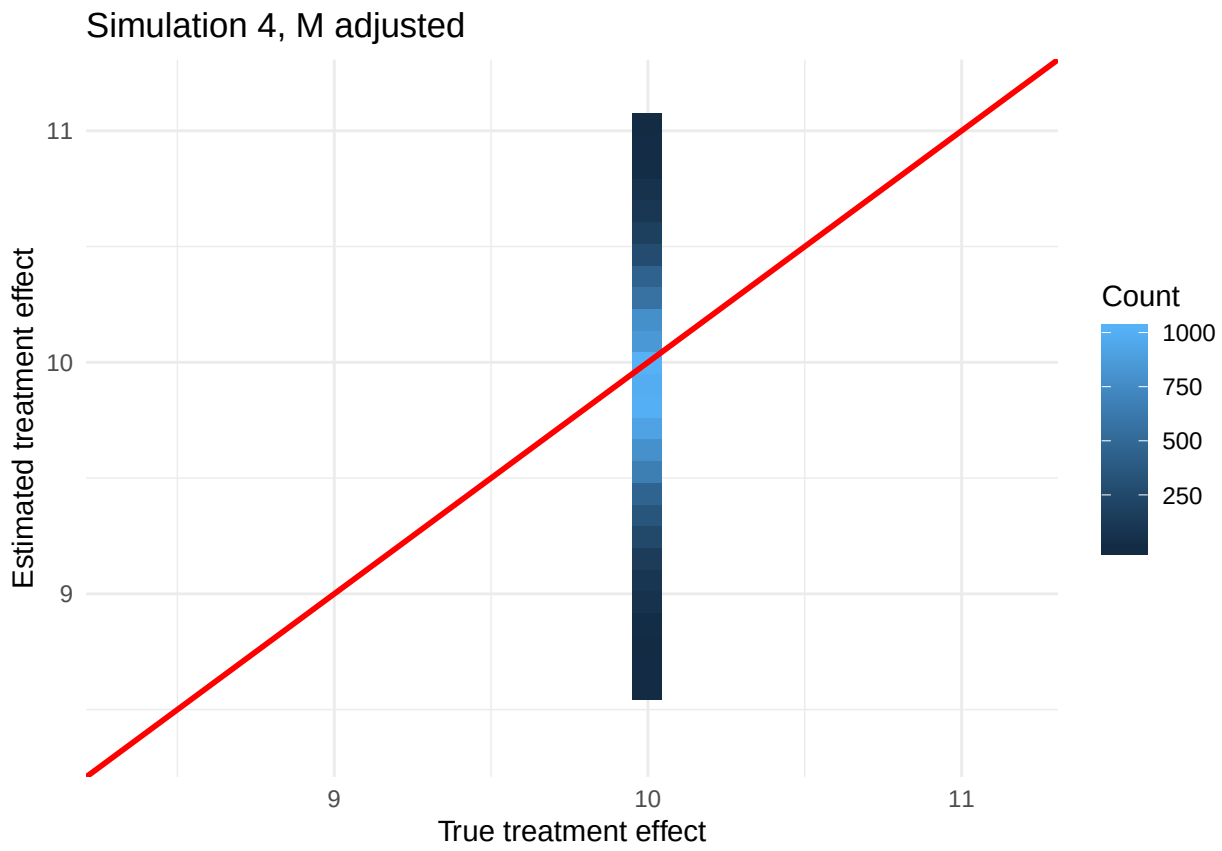
The *proportional difference in the ATE estimates* for the whole population:

```r
fun.diff_ATE(ATE_est = ATE_est_4.with_M, ATE_true = tau)
```

```
## [1] "Proportional mean of the differences:"
##   estimate
## 0.01344948
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##     estimate     estimate
## -0.008054669  0.034953622
```

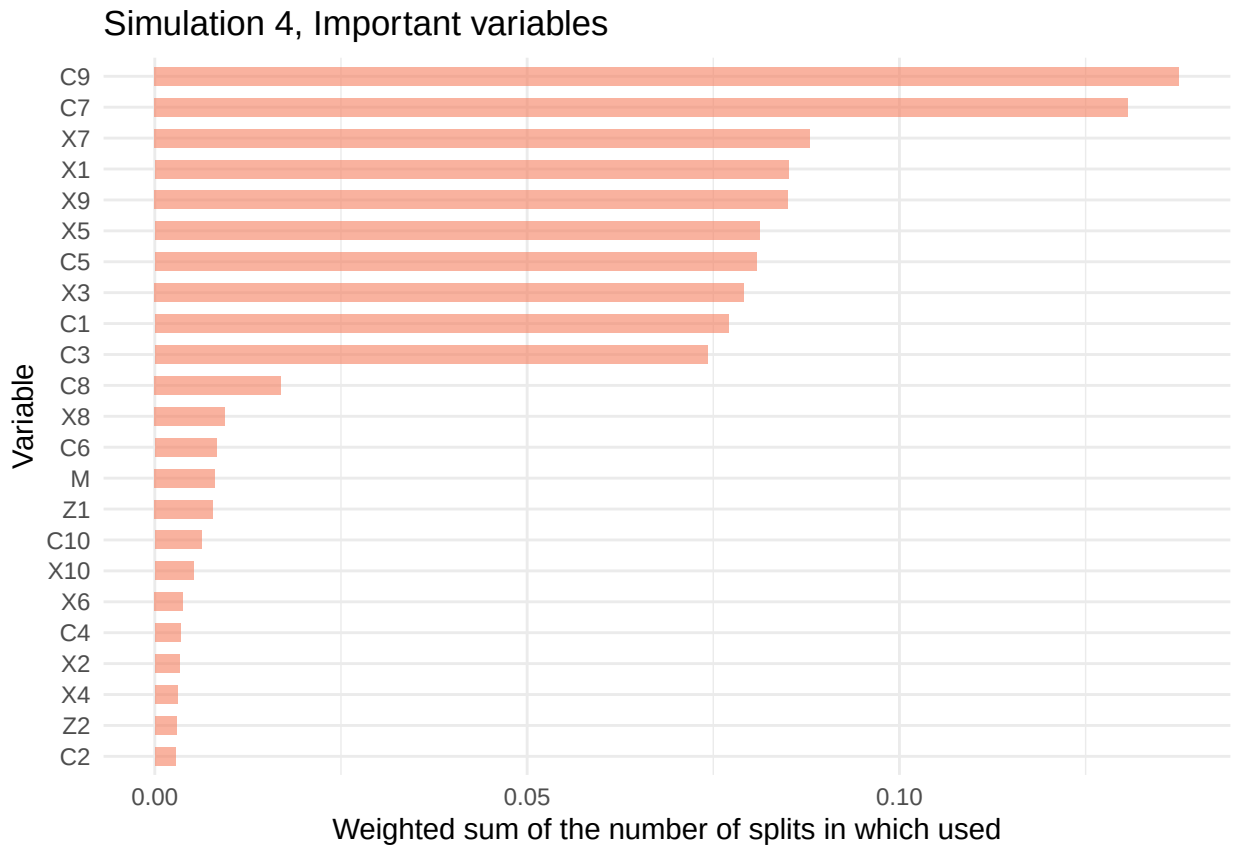
```r
true_vs_pred_4.with_M <- as.data.frame(cbind(tau, pred_tau_4.with_M$predictions))

colnames(true_vs_pred_4.with_M) <- c("tau", "pred_tau")

true_vs_pred_4.with_M$tau <- true_vs_pred_4.with_M$tau + rnorm(n, 0 , sd = 0.0001)

plot8 <- ggplot(data = true_vs_pred_4.with_M, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 4, M adjusted",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_4.with_M$pred_tau), max(true_vs_pred_4.with_M$pred_tau)),
       y = c(min(true_vs_pred_4.with_M$pred_tau), max(true_vs_pred_4.with_M$pred_tau)))

plot8
```

```
## Warning: Removed 1 rows containing missing values (geom_tile).
```



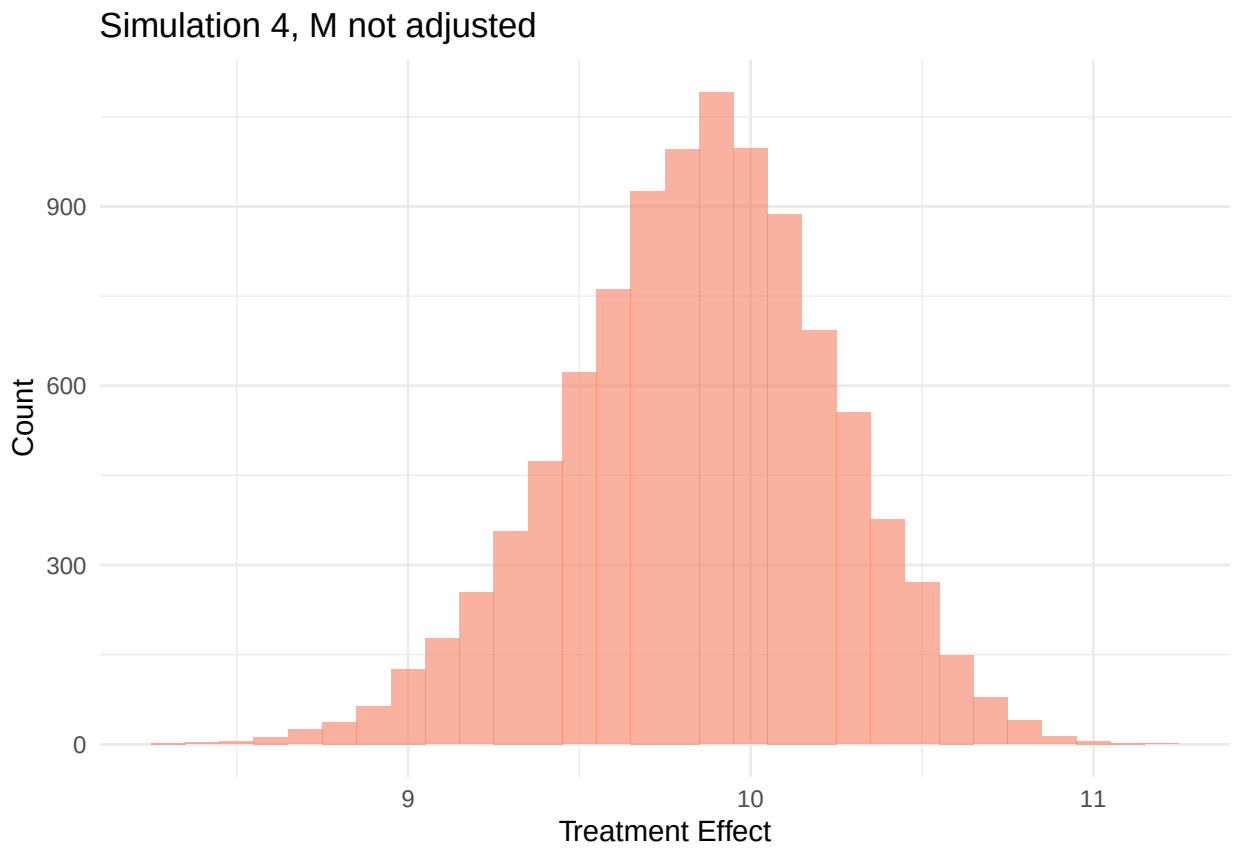
How "important" variable M was?

```
names4.with_M.X <- paste("X", 1:10, sep = "")

names4.with_M.Z <- paste("Z", 1:2, sep = "")

names4.with_M.C <- paste("C", 1:10, sep = "")

names4.with_M <- list(names4.with_M.X, names4.with_M.Z, names4.with_M.C, c("M"))

important_var_4.with_M <- as.data.frame(grf::variable_importance(cf4.with_M), row.names = Reduce(c, nam

important_var_4.with_M %>%
  mutate(name = fct_reorder(row.names(important_var_4.with_M), V1)) %>%
  ggplot(aes(x = name, y = V1)) +
  geom_bar(stat="identity", fill="#f68060", alpha=.6, width=.6) +
  coord_flip() +
  labs(title ="Simulation 4, Important variables", x = "Variable", y = "Weighted sum of the number of sp
  theme_minimal()
```



The following estimation is done by excluding the M from the ajusted set $\mathbb{S}$ ($X \cup Z \cup C \in \mathbb{S}$):

```
# Estimate causal forest
start_time_9 <- Sys.time() #Recording the running time

#Fitting the model
cf4.no_M <- grf::causal_forest(cbind(X, Z, C), y_4, w_4, orthog.boosting = TRUE)


end_time_9 <- Sys.time()

#Predicted values

pred_tau_4.no_M <- predict(cf4.no_M, estimate.variance = TRUE)

plot_pred_tau_9 <- ggplot(data = as.data.frame(pred_tau_4.no_M$predictions),
                          aes(x = (pred_tau_4.no_M$predictions))) +
  geom_histogram(binwidth = 0.1, fill="#f68060", alpha=.6) +
  labs(title ="Simulation 4, M not adjusted",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()

plot_pred_tau_9
```



Runing time:

```
start_time_9 - end_time_9
```

```
## Time difference of -1.202667 mins
```

RMSE:

```
rmse_4.no_M <- fun.rmse(predicted = pred_tau_4.no_M$predictions, true = tau)

rmse_4.no_M
```

```
## [1] 0.4186501
```

Coverage:

```
coverage_4.no_M <- fun.coverage(pred_tau_4.no_M, tau)

coverage_4.no_M
```

```
## [1] 0.9994
```

Estimated ATE:

```r
ATE_est_4.no_M <- average_treatment_effect(cf4.no_M)

ATE_est_4.no_M
```

```
##  estimate   std.err
## 9.8462622 0.2171587
```

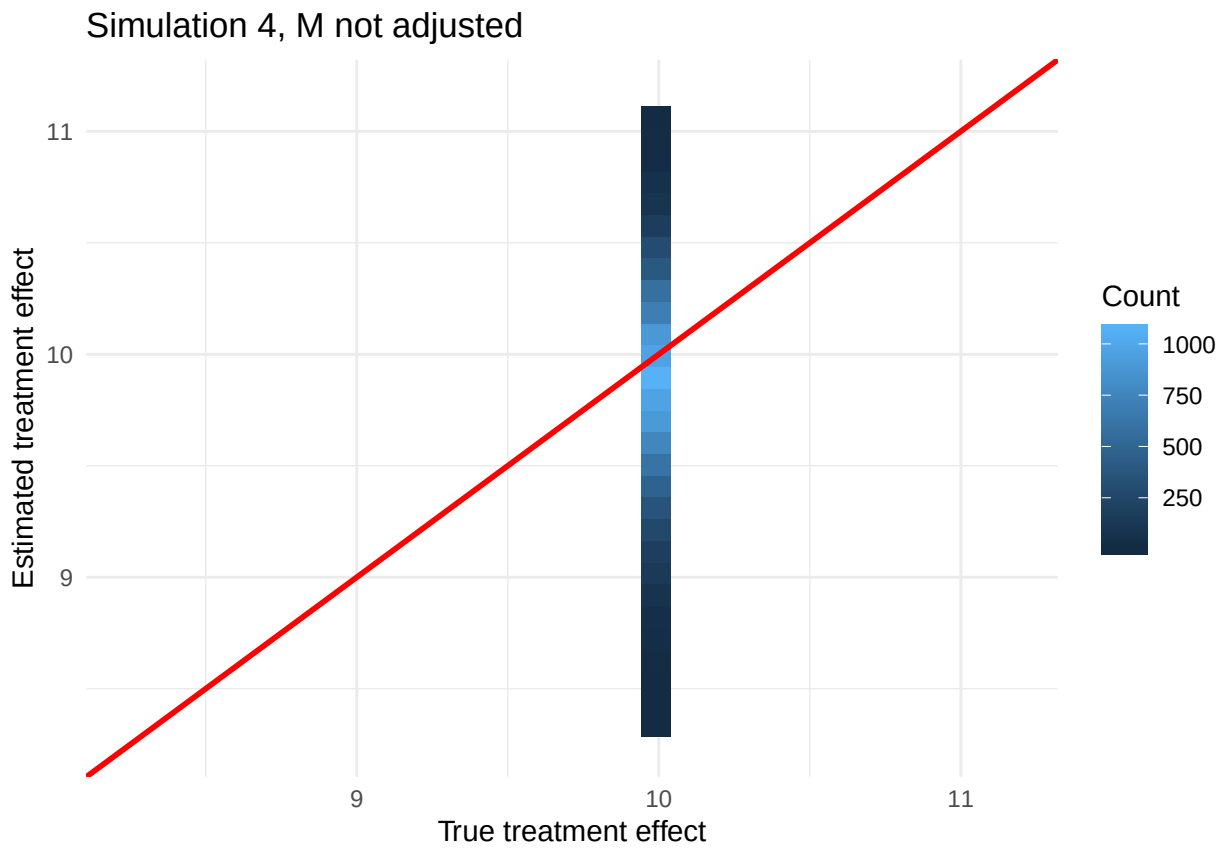
The *proportional difference in the ATE estimates* for the whole population:

```r
fun.diff_ATE(ATE_est = ATE_est_4.no_M, ATE_true = tau)
```

```
## [1] "Proportional mean of the differences:"
##   estimate
## 0.01537378
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##     estimate     estimate
## -0.006342088  0.037089648
```

```r
true_vs_pred_4.no_M <- as.data.frame(cbind(tau, pred_tau_4.no_M$predictions))

colnames(true_vs_pred_4.no_M) <- c("tau", "pred_tau")

true_vs_pred_4.no_M$tau <- true_vs_pred_4.no_M$tau + rnorm(n, 0 , sd = 0.0001)

plot9 <- ggplot(data = true_vs_pred_4.no_M, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 4, M not adjusted",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_4.no_M$pred_tau), max(true_vs_pred_4.no_M$pred_tau)),
       y = c(min(true_vs_pred_4.no_M$pred_tau), max(true_vs_pred_4.no_M$pred_tau)))

plot9
```

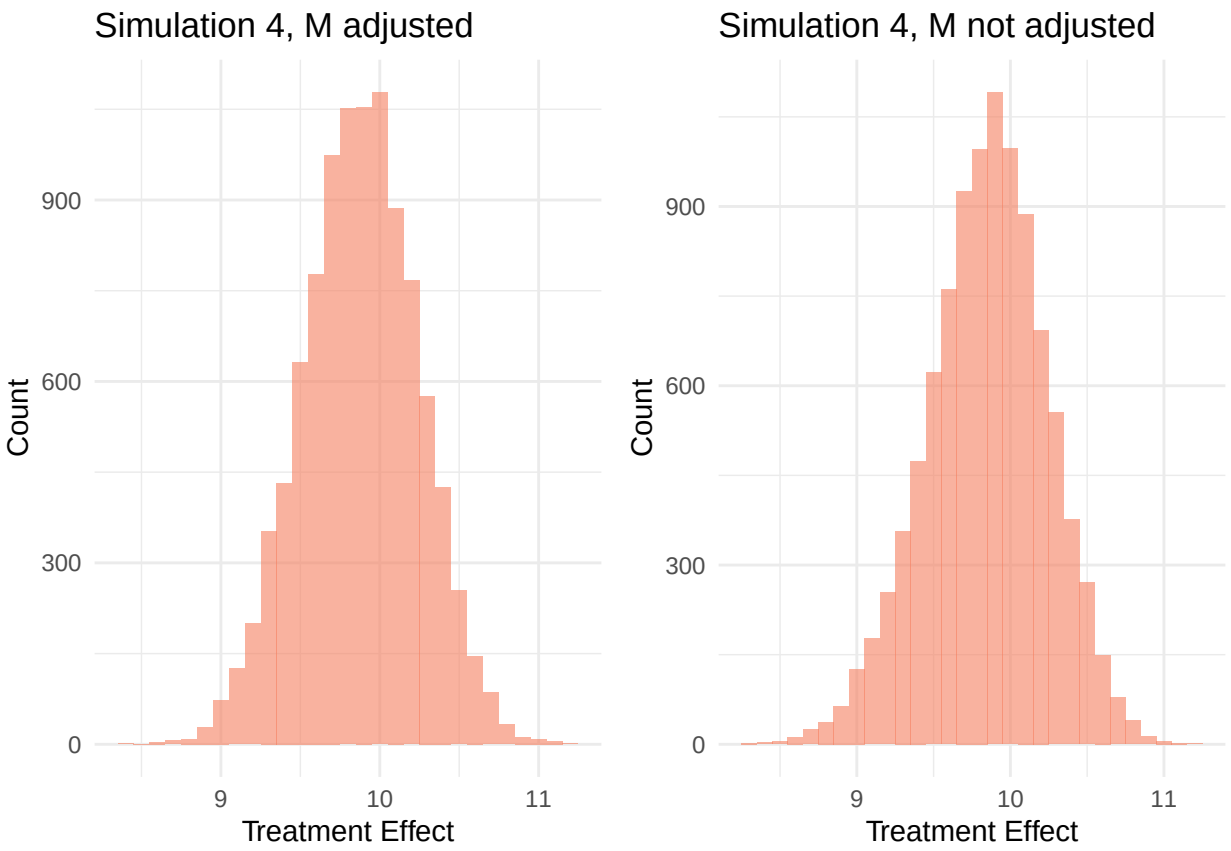
```
## Warning: Removed 1 rows containing missing values (geom_tile).
```



