Gerber and Green (2012) Chapter 3 Problem 7

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This script shows how to conduct the randomization inference procedure in Gerber and Green (2012) Chapter 3 Problem 7 three different ways: using the ri2 package, using the ri package, and by hand with a loop.

Chapter 3 Problem 7

A diet and exercise program advertises that it causes everyone who is currently starting a diet to lose at least seven pounds more than they otherwise would have during the rst two weeks. Use randomization inference (the procedure described in section 3.4) to test the hypothesis that ti = 7 for all i. e treatment group's weight losses a er two weeks are $\{2, 11, 14, 0, 3\}$ and the control group's weight losses are $\{1, 0, 0, 4, 3\}$. In order to test the hypothesis ti = 7 for all i using the randomization inference methods discussed in this chapter, subtract 7 from each outcome in the treatment group so that the exercise turns into the more familiar test of the sharp null hypothesis that ti = 0 for all i. When describ- ing your results, remember to state the null hypothesis clearly, and explain why you chose to use a one-sided or two-sided test.

```
# Create dataset

d <- rep(c(0, 1), c(5, 5))

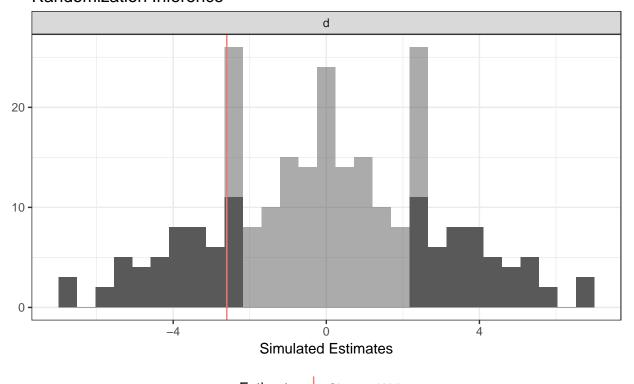
y <- rep(c(1, 0, 0, 4, 3, -5, 4, 7, -7, -4))

data3.7 <- data.frame(d, y)
```

In ri2

```
library(ri2)
# Declare randomization procedure
declaration <- declare_ra(N = 10, m = 5)
# Conduct Randomization Inference
ri2_out <- conduct_ri(y ~ d,
                      declaration = declaration,
                      assignment = "d",
                      sharp_hypothesis = 0,
                      data = data3.7)
summary(ri2_out)
     coefficient estimate two_tailed_p_value null_ci_lower null_ci_upper
## 1
                     -2.6
                                    0.4126984
                                                       -5.4
plot