Summary

Predicted $\hat{\tau}s$:

```
grid.arrange(plot_pred_tau_8, plot_pred_tau_9, nrow = 1)
```

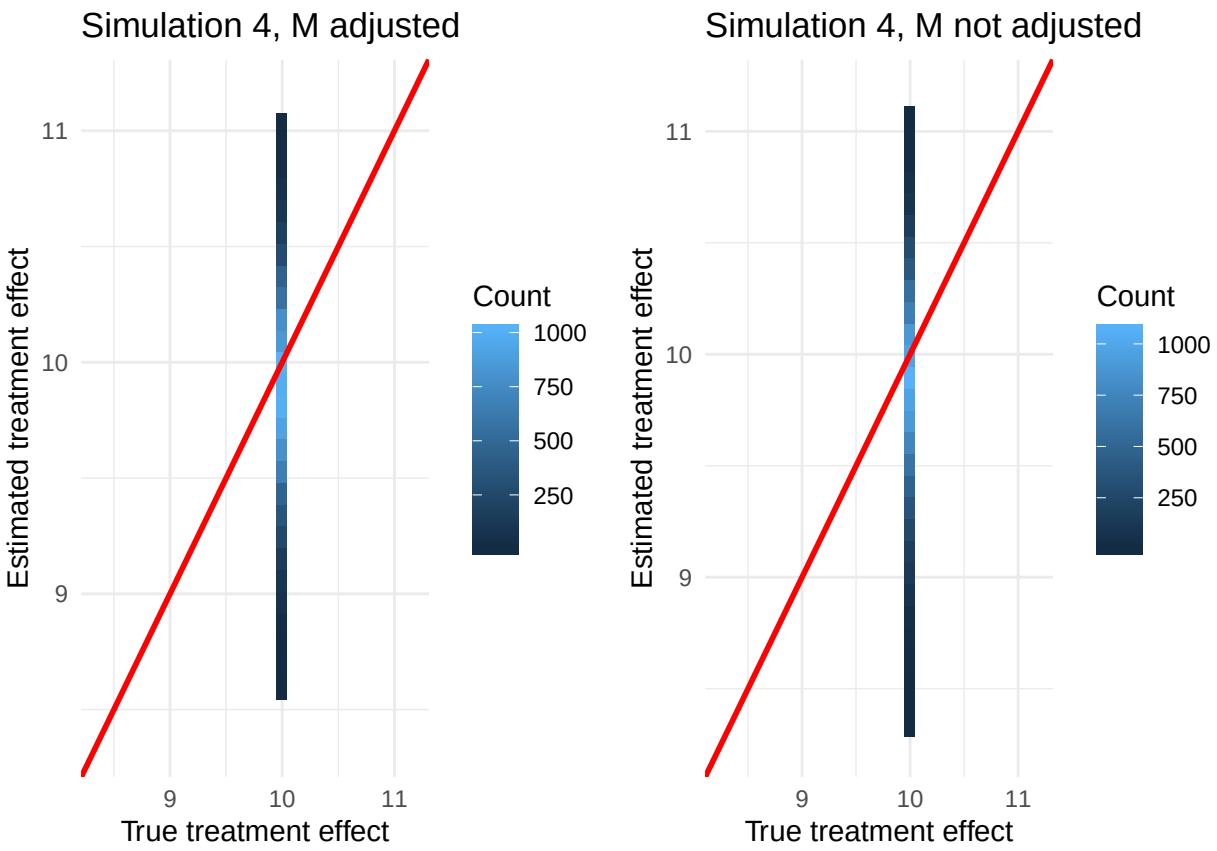


True τ vs. predicted $\hat{\tau}$:

```
grid.arrange(plot8, plot9, nrow = 1)
```

```
## Warning: Removed 1 rows containing missing values (geom_tile).
```

```
## Warning: Removed 1 rows containing missing values (geom_tile).
```



RMSEs:

```
rmse_4 <- as.data.frame(c(rmse_4.with_M, rmse_4.no_M))

rownames(rmse_4) <- c("$M$ adjusted", "$M$ not adjusted")

colnames(rmse_4) <- c("RMSE")

knitr::kable(rmse_4, escape = FALSE)
```

	RMSE
M adjusted	0.3844006
M not adjusted	0.4186501

Coverages:

```
coverage_4 <- as.data.frame(c(coverage_4.with_M, coverage_4.no_M))

rownames(coverage_4) <-  c("$M$ adjusted", "$M$ not adjusted")

colnames(coverage_4) <- c("Coverage")

knitr::kable(coverage_4, escape = FALSE)
```

	Coverage
M adjusted	0.9998
M not adjusted	0.9994

LaTeX:

```
knitr::kable(rmse_4, format = "latex",escape = FALSE)
```

	RMSE
M adjusted	0.3844006
M not adjusted	0.4186501

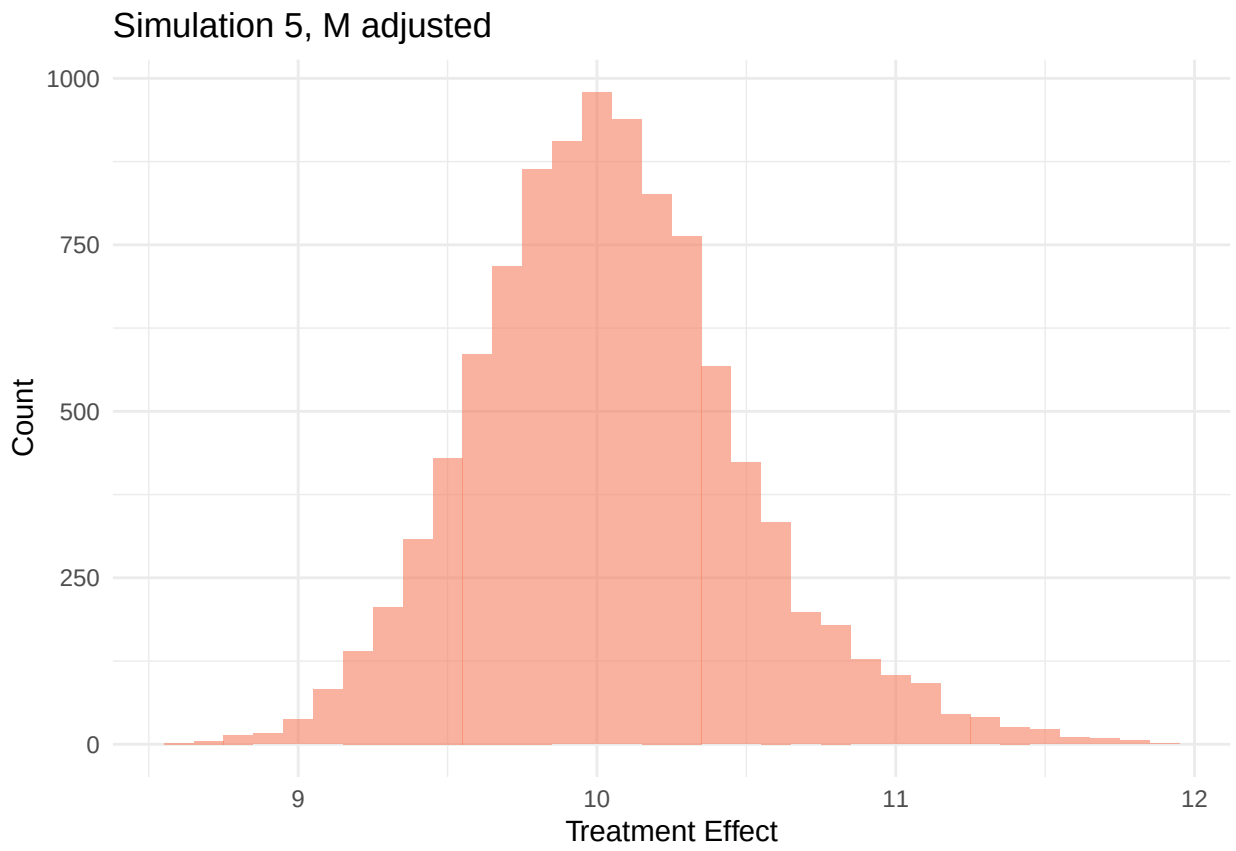
```
knitr::kable(coverage_4, format = "latex",escape = FALSE)
```

	Coverage
M adjusted	0.9998
M not adjusted	0.9994

3.5 Constant Treatment Effect with Confounded Assignment, Including Covariates Affecting to Output and a Impure Local M-Structure

The following estimation with $X \cup Z \cup C \cup M \in \mathbb{S}$:

```
# Estimate causal forest
start_time_10 <- Sys.time() #Recording the running time

#Fitting the model
cf5.with_M <- grf::causal_forest(cbind(X, Z, C, m), y_5, w_5, orthog.boosting = TRUE)


end_time_10 <- Sys.time()

#Predicted values

pred_tau_5.with_M <- predict(cf5.with_M, estimate.variance = TRUE)

plot_pred_tau_10 <- ggplot(data = as.data.frame(pred_tau_5.with_M$predictions),
       aes(x = (pred_tau_5.with_M$predictions))) +
  geom_histogram(binwidth = 0.1, fill="#f68060", alpha=.6) +
  labs(title ="Simulation 5, M adjusted",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()

plot_pred_tau_10
```



Runing time:

```
start_time_10 - end_time_10
```

```
## Time difference of -1.234566 mins
```

RMSE:

```
rmse_5.with_M <- fun.rmse(predicted = pred_tau_5.with_M$predictions, true = tau)

rmse_5.with_M
```

```
## [1] 0.4490187
```

Coverage:

```
coverage_5.with_M <- fun.coverage(pred_tau_5.with_M, tau)

coverage_5.with_M
```

```
## [1] 0.9996
```

Estimated ATE:

```r
ATE_est_5.with_M <- average_treatment_effect(cf5.with_M)

ATE_est_5.with_M
```

```
##   estimate    std.err
## 10.0542646  0.2154077
```

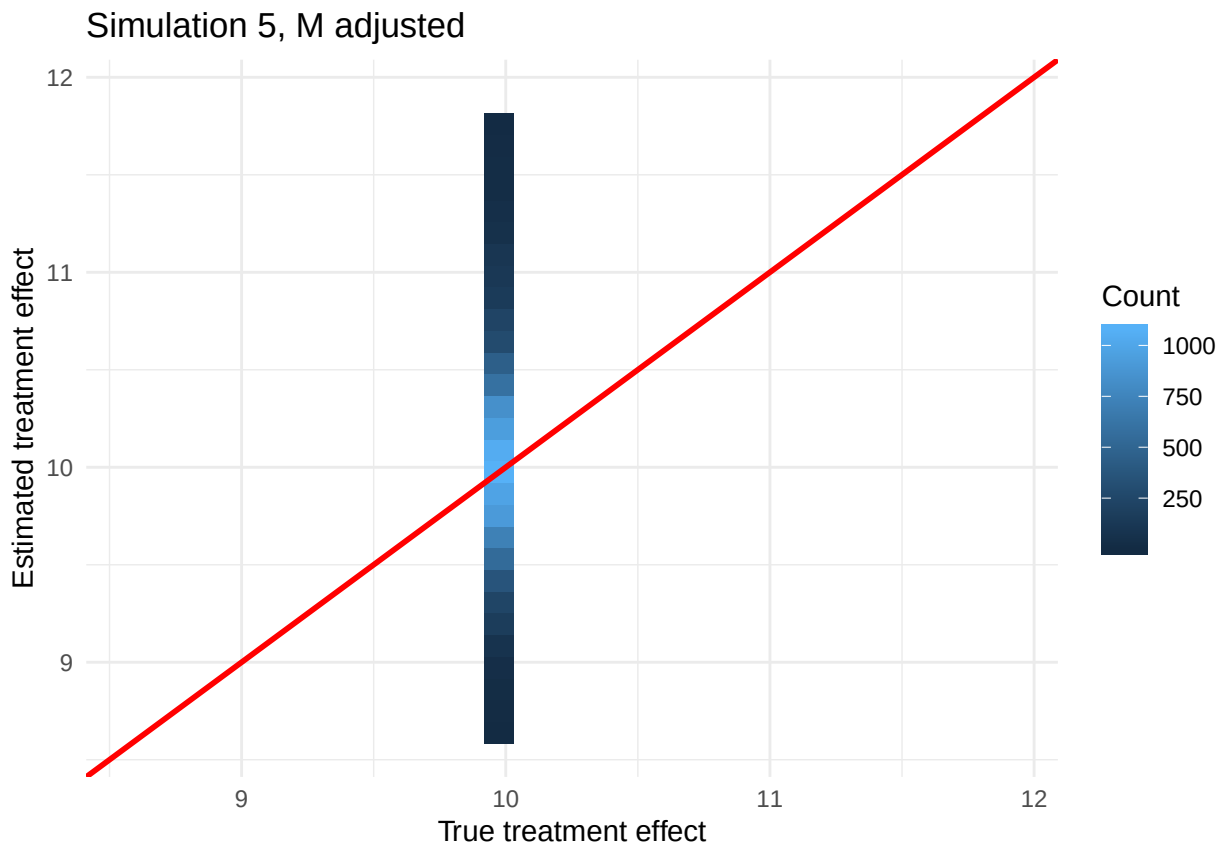
The *proportional difference in the ATE estimates* for the whole population:

```r
fun.diff_ATE(ATE_est = ATE_est_5.with_M, ATE_true = tau)
```

```
## [1] "Proportional mean of the differences:"
##     estimate
## -0.005426457
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##    estimate    estimate
## -0.02696723  0.01611432
```

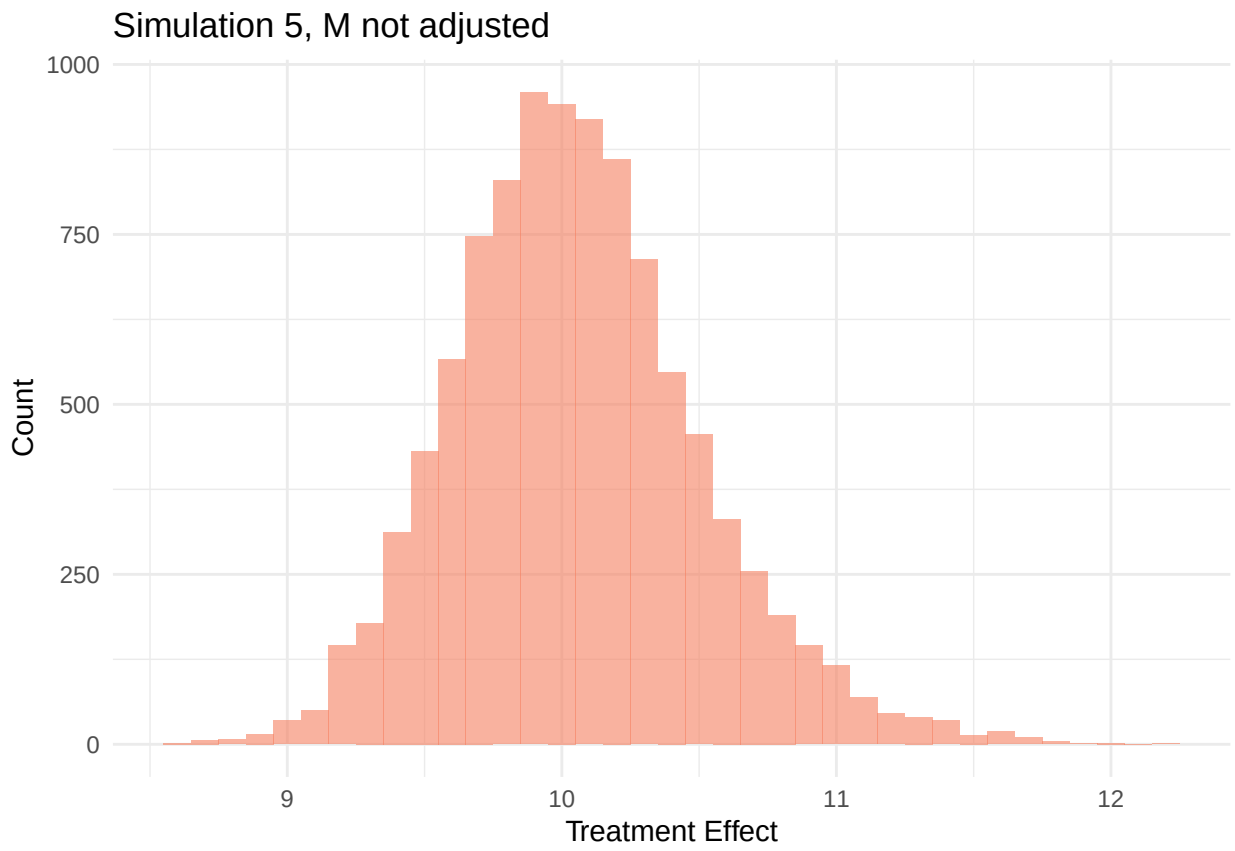
```r
true_vs_pred_5.with_M <- as.data.frame(cbind(tau, pred_tau_5.with_M$predictions))

colnames(true_vs_pred_5.with_M) <- c("tau", "pred_tau")

true_vs_pred_5.with_M$tau <- true_vs_pred_5.with_M$tau + rnorm(n, 0 , sd = 0.0001)

plot10 <- ggplot(data = true_vs_pred_5.with_M, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 5, M adjusted",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_5.with_M$pred_tau), max(true_vs_pred_5.with_M$pred_tau)),
       y = c(min(true_vs_pred_5.with_M$pred_tau), max(true_vs_pred_5.with_M$pred_tau)))

plot10
```

```
## Warning: Removed 1 rows containing missing values (geom_tile).
```



The following estimation with $M \notin \mathbb{S}$ ($X \cup Z \cup C \in \mathbb{S}$):

```
# Estimate causal forest
start_time_11 <- Sys.time() #Recording the running time

#Fitting the model
cf5.no_M <- grf::causal_forest(cbind(X, Z, C), y_5, w_5, orthog.boosting = TRUE)


end_time_11 <- Sys.time()

#Predicted values

pred_tau_5.no_M <- predict(cf5.no_M, estimate.variance = TRUE)

plot_pred_tau_11 <- ggplot(data = as.data.frame(pred_tau_5.no_M$predictions),
       aes(x = (pred_tau_5.no_M$predictions))) +
  geom_histogram(binwidth = 0.1, fill="#f68060", alpha=.6) +
  labs(title ="Simulation 5, M not adjusted",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()

plot_pred_tau_11
```



Runing time:

```
start_time_11 - end_time_11
```

```
## Time difference of -1.262756 mins
```

RMSE:

```
rmse_5.no_M <- fun.rmse(predicted = pred_tau_5.no_M$predictions, true = tau)

rmse_5.no_M
```

```
## [1] 0.4513016
```

Coverage:

```
coverage_5.no_M <- fun.coverage(pred_tau_5.no_M, tau)

coverage_5.no_M
```

```
## [1] 0.9986
```

Estimated ATE:

```r
ATE_est_5.no_M <- average_treatment_effect(cf5.no_M)

ATE_est_5.no_M
```

```
##   estimate    std.err
## 10.0524049  0.2171627
```

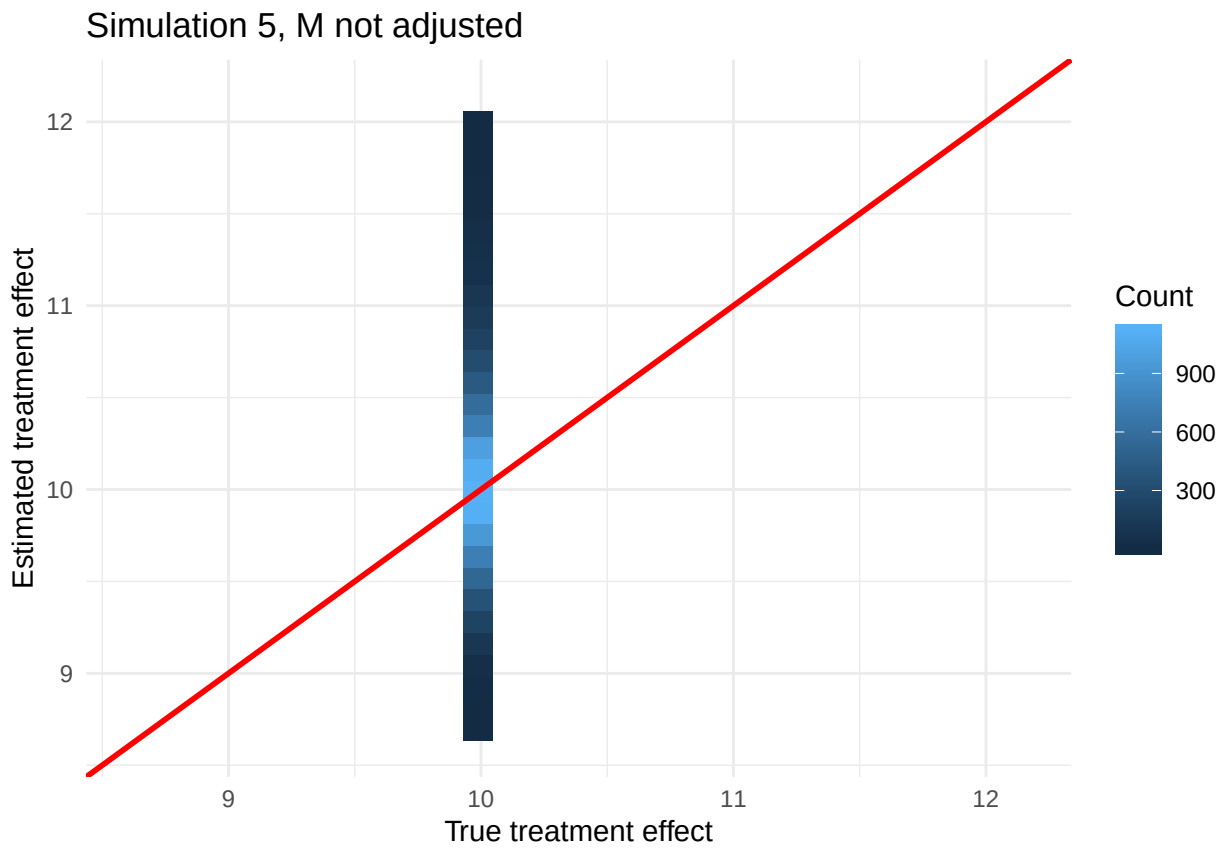
The *proportional difference in the ATE estimates* for the whole population:

```r
fun.diff_ATE(ATE_est = ATE_est_5.no_M, ATE_true = tau)
```

```
## [1] "Proportional mean of the differences:"
##     estimate
## -0.005240495
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##    estimate    estimate
## -0.02695676  0.01647577
```

```r
true_vs_pred_5.no_M <- as.data.frame(cbind(tau, pred_tau_5.no_M$predictions))

colnames(true_vs_pred_5.no_M) <- c("tau", "pred_tau")

true_vs_pred_5.no_M$tau <- true_vs_pred_5.no_M$tau + rnorm(n, 0 , sd = 0.0001)

plot11 <- ggplot(data = true_vs_pred_5.no_M, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 5, M not adjusted",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_5.no_M$pred_tau), max(true_vs_pred_5.no_M$pred_tau)),
       y = c(min(true_vs_pred_5.no_M$pred_tau), max(true_vs_pred_5.no_M$pred_tau)))

plot11
```

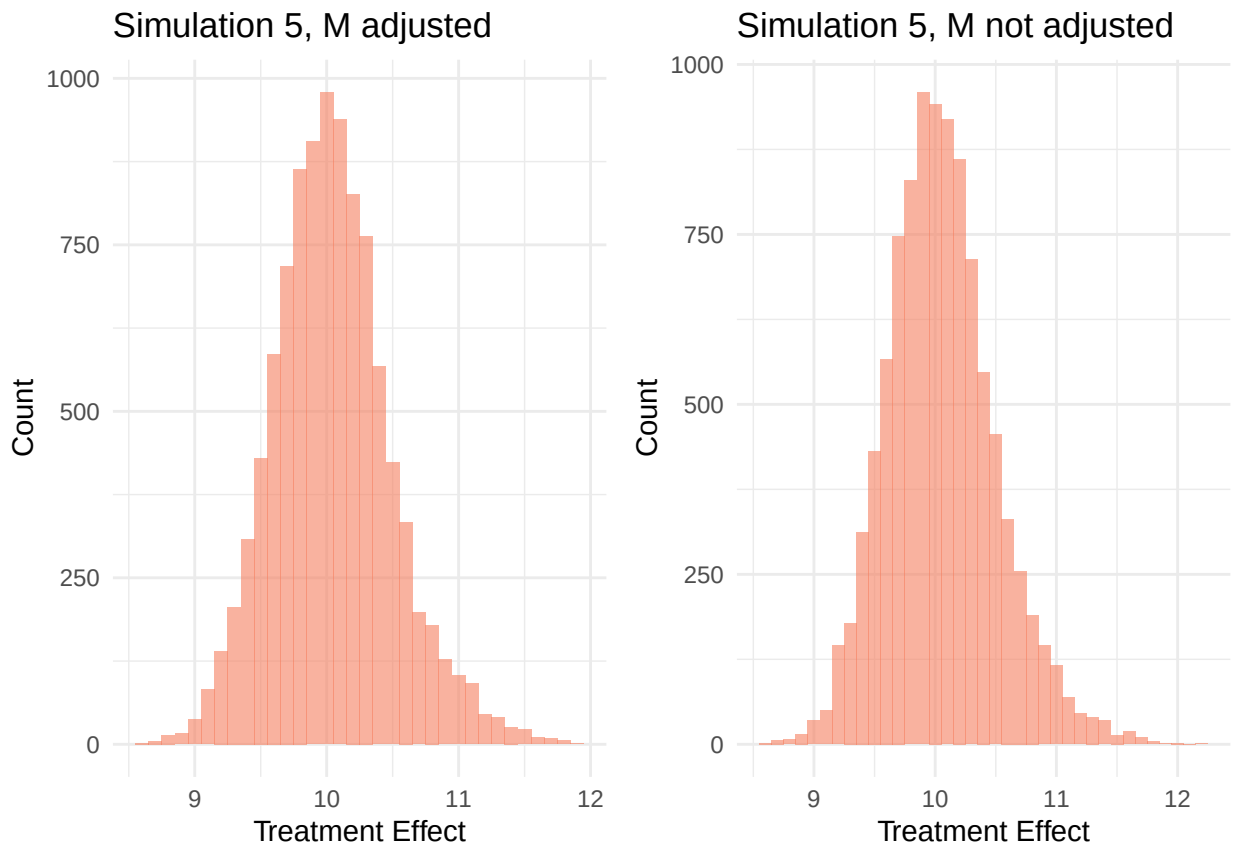
```
## Warning: Removed 1 rows containing missing values (geom_tile).
```



Summary

Predicted $\hat{\tau}s$:

```
grid.arrange(plot_pred_tau_10, plot_pred_tau_11, nrow = 1)
```

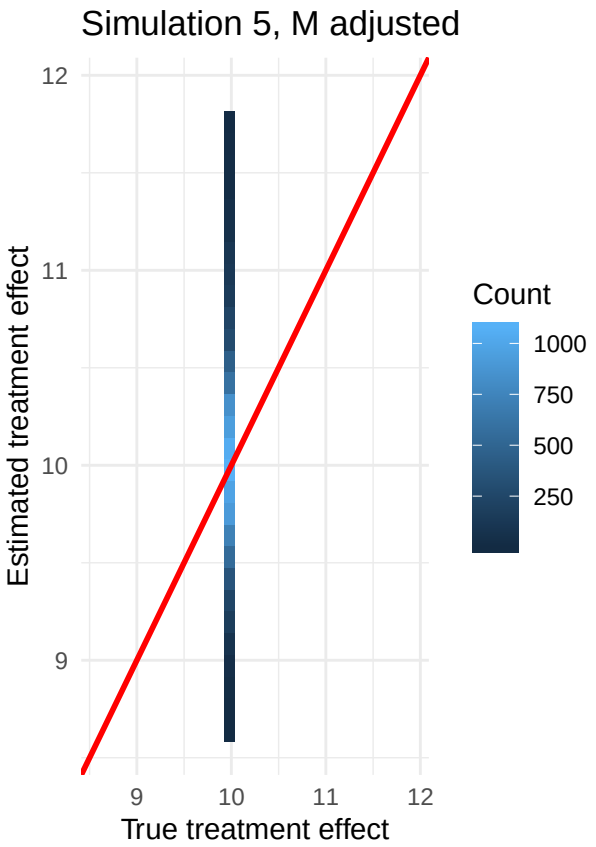


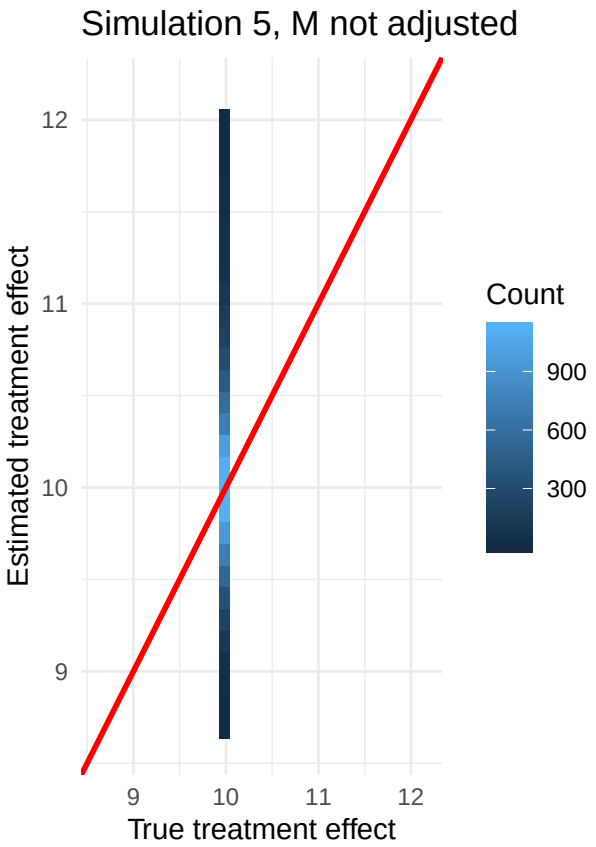
True τ vs. predicted $\hat{\tau}$:

```
grid.arrange(plot10, plot11, nrow = 1)
```

```
## Warning: Removed 1 rows containing missing values (geom_tile).
```

```
## Warning: Removed 1 rows containing missing values (geom_tile).
```





RMSEs:

```
rmse_5 <- as.data.frame(c(rmse_5.with_M, rmse_5.no_M))

rownames(rmse_5) <- c("$M$ adjusted", "$M$ not adjusted")

colnames(rmse_5) <- c("RMSE")

knitr::kable(rmse_5, escape = FALSE)
```

	RMSE
M adjusted	0.4490187
M not adjusted	0.4513016

Coverages:

```
coverage_5 <- as.data.frame(c(coverage_5.with_M, coverage_5.no_M))

rownames(coverage_5) <-  c("$M$ adjusted", "$M$ not adjusted")

colnames(coverage_5) <- c("Coverage")

knitr::kable(coverage_5, escape = FALSE)
```

	Coverage
M adjusted	0.9996
M not adjusted	0.9986

LaTeX:

```
knitr::kable(rmse_5, format = "latex",escape = FALSE)
```

	RMSE
M adjusted	0.4490187
M not adjusted	0.4513016

```
knitr::kable(coverage_5, format = "latex",escape = FALSE)
```

	Coverage
M adjusted	0.9996
M not adjusted	0.9986

3.6 Randomized Controlled Trial with Heterogeneous Treatment Effect, Including Covariates Affecting to Output

The first estimation for a heterogeneous treatment effect. At first, let's test with the full set of observed variables ($X \in \mathbb{S}$)::

```
# Estimate causal forest
start_time_12 <- Sys.time() #Recording the running time

#Fitting the model
cf6.full <- grf::causal_forest(X, y_6, w_1, orthog.boosting = FALSE)


end_time_12 <- Sys.time()

#Predicted values

pred_tau_6.full <- predict(cf6.full, estimate.variance = TRUE)

plot_pred_tau_12 <- cbind(pred_tau_6.full$predictions, tau_1) %>%
  as.data.frame() %>%
  dplyr::rename(Predicted = V1) %>%
  dplyr::rename(True = tau_1) %>%
  gather(key = "key", value = "value") %>%
  ggplot(aes(x = value, fill = key)) +
  geom_histogram(binwidth = 0.1, alpha=.6) +
  scale_fill_manual(name = "", values=c("#f68060", "#57b2eb")) +
  labs(title ="Simulation 6 with the whole set X",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()

plot_pred_tau_12
```

Runing time:

```
start_time_12 - end_time_12
```

```
## Time difference of -35.61582 secs
```

RMSE:

```
rmse_6.full <- fun.rmse(predicted = pred_tau_6.full$predictions, true = tau_1)

rmse_6.full
```

```
## [1] 2.274664
```

Coverage:

```
coverage_6.full <- fun.coverage(pred_tau_6.full, tau_1)

coverage_6.full
```

```
## [1] 0.7734
```

Estimated ATE:

```r
ATE_est_6.full <- average_treatment_effect(cf6.full)

ATE_est_6.full
```

```
##  estimate   std.err
## 2.2208766 0.2069256
```

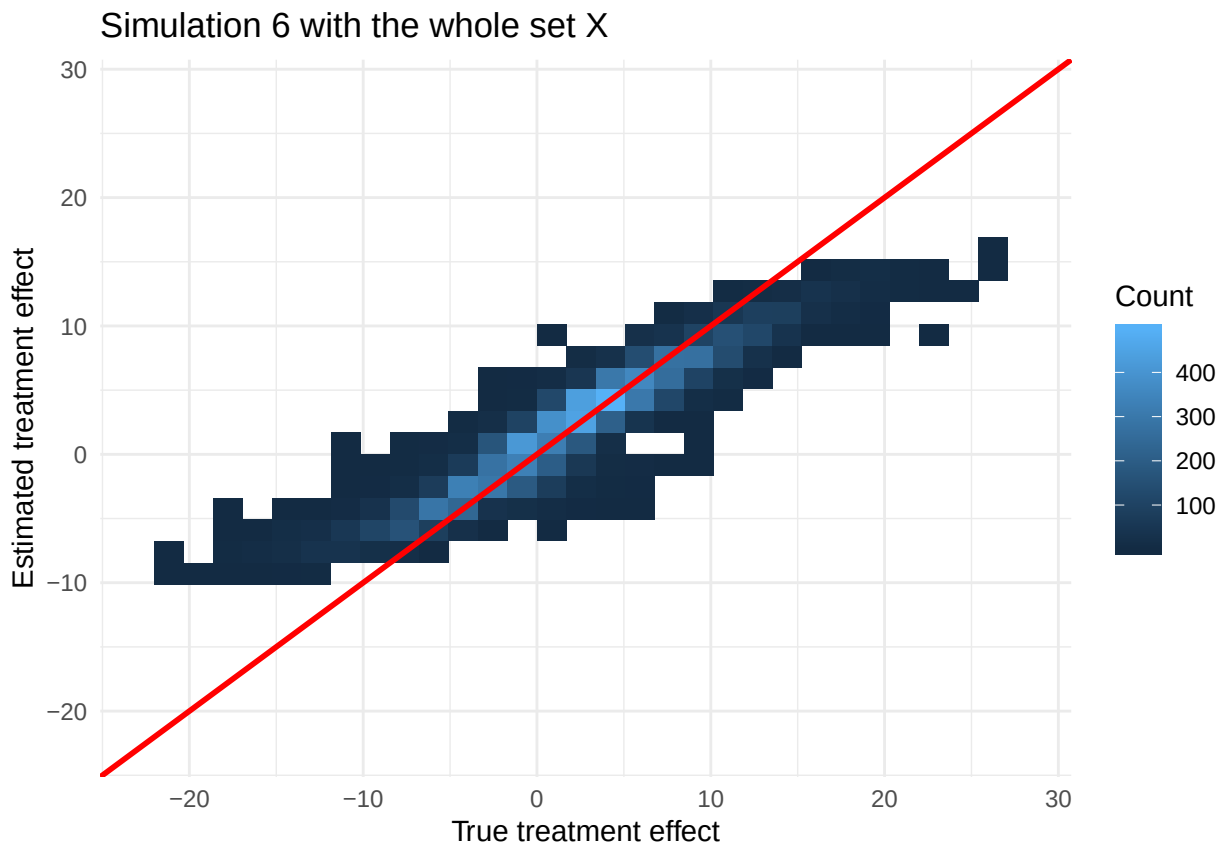
The *proportional difference in the ATE estimates* for the whole population:

```r
fun.diff_ATE(ATE_est = ATE_est_6.full, ATE_true = mean(tau_1))
```

```
## [1] "Proportional mean of the differences:"
##   estimate
## -0.1242247
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##    estimate    estimate
## -0.22897195 -0.01947736
```

```r
true_vs_pred_6.full <- as.data.frame(cbind(tau_1, pred_tau_6.full$predictions))

colnames(true_vs_pred_6.full) <- c("tau", "pred_tau")

plot12 <- ggplot(data = true_vs_pred_6.full, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 6 with the whole set X",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_6.full), max(true_vs_pred_6.full)),
       y = c(min(true_vs_pred_6.full), max(true_vs_pred_6.full)))

plot12
```

```
## Warning: Removed 1 rows containing missing values (geom_tile).
```

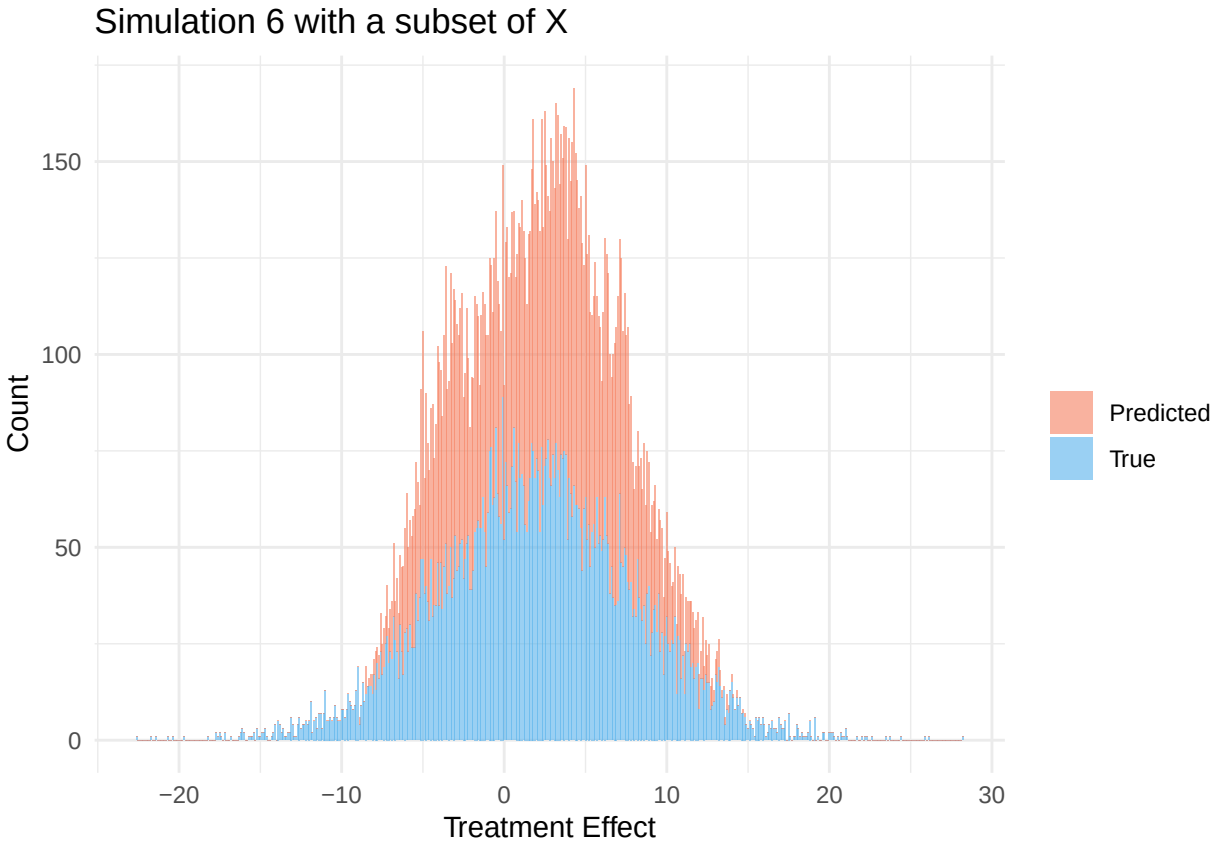


Let's use only the most important variables and see how it affects in the predictions:

```
important_var_6 <- which(variable_importance(cf6.full) >= median(variable_importance(cf6.full))) #Varia
```

```
# Estimate causal forest
start_time_13 <- Sys.time() #Recording the running time

#Fitting the model
cf6.important <- grf::causal_forest(X[, important_var_6], y_6, w_1, orthog.boosting = FALSE)


end_time_13 <- Sys.time()

#Predicted values

pred_tau_6.important <- predict(cf6.important, estimate.variance = TRUE)

plot_pred_tau_13 <- cbind(pred_tau_6.important$predictions, tau_1) %>%
  as.data.frame() %>%
  dplyr::rename(Predicted = V1) %>%
  dplyr::rename(True = tau_1) %>%
  gather(key = "key", value = "value") %>%
  ggplot(aes(x = value, fill = key)) +
  geom_histogram(binwidth = 0.1, alpha=.6) +
  scale_fill_manual(name = "", values=c("#f68060", "#57b2eb")) +
  labs(title ="Simulation 6 with a subset of X",
```

```
       x = "Treatment Effect", y = "Count") +
  theme_minimal()

plot_pred_tau_13
```



Runing time:

```
start_time_13 - end_time_13
```

```
## Time difference of -35.88995 secs
```

RMSE:

```
rmse_6.important <- fun.rmse(predicted = pred_tau_6.important$predictions, true = tau_1)
```

Coverage:

```
coverage_6.important <- fun.coverage(pred_tau_6.important, tau_1)

coverage_6.important
```

```
## [1] 0.6238
```

Estimated ATE:

```r
ATE_est_6.important <- average_treatment_effect(cf6.important)

ATE_est_6.important
```

```
##  estimate   std.err
## 2.2190782 0.2102267
```

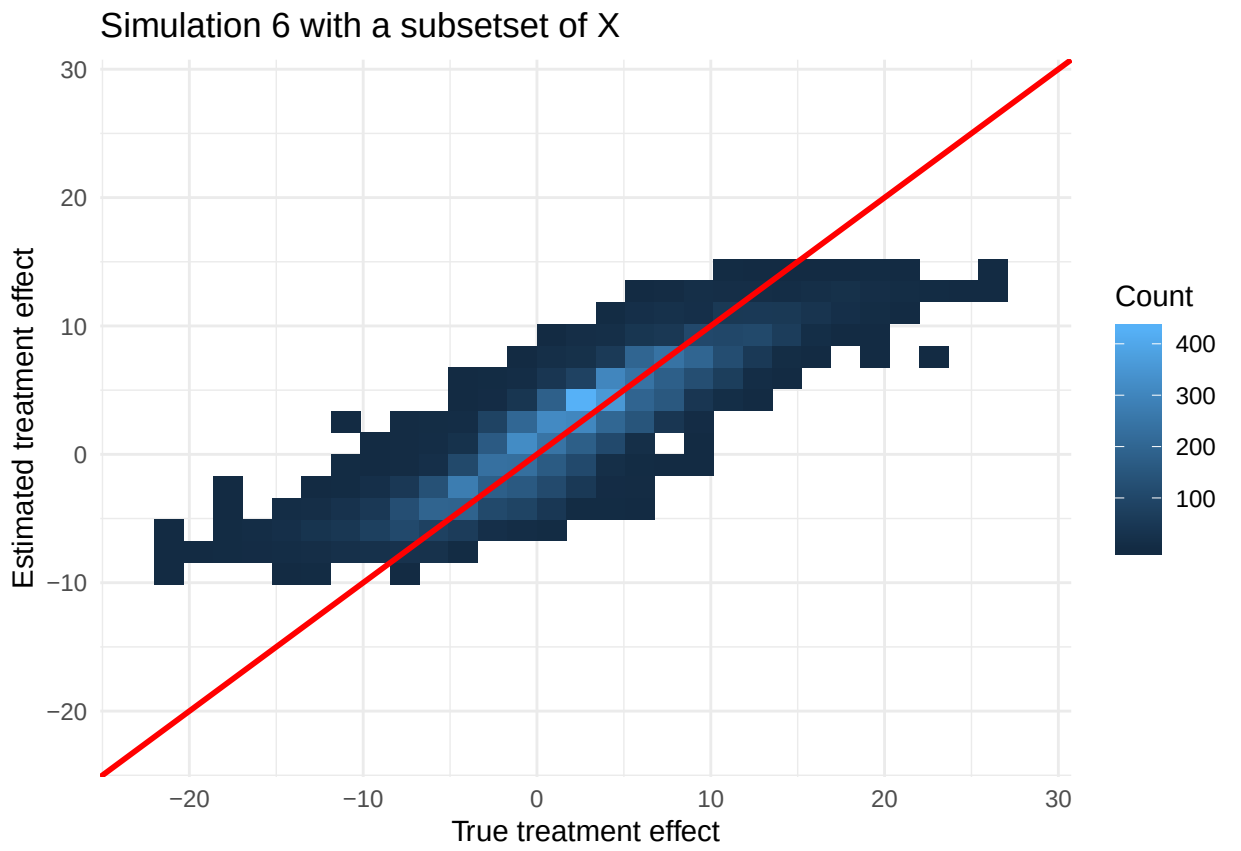
The *proportional difference in the ATE estimates* for the whole population:

```r
fun.diff_ATE(ATE_est = ATE_est_6.important, ATE_true = mean(tau_1))
```

```
## [1] "Proportional mean of the differences:"
##   estimate
## -0.1233143
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##    estimate    estimate
## -0.22973267 -0.01689592
```

```r
true_vs_pred_6.important <- as.data.frame(cbind(tau_1, pred_tau_6.important$predictions))

colnames(true_vs_pred_6.important) <- c("tau", "pred_tau")

plot13 <- ggplot(data = true_vs_pred_6.important, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 6 with a subsetset of X",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_6.important), max(true_vs_pred_6.important)),
       y = c(min(true_vs_pred_6.important), max(true_vs_pred_6.important)))

plot13
```

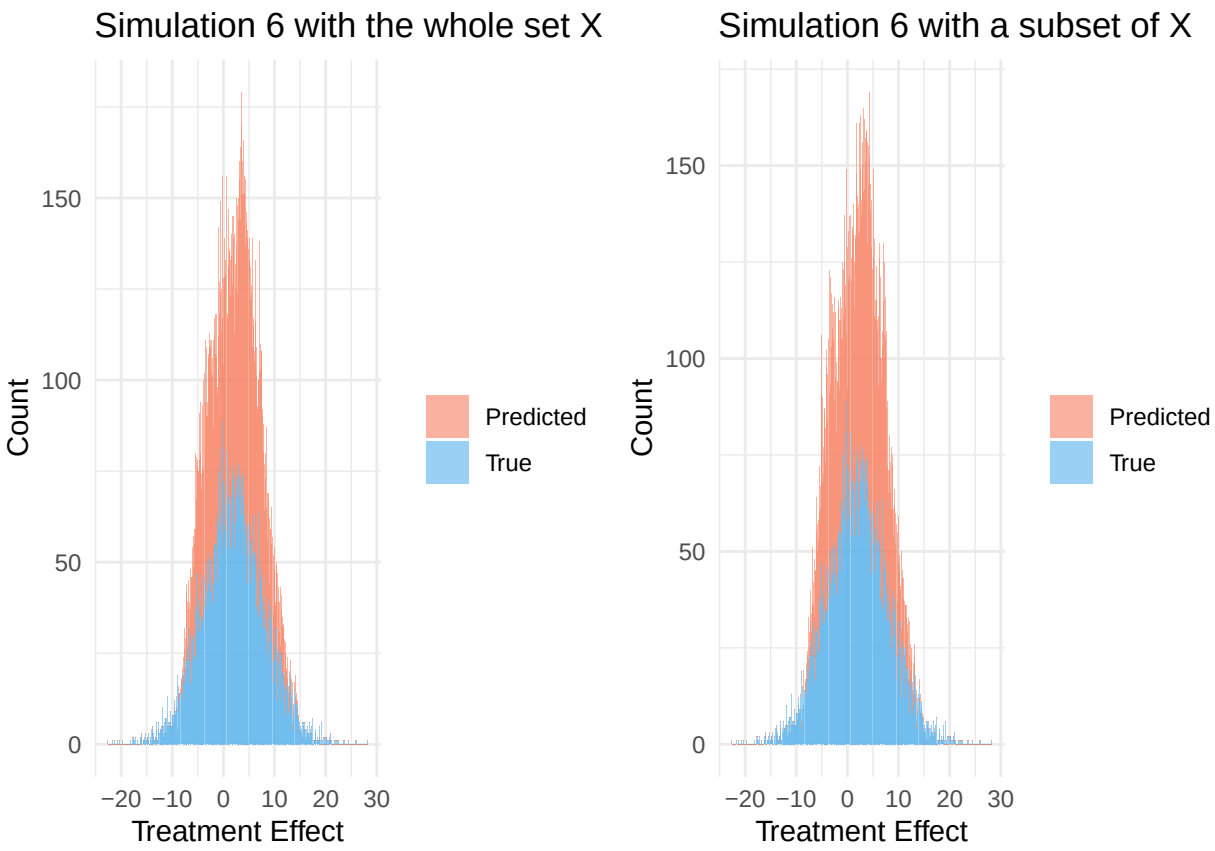
```
## Warning: Removed 1 rows containing missing values (geom_tile).
```



Summary

Predicted $\hat{\tau}s$:

```
grid.arrange(plot_pred_tau_12, plot_pred_tau_13, nrow = 1)
```

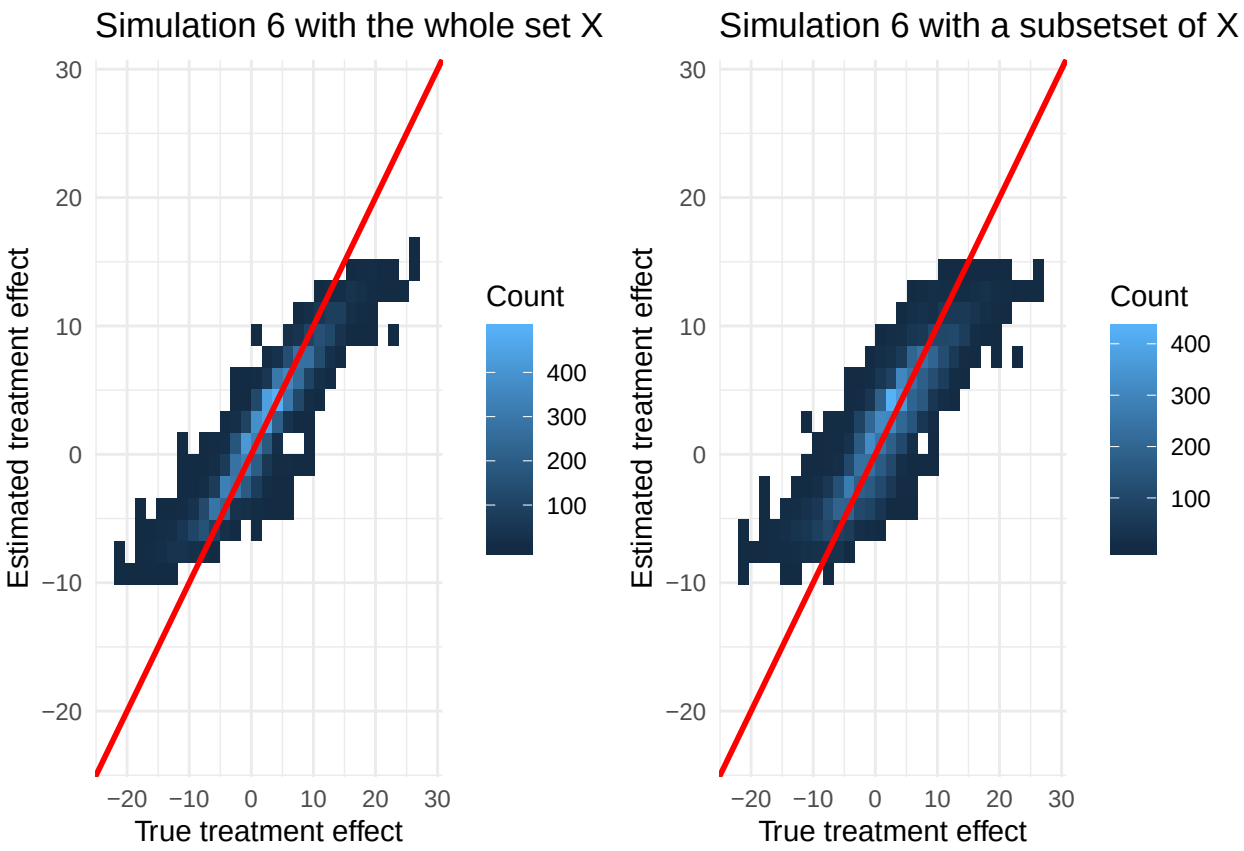


True τ vs. predicted $\hat{\tau}$:

```
grid.arrange(plot12, plot13, nrow = 1)
```

```
## Warning: Removed 1 rows containing missing values (geom_tile).
```

```
## Warning: Removed 1 rows containing missing values (geom_tile).
```



RMSEs:

```
rmse_6 <- as.data.frame(c(rmse_6.full, rmse_6.important))

rownames(rmse_6) <- c("Full set $X$", "Subset of $X$")

colnames(rmse_6) <- c("RMSE")

knitr::kable(rmse_6, escape = FALSE)
```

	RMSE
Full set X	2.274664
Subset of X	2.877371

Coverages:

```
coverage_6 <- as.data.frame(c(coverage_6.full, coverage_6.important))

rownames(coverage_6) <-  c("Full set $X$", "Subset of $X$")

colnames(coverage_6) <- c("Coverage")

knitr::kable(coverage_6, escape = FALSE)
```

	Coverage
Full set X	0.7734
Subset of X	0.6238

LaTeX:

```
knitr::kable(rmse_6, format = "latex",escape = FALSE)
```

	RMSE
Full set X	2.274664
Subset of X	2.877371

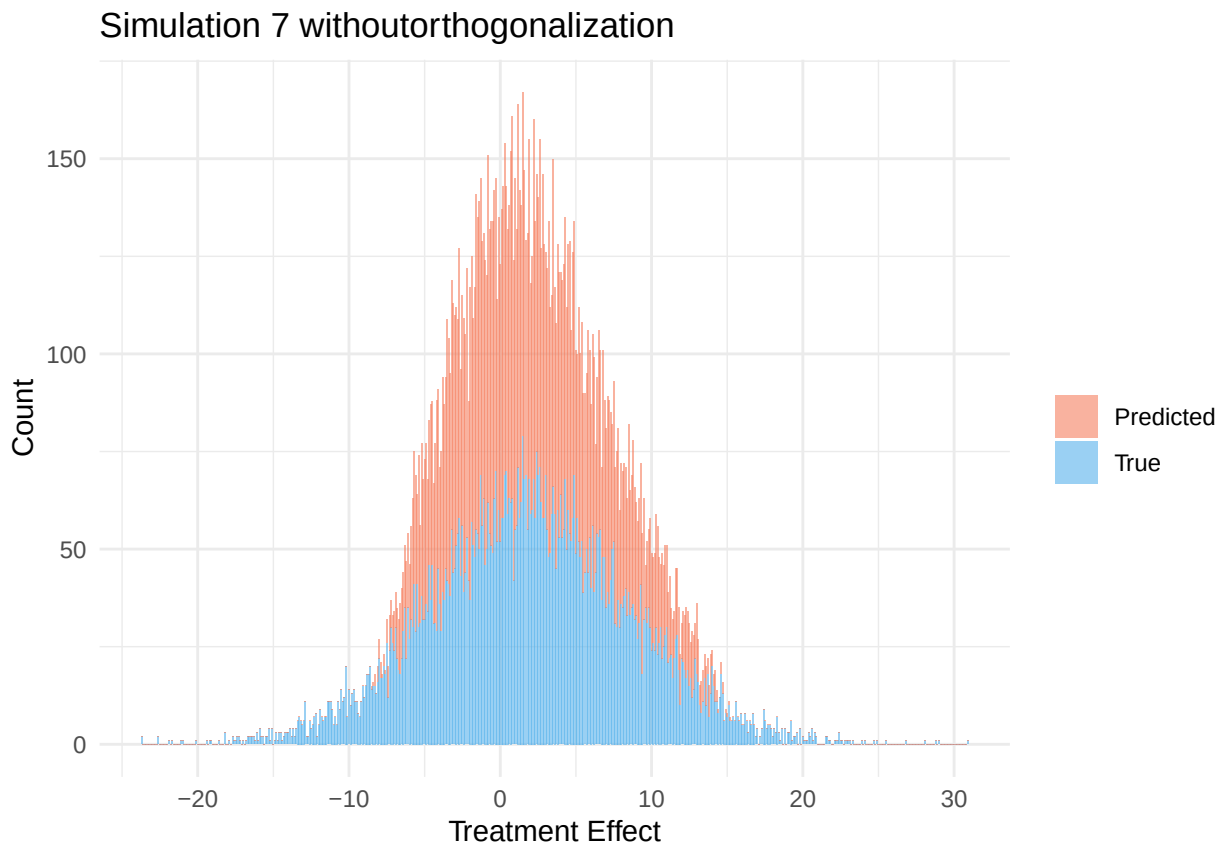
```
knitr::kable(coverage_6, format = "latex",escape = FALSE)
```

	Coverage
Full set X	0.7734
Subset of X	0.6238

3.7 Heterogeneous Treatment Effect with the Confounded Assignment, Including Covariates Affecting to Output

Without orthogonalization:

```
# Estimate causal forest
start_time_14 <- Sys.time() #Recording the running time

#Fitting the model
cf7.no_ort <- grf::causal_forest(cbind(X, Z, C), y_7, w_3, orthog.boosting = FALSE)


end_time_14 <- Sys.time()

#Predicted values

pred_tau_7.no_ort <- predict(cf7.no_ort, estimate.variance = TRUE)

plot_pred_tau_14 <- cbind(pred_tau_7.no_ort$predictions, tau_2) %>%
  as.data.frame() %>%
  dplyr::rename(Predicted = V1) %>%
  dplyr::rename(True = tau_2) %>%
  gather(key = "key", value = "value") %>%
  ggplot(aes(x = value, fill = key)) +
  geom_histogram(binwidth = 0.1, alpha=.6) +
  scale_fill_manual(name = "", values=c("#f68060", "#57b2eb")) +
  labs(title ="Simulation 7 withoutorthogonalization", x = "Treatment Effect", y = "Count") +
  theme_minimal()

plot_pred_tau_14
```



Runing time:

```
start_time_14 - end_time_14
```

```
## Time difference of -56.95369 secs
```

RMSE:

```
rmse_7.no_ort <- fun.rmse(predicted = pred_tau_7.no_ort$predictions, true = tau_2)

rmse_7.no_ort
```

```
## [1] 3.157229
```

Coverage:

```
coverage_7.no_ort <- fun.coverage(pred_tau_7.no_ort, tau_2)

coverage_7.no_ort
```

```
## [1] 0.6832
```

Estimated ATE:

```r
ATE_est_7.no_ort <- average_treatment_effect(cf7.no_ort)

ATE_est_7.no_ort
```

```
##  estimate   std.err
## 2.0263906 0.2233486
```

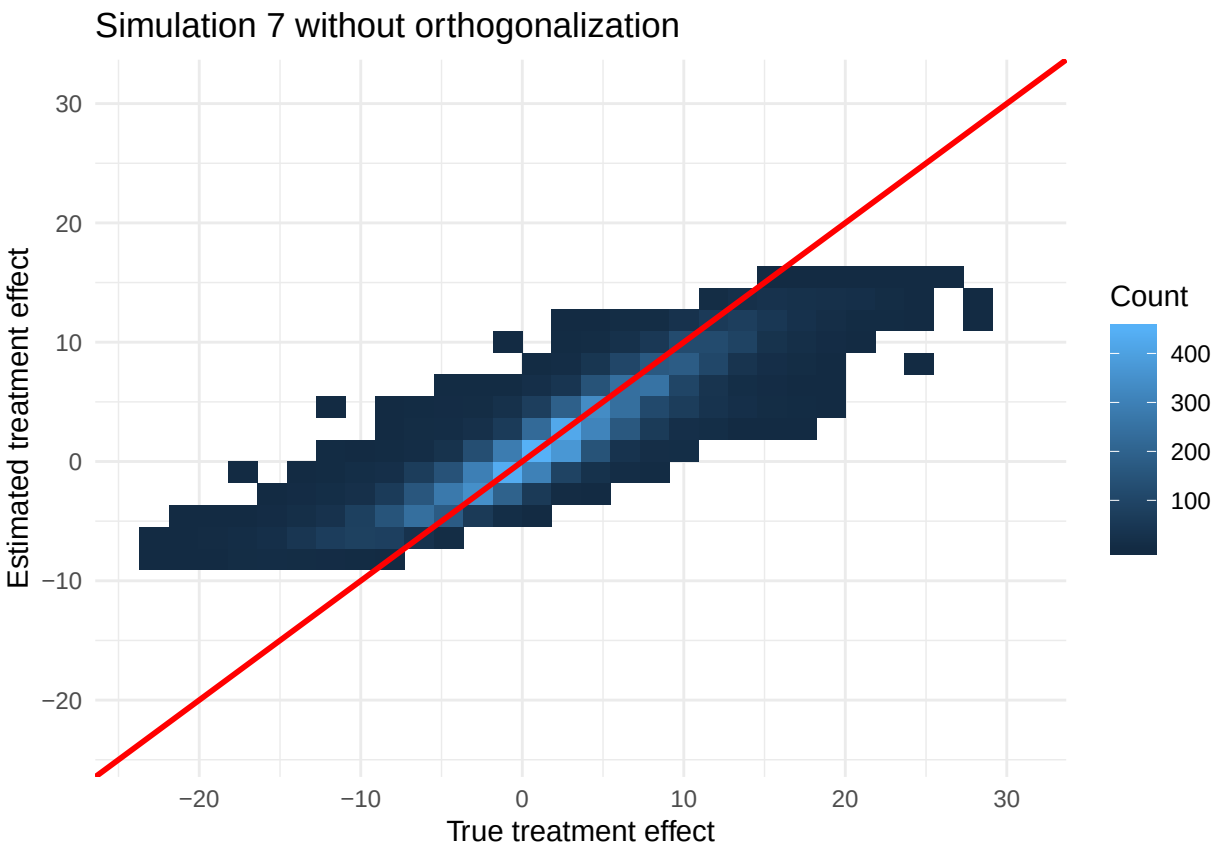
The *proportional difference in the ATE estimates* for the whole population:

```r
fun.diff_ATE(ATE_est = ATE_est_7.no_ort, ATE_true = mean(tau_2))
```

```
## [1] "Proportional mean of the differences:"
##    estimate
## -0.01723146
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##   estimate   estimate
## -0.1293506  0.0948877
```

```r
true_vs_pred_7.no_ort <- as.data.frame(cbind(tau_2, pred_tau_7.no_ort$predictions))

colnames(true_vs_pred_7.no_ort) <- c("tau", "pred_tau")

plot14 <- ggplot(data = true_vs_pred_7.no_ort, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 7 without orthogonalization",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_7.no_ort), max(true_vs_pred_7.no_ort)),
       y = c(min(true_vs_pred_7.no_ort), max(true_vs_pred_7.no_ort)))

plot14
```

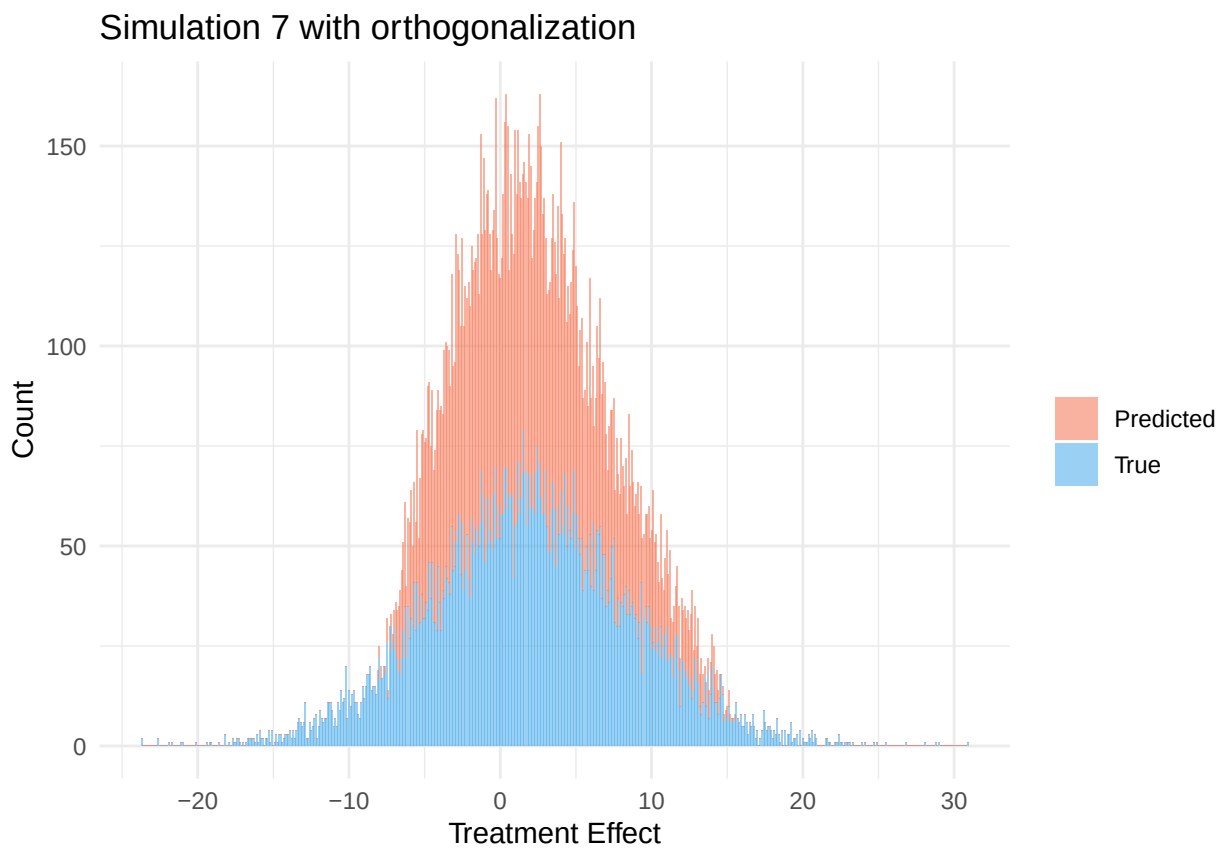
```
## Warning: Removed 2 rows containing missing values (geom_tile).
```



With orthogonalization:

```
# Estimate causal forest
start_time_15 <- Sys.time() #Recording the running time

#Fitting the model
cf7.with_ort <- grf::causal_forest(cbind(X,Z, C), y_7, w_3, orthog.boosting = TRUE)


end_time_15 <- Sys.time()

#Predicted values

pred_tau_7.with_ort <- predict(cf7.with_ort, estimate.variance = TRUE)

plot_pred_tau_15 <- cbind(pred_tau_7.with_ort$predictions, tau_2) %>%
  as.data.frame() %>%
  dplyr::rename(Predicted = V1) %>%
  dplyr::rename(True = tau_2) %>%
  gather(key = "key", value = "value") %>%
  ggplot(aes(x = value, fill = key)) +
  geom_histogram(binwidth = 0.1, alpha=.6) +
  scale_fill_manual(name = "", values=c("#f68060", "#57b2eb")) +
  labs(title ="Simulation 7 with orthogonalization",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()
```

```
plot_pred_tau_15
```



Runing time:

```
start_time_15 - end_time_15
```

```
## Time difference of -1.205449 mins
```

RMSE:

```
rmse_7.with_ort <- fun.rmse(predicted = pred_tau_7.with_ort$predictions, true = tau_2)

rmse_7.with_ort
```

```
## [1] 3.101125
```

Coverage:

```
coverage_7.with_ort <- fun.coverage(pred_tau_7.with_ort, tau_2)

coverage_7.with_ort
```

```
## [1] 0.6911
```

Estimated ATE:

```
ATE_est_7.with_ort <- average_treatment_effect(cf7.with_ort)

ATE_est_7.with_ort
```

```
##  estimate   std.err
## 2.0533831 0.2162684
```

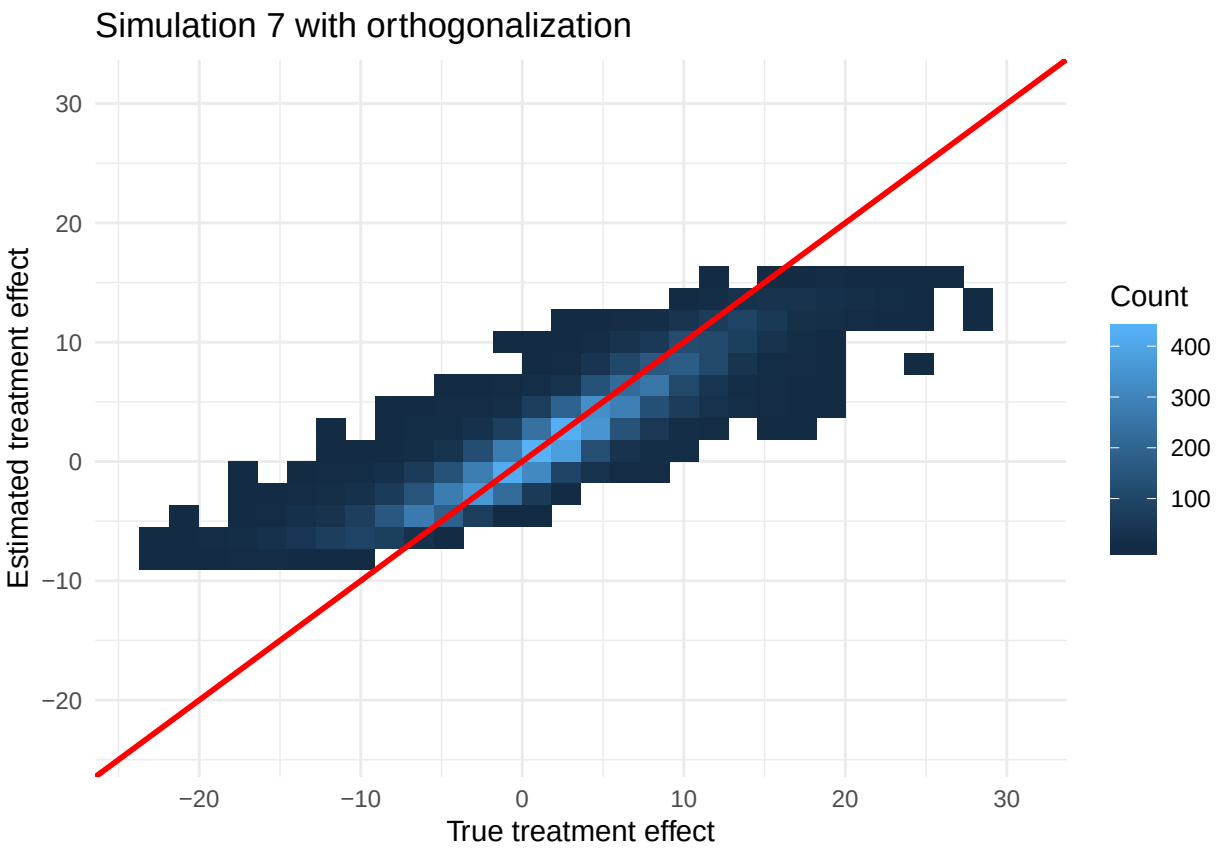
The *proportional difference in the ATE estimates* for the whole population:

```
fun.diff_ATE(ATE_est = ATE_est_7.with_ort, ATE_true = mean(tau_2))
```

```
## [1] "Proportional mean of the differences:"
##    estimate
## -0.03078146
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##    estimate    estimate
## -0.13934645  0.07778353
```

```
true_vs_pred_7.with_ort <- as.data.frame(cbind(tau_2, pred_tau_7.with_ort$predictions))

colnames(true_vs_pred_7.with_ort) <- c("tau", "pred_tau")

plot15 <- ggplot(data = true_vs_pred_7.with_ort, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 7 with orthogonalization",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_7.with_ort), max(true_vs_pred_7.with_ort)),
       y = c(min(true_vs_pred_7.with_ort), max(true_vs_pred_7.with_ort)))

plot15
```

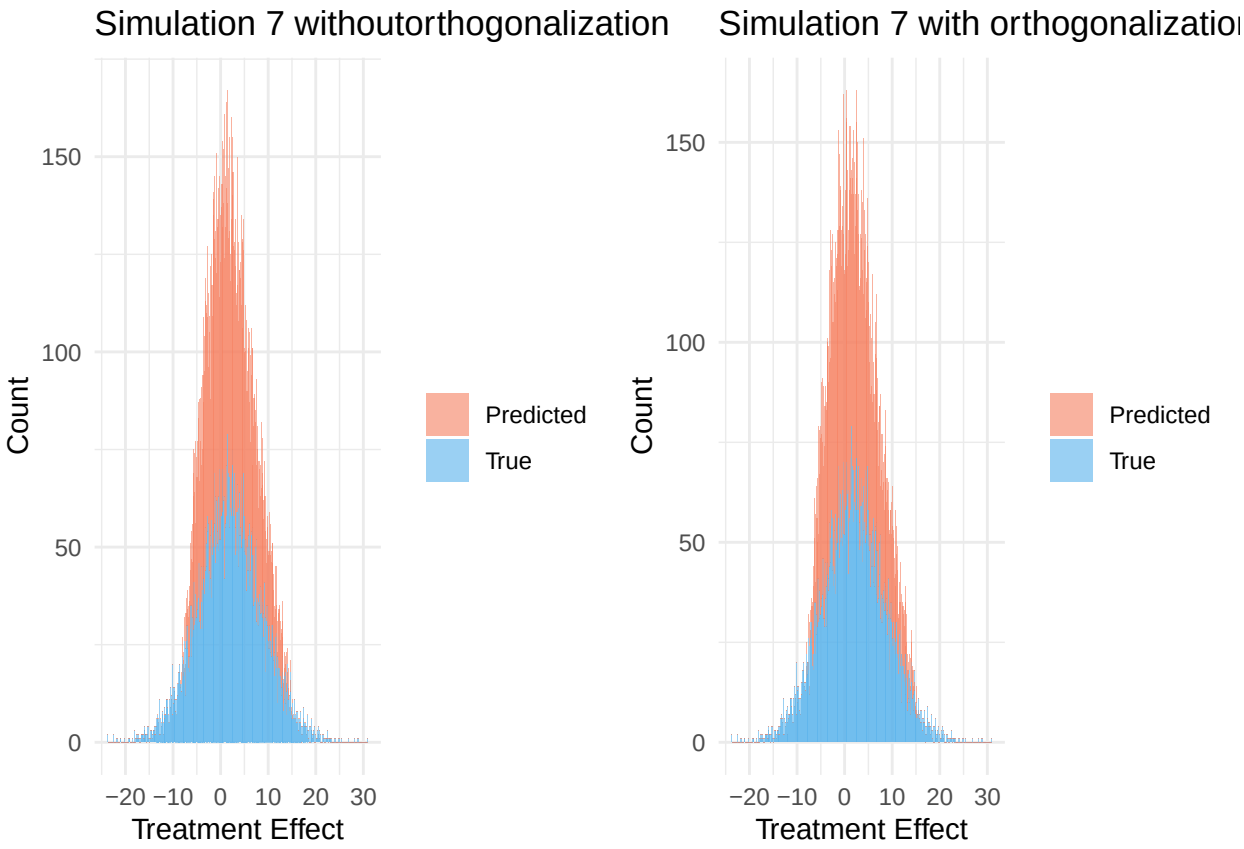
```
## Warning: Removed 2 rows containing missing values (geom_tile).
```



Summary

Predicted $\hat{\tau}s$:

```
grid.arrange(plot_pred_tau_14, plot_pred_tau_15, nrow = 1)
```

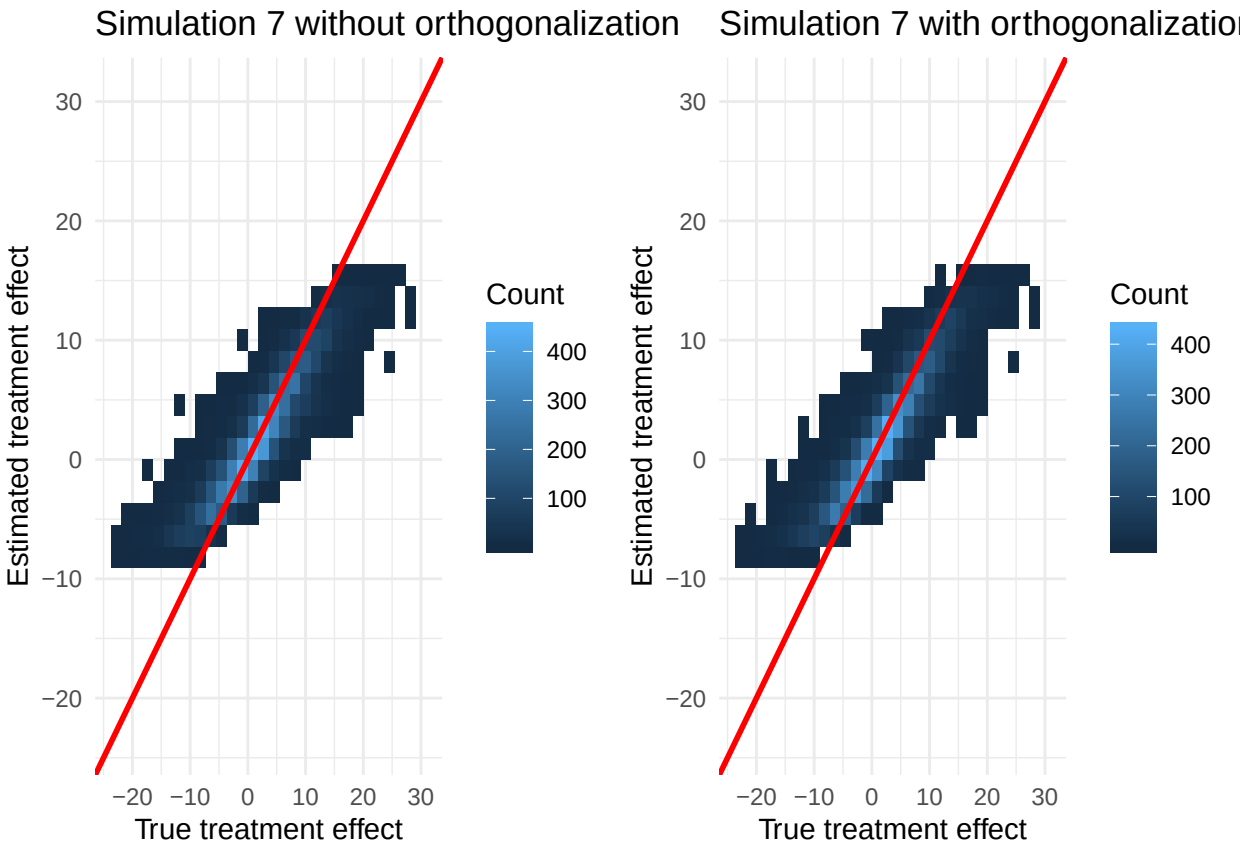


True τ vs. predicted $\hat{\tau}$:

```
grid.arrange(plot14, plot15, nrow = 1)
```

```
## Warning: Removed 2 rows containing missing values (geom_tile).
```

```
## Warning: Removed 2 rows containing missing values (geom_tile).
```



RMSEs:

```
rmse_7 <- as.data.frame(c(rmse_7.no_ort, rmse_7.with_ort))

rownames(rmse_7) <- c("With orthogonalization", "Without orthogonalization")

colnames(rmse_7) <- c("RMSE")

knitr::kable(rmse_7, escape = FALSE)
```

	RMSE
With orthogonalization	3.157229
Without orthogonalization	3.101125

Coverages:

```
coverage_7 <- as.data.frame(c(coverage_7.no_ort, coverage_7.with_ort))

rownames(coverage_7) <-  c("With orthogonalization", "Without orthogonalization")

colnames(coverage_7) <- c("Coverage")

knitr::kable(coverage_7, escape = FALSE)
```

	Coverage
With orthogonalization	0.6832
Without orthogonalization	0.6911

LaTeX:

```
knitr::kable(rmse_7, format = "latex",escape = FALSE)
```

	RMSE
With orthogonalization	3.157229
Without orthogonalization	3.101125

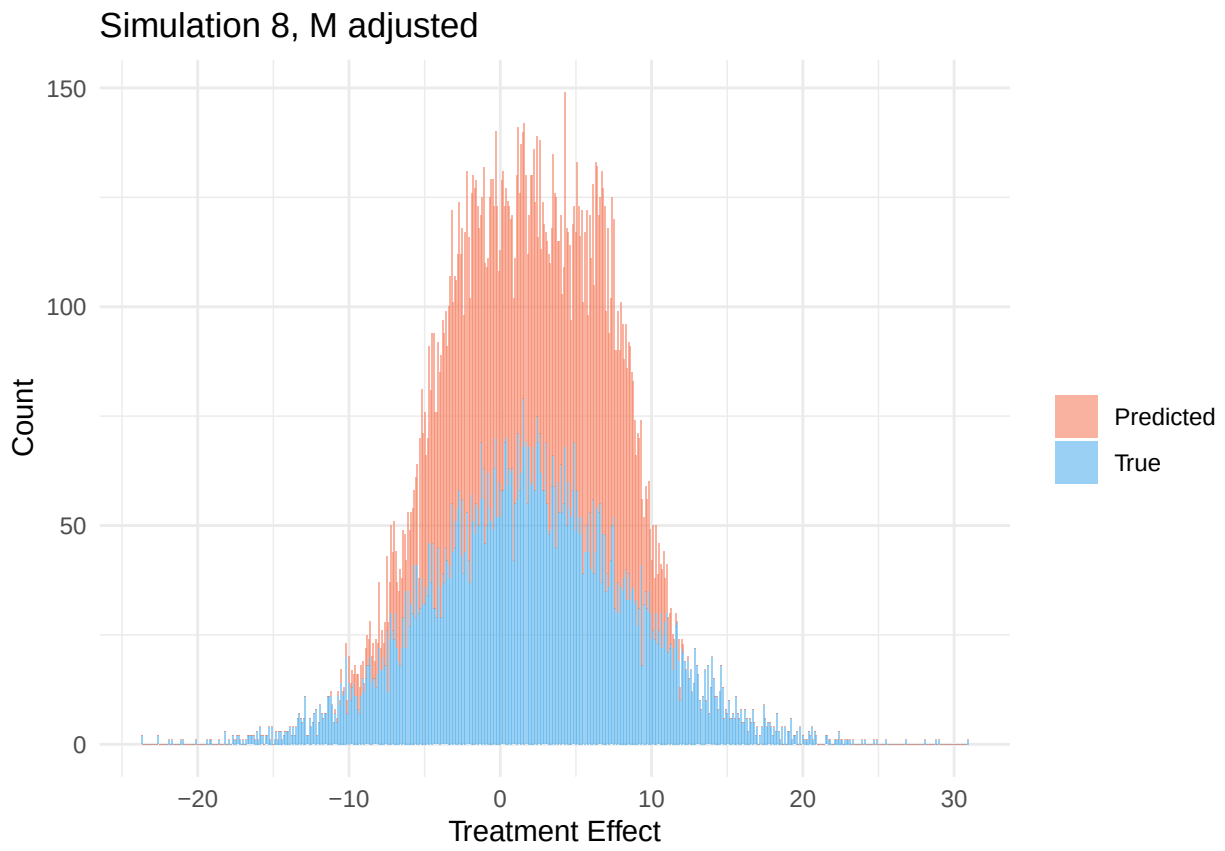
```
knitr::kable(coverage_7, format = "latex",escape = FALSE)
```

	Coverage
With orthogonalization	0.6832
Without orthogonalization	0.6911

3.8 Heterogeneous Treatment Effect with Confounded Assignment, Including Covariates Affecting to Output and a Pure Local M-Structure

With M ($X \cup Z \cup C \cup M \in \mathbb{S}$):

```
# Estimate causal forest
start_time_16 <- Sys.time() #Recording the running time

#Fitting the model
cf8.with_M <- grf::causal_forest(cbind(X, Z, C, m), y_8, w_4, orthog.boosting = TRUE)


end_time_16 <- Sys.time()

#Predicted values

pred_tau_8.with_M <- predict(cf8.with_M, estimate.variance = TRUE)

plot_pred_tau_16 <- cbind(pred_tau_8.with_M$predictions, tau_2) %>%
  as.data.frame() %>%
  dplyr::rename(Predicted = V1) %>%
  dplyr::rename(True = tau_2) %>%
  gather(key = "key", value = "value") %>%
  ggplot(aes(x = value, fill = key)) +
  geom_histogram(binwidth = 0.1, alpha=.6) +
  scale_fill_manual(name = "", values=c("#f68060", "#57b2eb")) +
  labs(title ="Simulation 8, M adjusted",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()

plot_pred_tau_16
```



Runing time:

```
start_time_16 - end_time_16
```

```
## Time difference of -1.733859 mins
```

RMSE:

```
rmse_8.with_M <- fun.rmse(predicted = pred_tau_8.with_M$predictions, true = tau_2)

rmse_8.with_M
```

```
## [1] 3.201408
```

Coverage:

```
coverage_8.with_M <- fun.coverage(pred_tau_8.with_M, tau_2)

coverage_8.with_M
```

```
## [1] 0.67
```

Estimated ATE:

```r
ATE_est_8.with_M <- average_treatment_effect(cf8.with_M)

ATE_est_8.with_M
```

```
##  estimate   std.err
## 1.8739371 0.2197631
```

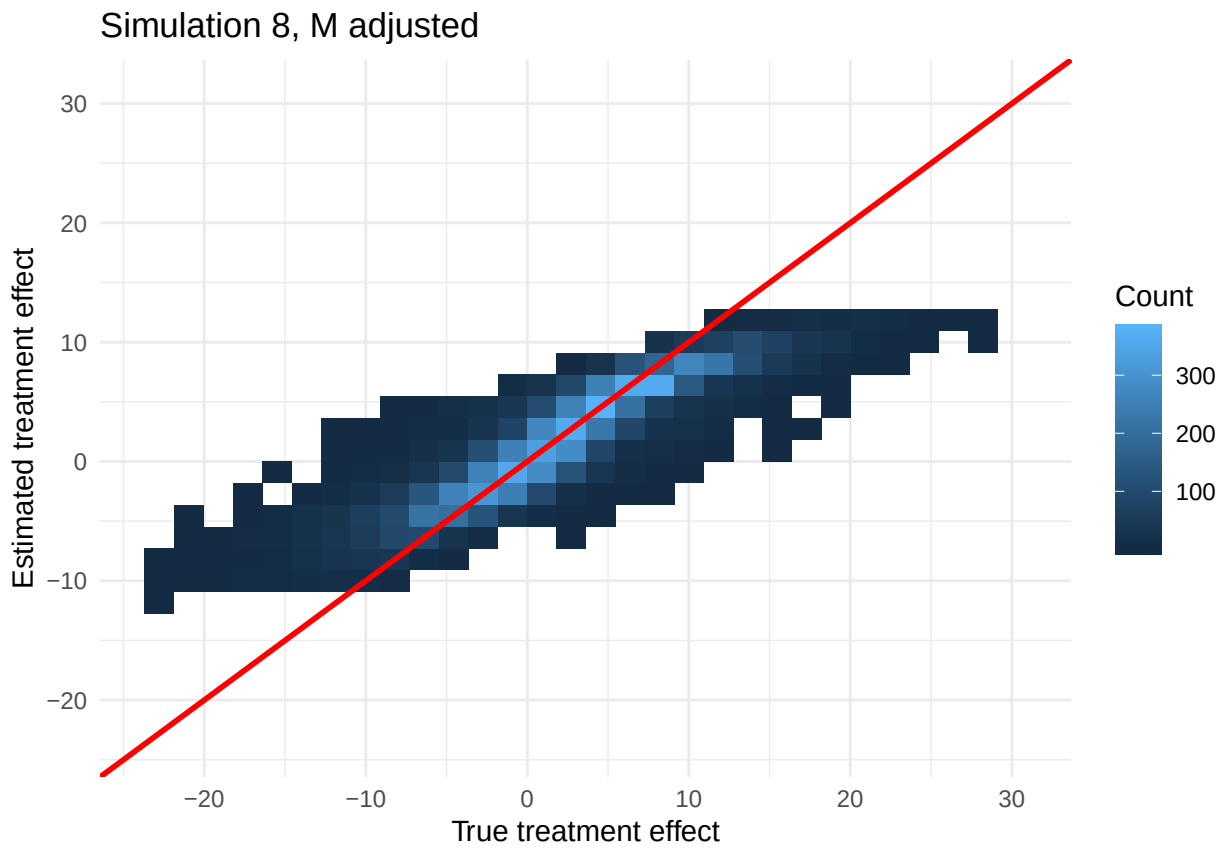
The *proportional difference in the ATE estimates* for the whole population:

```r
fun.diff_ATE(ATE_est = ATE_est_8.with_M, ATE_true = mean(tau_2))
```

```
## [1] "Proportional mean of the differences:"
##   estimate
## 0.05929896
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##    estimate    estimate
## -0.05102032  0.16961823
```

```r
true_vs_pred_8.with_M <- as.data.frame(cbind(tau_2, pred_tau_8.with_M$predictions))

colnames(true_vs_pred_8.with_M) <- c("tau", "pred_tau")

plot16 <- ggplot(data = true_vs_pred_8.with_M, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 8, M adjusted",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_8.with_M), max(true_vs_pred_8.with_M)),
       y = c(min(true_vs_pred_8.with_M), max(true_vs_pred_8.with_M)))

plot16
```

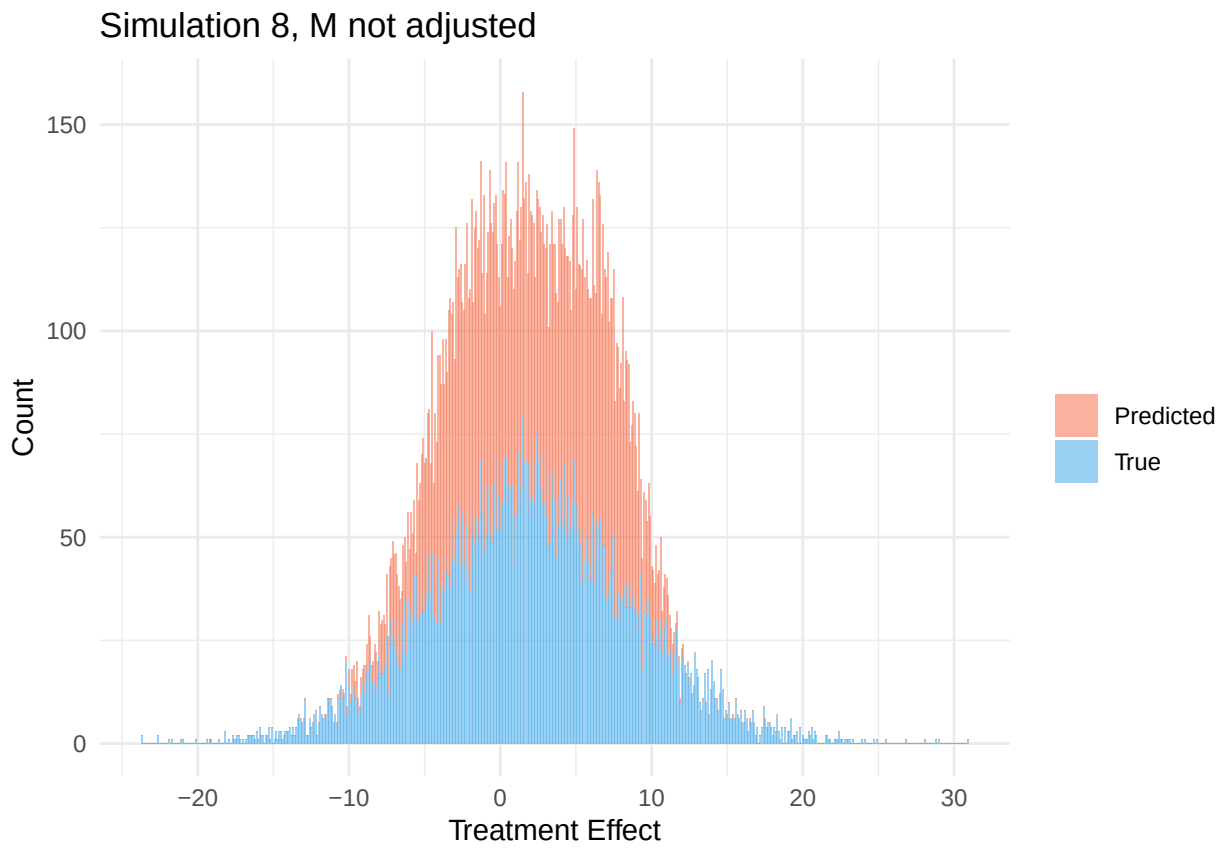
```
## Warning: Removed 2 rows containing missing values (geom_tile).
```



$M \notin \mathbb{S}$ $(X \cup Z \cup C \in \mathbb{S})$:

```
# Estimate causal forest
start_time_17 <- Sys.time() #Recording the running time

#Fitting the model
cf8.no_M <- grf::causal_forest(cbind(X, Z, C), y_8, w_4, orthog.boosting = TRUE)


end_time_17 <- Sys.time()

#Predicted values

pred_tau_8.no_M <- predict(cf8.no_M, estimate.variance = TRUE)

plot_pred_tau_17 <- cbind(pred_tau_8.no_M$predictions, tau_2) %>%
  as.data.frame() %>%
  dplyr::rename(Predicted = V1) %>%
  dplyr::rename(True = tau_2) %>%
  gather(key = "key", value = "value") %>%
  ggplot(aes(x = value, fill = key)) +
  geom_histogram(binwidth = 0.1, alpha=.6) +
  scale_fill_manual(name = "", values=c("#f68060", "#57b2eb")) +
  labs(title ="Simulation 8, M not adjusted",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()
```

```
plot_pred_tau_17
```



Runing time:

```
start_time_17 - end_time_17
```

```
## Time difference of -1.204982 mins
```

RMSE:

```
rmse_8.no_M <- fun.rmse(predicted = pred_tau_8.no_M$predictions, true = tau_2)
```

Coverage:

```
coverage_8.no_M <- fun.coverage(pred_tau_8.no_M, tau_2)

coverage_8.no_M
```

```
## [1] 0.6671
```

Estimated ATE:

```r
ATE_est_8.no_M <- average_treatment_effect(cf8.no_M)

ATE_est_8.no_M
```

```
##  estimate   std.err
## 1.8671429 0.2218439
```

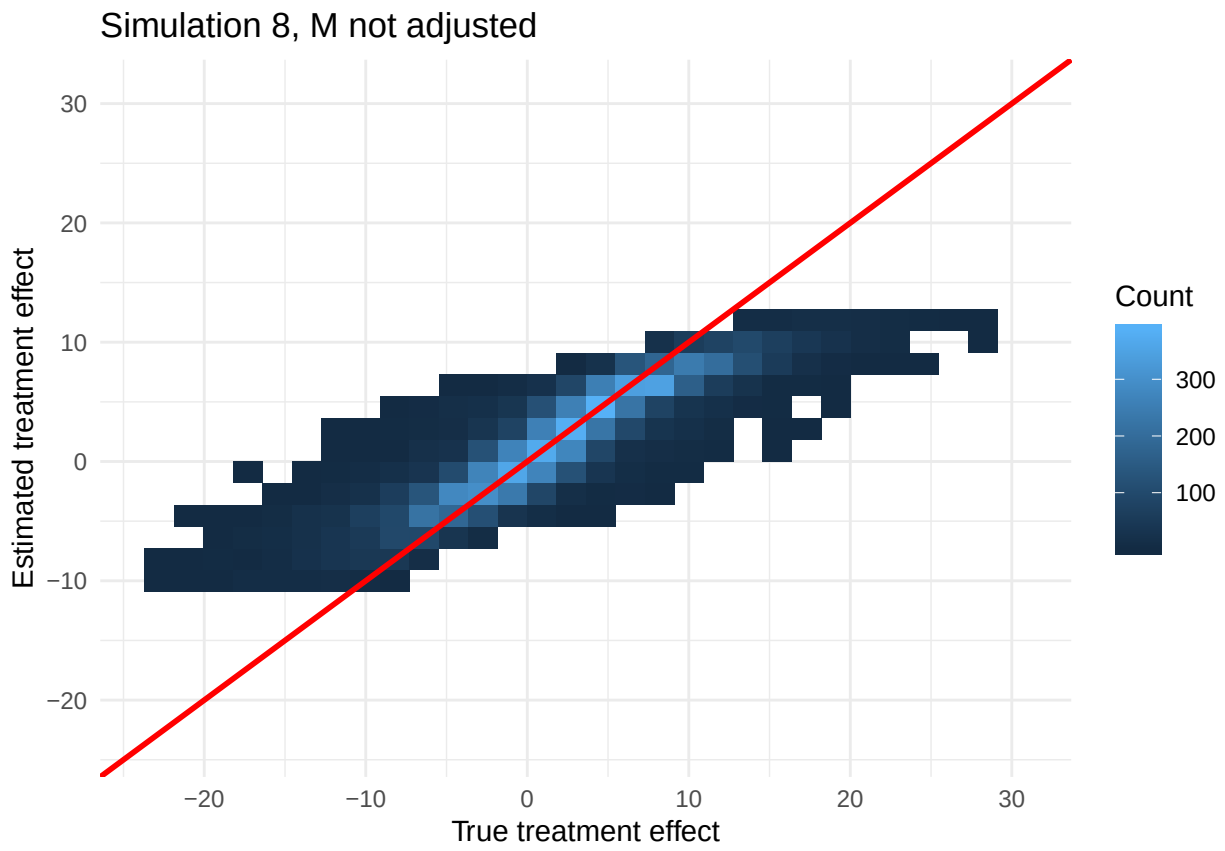
The *proportional difference in the ATE estimates* for the whole population:

```r
fun.diff_ATE(ATE_est = ATE_est_8.no_M, ATE_true = mean(tau_2))
```

```
## [1] "Proportional mean of the differences:"
##   estimate
## 0.06270957
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##    estimate    estimate
## -0.04865424  0.17407338
```

```r
true_vs_pred_8.no_M <- as.data.frame(cbind(tau_2, pred_tau_8.no_M$predictions))

colnames(true_vs_pred_8.no_M) <- c("tau", "pred_tau")

plot17 <- ggplot(data = true_vs_pred_8.no_M, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 8, M not adjusted",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_8.no_M), max(true_vs_pred_8.no_M)),
       y = c(min(true_vs_pred_8.no_M), max(true_vs_pred_8.no_M)))

plot17
```

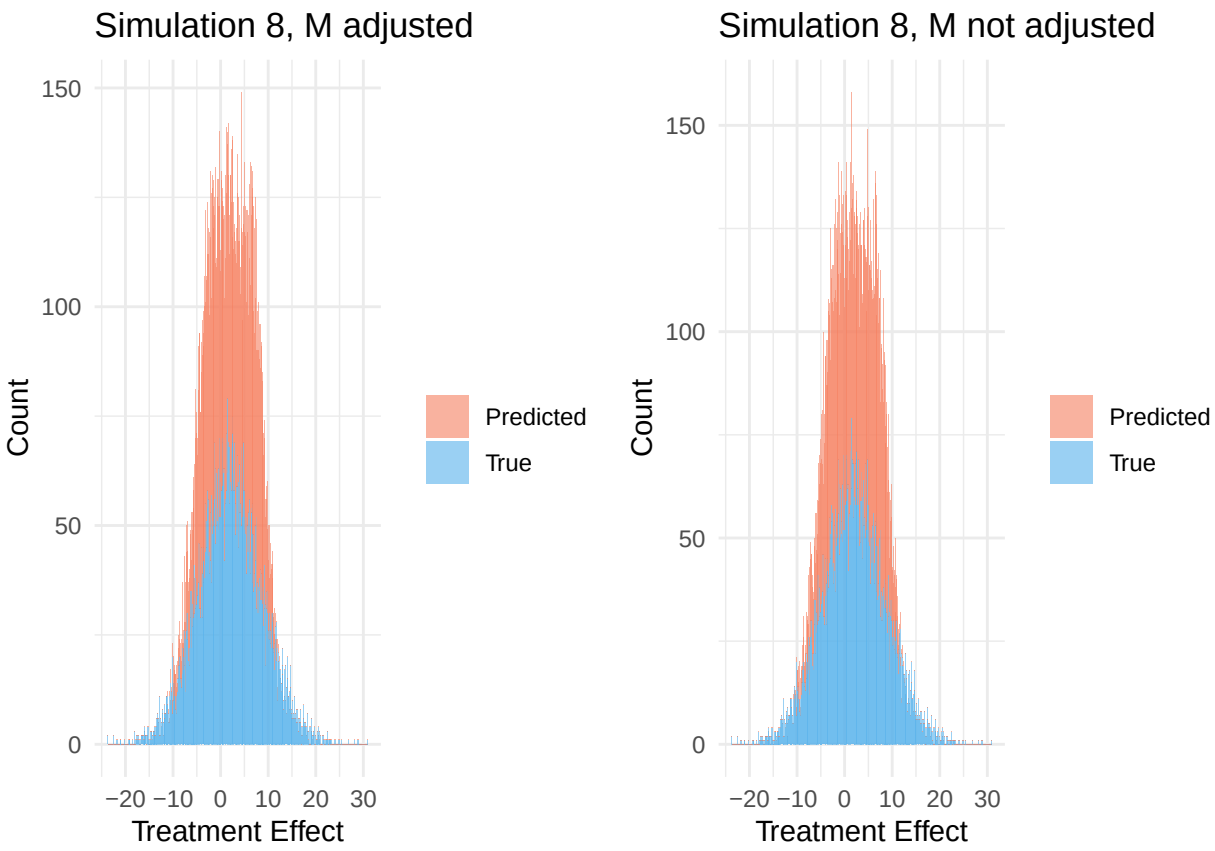
```
## Warning: Removed 2 rows containing missing values (geom_tile).
```



Summary

Predicted $\hat{\tau}s$:

```
grid.arrange(plot_pred_tau_16, plot_pred_tau_17, nrow = 1)
```

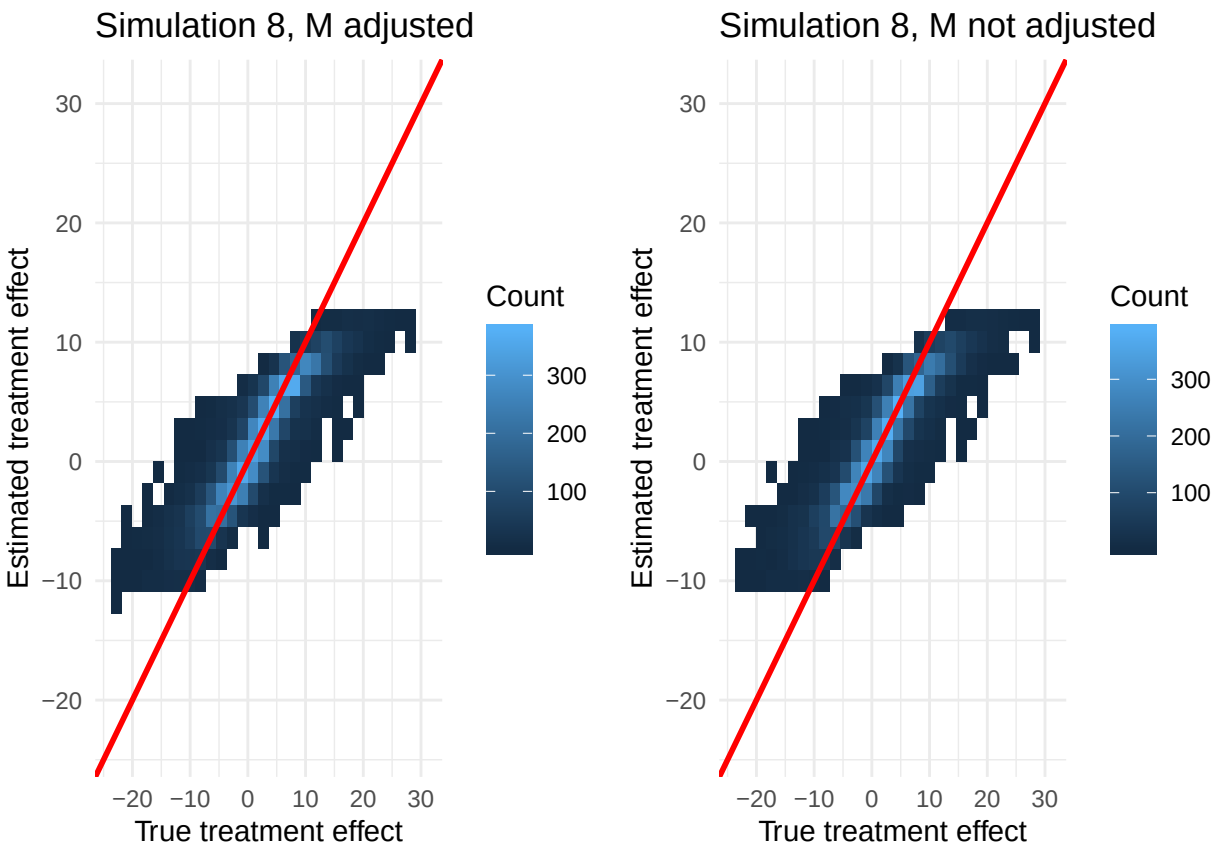


True τ vs. predicted $\hat{\tau}$:

```
grid.arrange(plot16, plot17, nrow = 1)
```

```
## Warning: Removed 2 rows containing missing values (geom_tile).
```

```
## Warning: Removed 2 rows containing missing values (geom_tile).
```



RMSEs:

```
rmse_8 <- as.data.frame(c(rmse_8.with_M, rmse_8.no_M))

rownames(rmse_8) <- c("$M$ adjusted", "$M$ not adjusted")

colnames(rmse_8) <- c("RMSE")

knitr::kable(rmse_8, escape = FALSE)
```

	RMSE
M adjusted	3.201408
M not adjusted	3.218593

Coverages:

```
coverage_8 <- as.data.frame(c(coverage_8.with_M, coverage_8.no_M))

rownames(coverage_8) <-  c("$M$ adjusted", "$M$ not adjusted")

colnames(coverage_8) <- c("Coverage")

knitr::kable(coverage_8, escape = FALSE)
```

	Coverage
M adjusted	0.6700
M not adjusted	0.6671

LaTeX:

```
knitr::kable(rmse_8, format = "latex",escape = FALSE)
```

	RMSE
M adjusted	3.201408
M not adjusted	3.218593

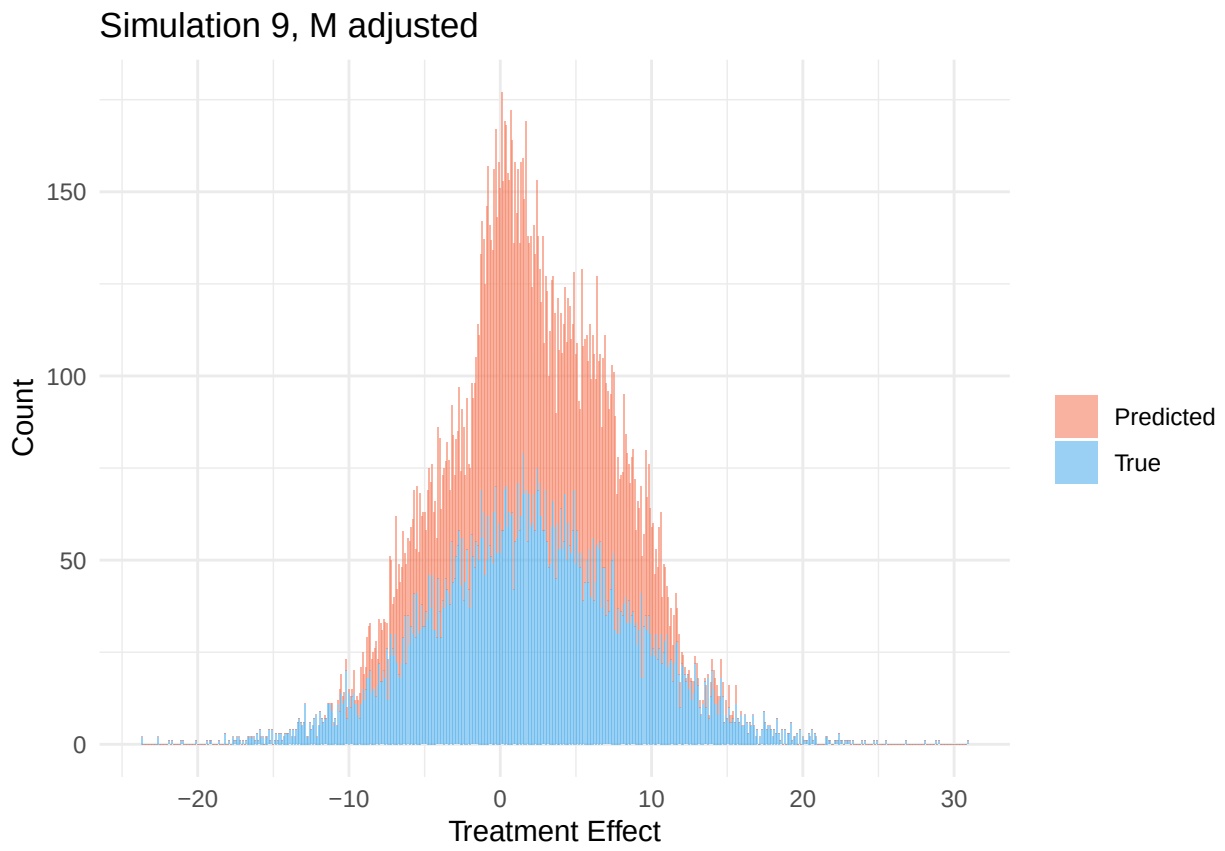
```
knitr::kable(coverage_8, format = "latex",escape = FALSE)
```

	Coverage
M adjusted	0.6700
M not adjusted	0.6671

3.9 Heterogeneous Treatment Effect with Confounded Assignment, Including Covariates Affecting to Output and a Impure Local M-Structure

With M ($X \cup Z \cup C \cup M \in \mathbb{S}$):

```
# Estimate causal forest
start_time_18 <- Sys.time() #Recording the running time

#Fitting the model
cf9.with_M <- grf::causal_forest(cbind(X, Z, C, m), y_9, w_5, orthog.boosting = TRUE)


end_time_18 <- Sys.time()

#Predicted values

pred_tau_9.with_M <- predict(cf9.with_M, estimate.variance = TRUE)

plot_pred_tau_18 <- cbind(pred_tau_9.with_M$predictions, tau_2) %>%
  as.data.frame() %>%
  dplyr::rename(Predicted = V1) %>%
  dplyr::rename(True = tau_2) %>%
  gather(key = "key", value = "value") %>%
  ggplot(aes(x = value, fill = key)) +
  geom_histogram(binwidth = 0.1, alpha=.6) +
  scale_fill_manual(name = "", values=c("#f68060", "#57b2eb")) +
  labs(title ="Simulation 9, M adjusted",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()

plot_pred_tau_18
```



Runing time:

```
start_time_18 - end_time_18
```

```
## Time difference of -1.2066 mins
```

RMSE:

```
rmse_9.with_M <- fun.rmse(predicted = pred_tau_9.with_M$predictions, true = tau_2)

rmse_9.with_M
```

```
## [1] 3.291505
```

Coverage:

```
coverage_9.with_M <- fun.coverage(pred_tau_9.with_M, tau_2)

coverage_9.with_M
```

```
## [1] 0.6589
```

Estimated ATE:

```r
ATE_est_9.with_M <- average_treatment_effect(cf9.with_M)

ATE_est_9.with_M
```

```
##  estimate   std.err
## 2.0312799 0.2196883
```

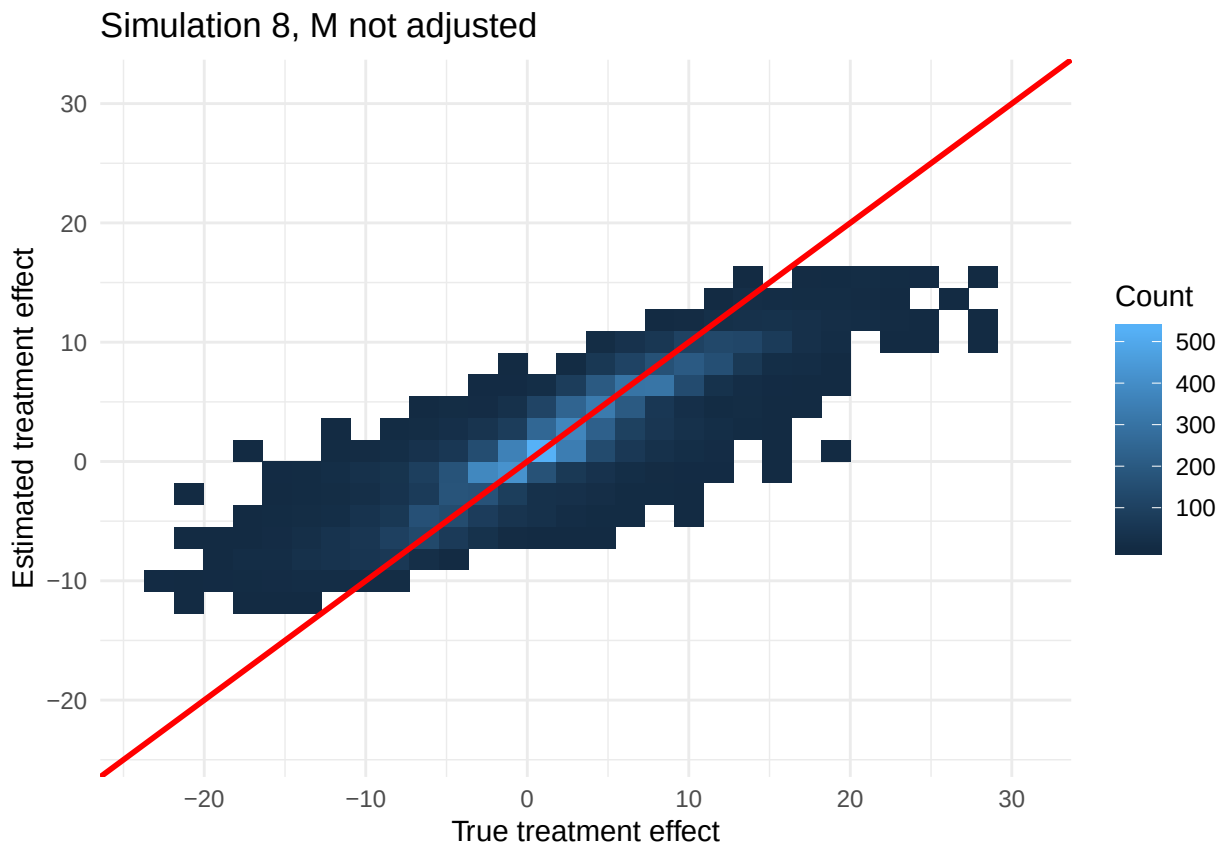
The *proportional difference in the ATE estimates* for the whole population:

```r
fun.diff_ATE(ATE_est = ATE_est_9.with_M, ATE_true = mean(tau_2))
```

```
## [1] "Proportional mean of the differences:"
##    estimate
## -0.01968584
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##   estimate   estimate
## -0.1299676  0.0905959
```

```r
true_vs_pred_9.with_M <- as.data.frame(cbind(tau_2, pred_tau_9.with_M$predictions))

colnames(true_vs_pred_9.with_M) <- c("tau", "pred_tau")

plot18 <- ggplot(data = true_vs_pred_9.with_M, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 8, M not adjusted",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_9.with_M), max(true_vs_pred_9.with_M)),
       y = c(min(true_vs_pred_9.with_M), max(true_vs_pred_9.with_M)))

plot18
```

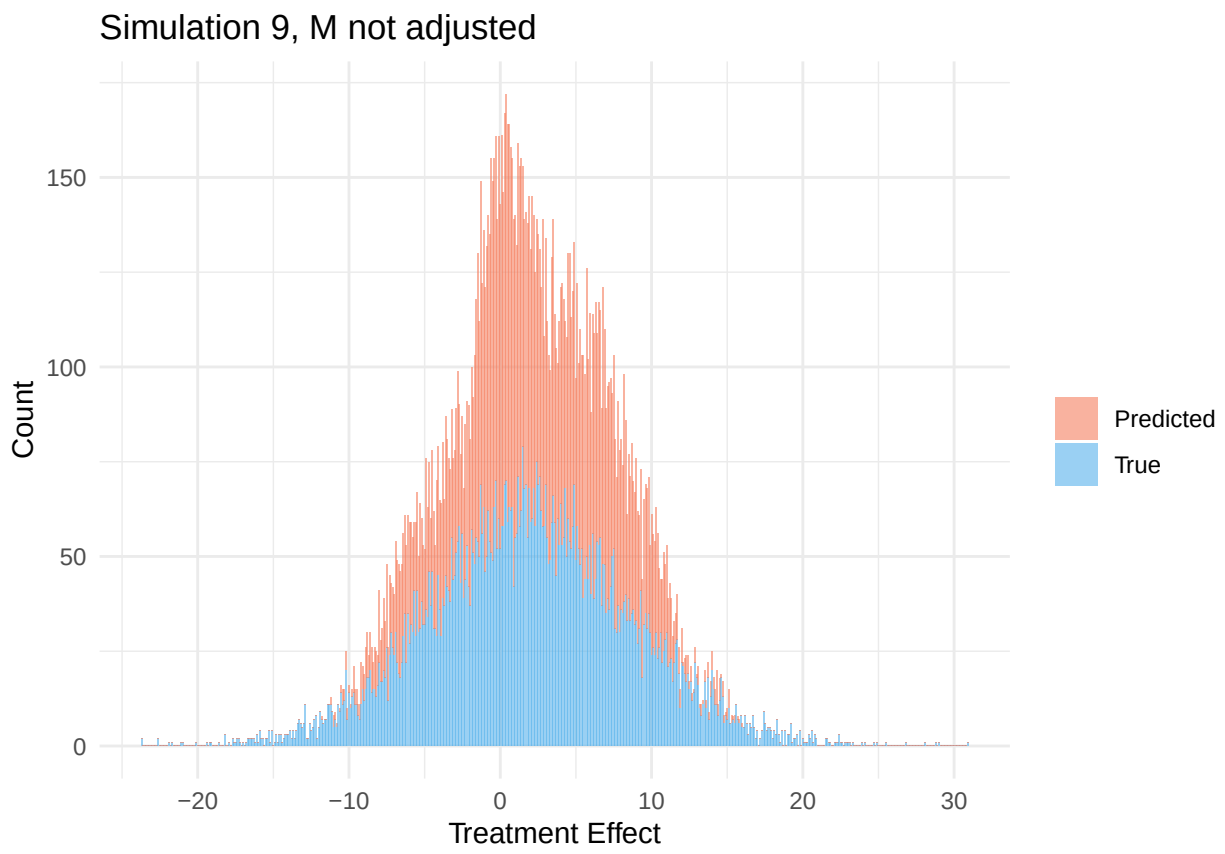
```
## Warning: Removed 2 rows containing missing values (geom_tile).
```



$M \notin \mathbb{S}$ $(X \cup Z \cup C \in \mathbb{S})$:

```
# Estimate causal forest
start_time_19 <- Sys.time() #Recording the running time

#Fitting the model
cf9.no_M <- grf::causal_forest(cbind(X, Z, C), y_9, w_5, orthog.boosting = TRUE)


end_time_19 <- Sys.time()

#Predicted values

pred_tau_9.no_M <- predict(cf9.no_M, estimate.variance = TRUE)

plot_pred_tau_19 <- cbind(pred_tau_9.no_M$predictions, tau_2) %>%
  as.data.frame() %>%
  dplyr::rename(Predicted = V1) %>%
  dplyr::rename(True = tau_2) %>%
  gather(key = "key", value = "value") %>%
  ggplot(aes(x = value, fill = key)) +
  geom_histogram(binwidth = 0.1, alpha=.6) +
  scale_fill_manual(name = "", values=c("#f68060", "#57b2eb")) +
  labs(title ="Simulation 9, M not adjusted",
       x = "Treatment Effect", y = "Count") +
  theme_minimal()
```

```
plot_pred_tau_19
```



Runing time:

```
start_time_19 - end_time_19
```

```
## Time difference of -1.202041 mins
```

RMSE:

```
rmse_9.no_M <- fun.rmse(predicted = pred_tau_9.no_M$predictions, true = tau_2)

rmse_9.no_M
```

```
## [1] 3.279869
```

Coverage:

```
coverage_9.no_M <- fun.coverage(pred_tau_9.no_M, tau_2)

coverage_9.no_M
```

```
## [1] 0.6664
```

Estimated ATE:

```
ATE_est_9.no_M <- average_treatment_effect(cf9.no_M)

ATE_est_9.no_M
```

```
##  estimate   std.err
## 2.0584609 0.2217999
```

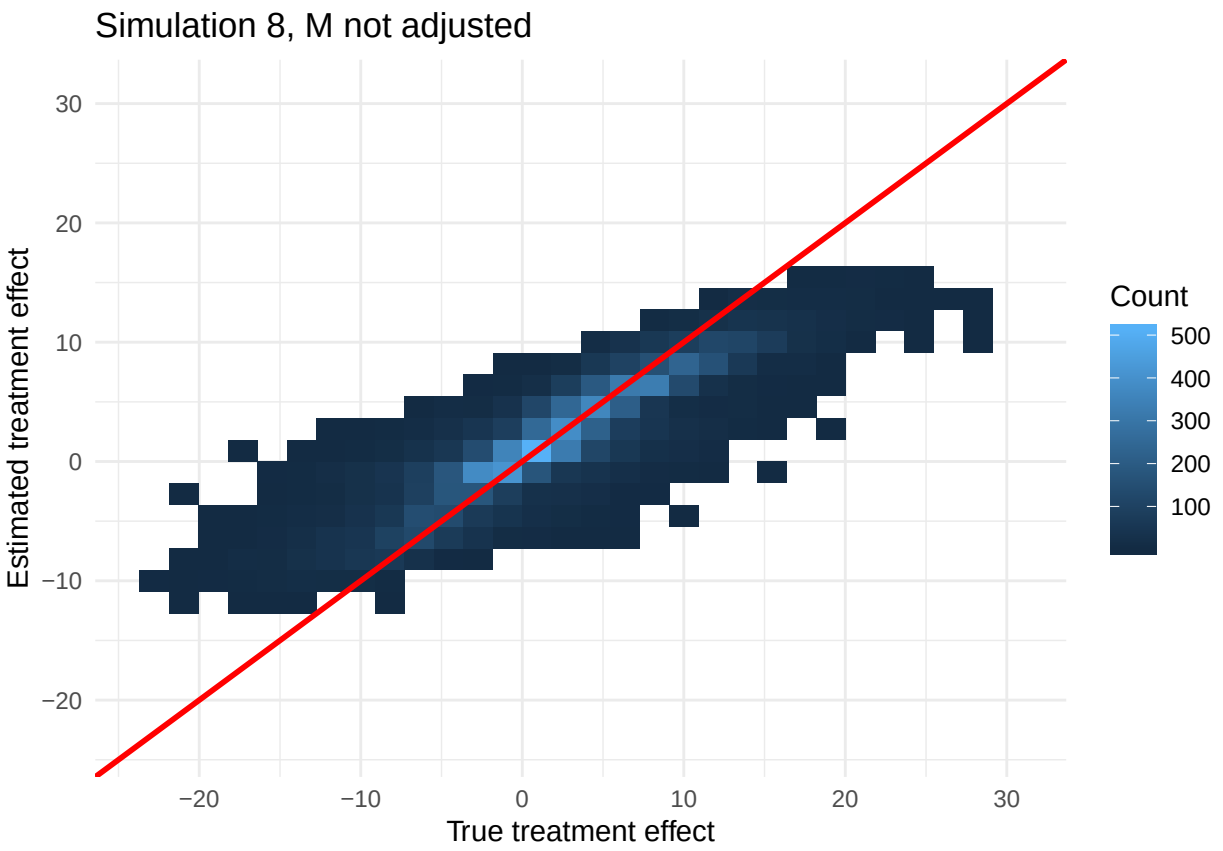
The *proportional difference in the ATE estimates* for the whole population:

```
fun.diff_ATE(ATE_est = ATE_est_9.no_M, ATE_true = mean(tau_2))
```

```
## [1] "Proportional mean of the differences:"
##   estimate
## -0.0333305
## [1] "Proportional mean of the differences, 95 % confidence intervals:"
##    estimate    estimate
## -0.14467221  0.07801121
```

```
true_vs_pred_9.no_M <- as.data.frame(cbind(tau_2, pred_tau_9.no_M$predictions))

colnames(true_vs_pred_9.no_M) <- c("tau", "pred_tau")

plot19<- ggplot(data = true_vs_pred_9.no_M, aes(x = tau, y = pred_tau)) +
  geom_bin2d() +
  geom_abline(slope = 1, intercept = 0, colour = "red", size = 1) +
  theme_minimal() +
  labs(title = "Simulation 8, M not adjusted",
       x = "True treatment effect", y = "Estimated treatment effect", fill = "Count") +
  lims(x = c(min(true_vs_pred_9.no_M), max(true_vs_pred_9.no_M)),
       y = c(min(true_vs_pred_9.no_M), max(true_vs_pred_9.no_M)))

plot19
```

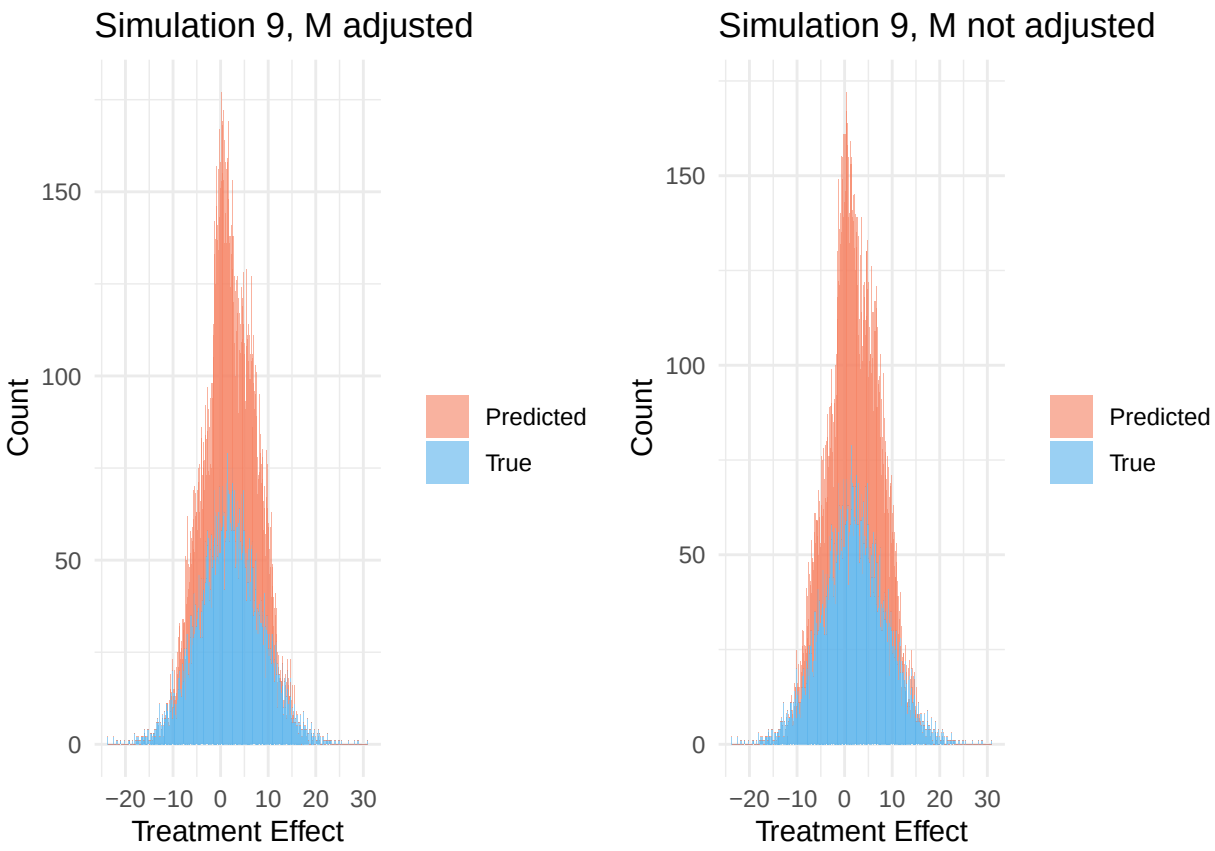
```
## Warning: Removed 2 rows containing missing values (geom_tile).
```



Summary

Predicted $\hat{\tau}s$:

```
grid.arrange(plot_pred_tau_18, plot_pred_tau_19, nrow = 1)
```

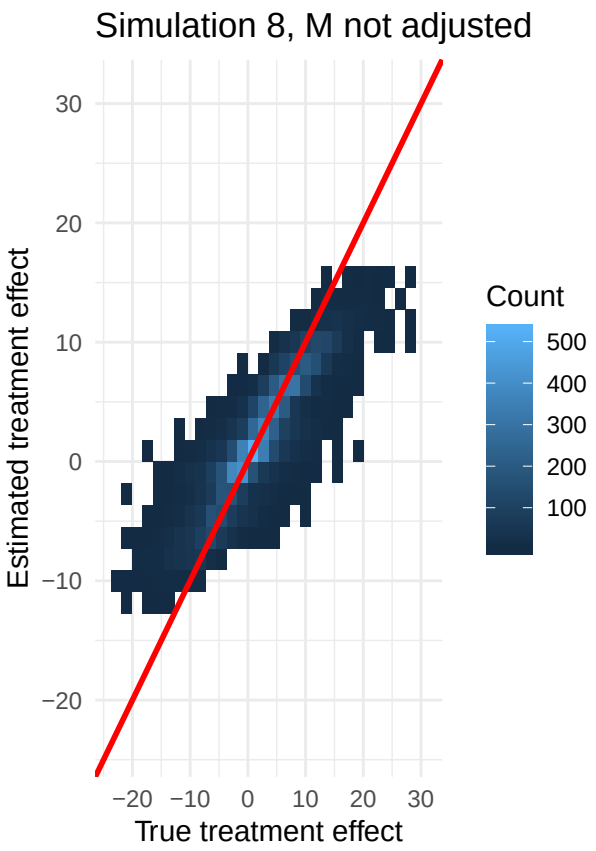


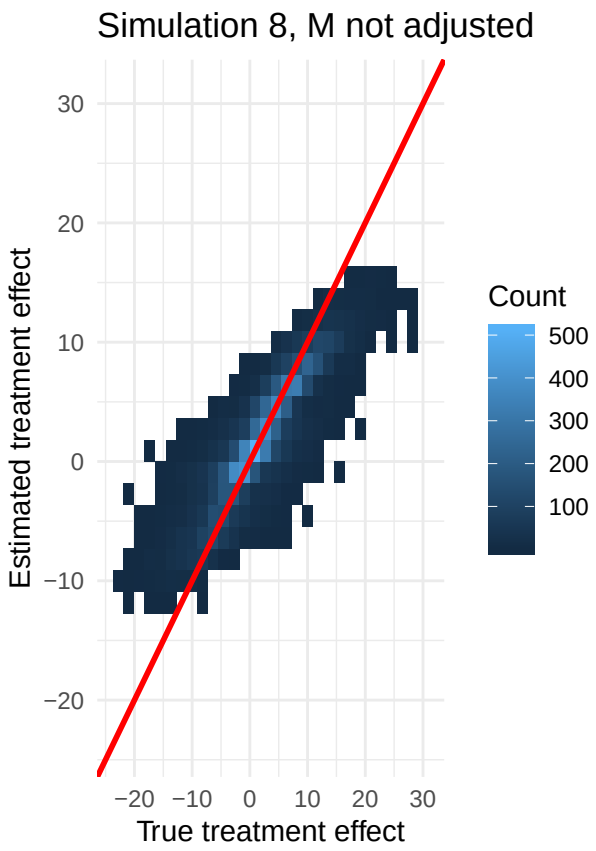
True τ vs. predicted $\hat{\tau}$:

```
grid.arrange(plot18, plot19, nrow = 1)
```

```
## Warning: Removed 2 rows containing missing values (geom_tile).
```

```
## Warning: Removed 2 rows containing missing values (geom_tile).
```





RMSEs:

```
rmse_9 <- as.data.frame(c(rmse_9.with_M, rmse_9.no_M))

rownames(rmse_9) <- c("$M$ adjusted", "$M$ not adjusted")

colnames(rmse_9) <- c("RMSE")

knitr::kable(rmse_9, escape = FALSE)
```

	RMSE
M adjusted	3.291505
M not adjusted	3.279869

Coverages:

```
coverage_9 <- as.data.frame(c(coverage_9.with_M, coverage_9.no_M))

rownames(coverage_9) <-  c("$M$ adjusted", "$M$ not adjusted")

colnames(coverage_9) <- c("Coverage")

knitr::kable(coverage_9, escape = FALSE)
```

	Coverage
M adjusted	0.6589
M not adjusted	0.6664

LaTeX:

```
knitr::kable(rmse_9, format = "latex",escape = FALSE)
```

	RMSE
M adjusted	3.291505
M not adjusted	3.279869

```
knitr::kable(coverage_9, format = "latex",escape = FALSE)
```

	Coverage
M adjusted	0.6589
M not adjusted	0.6664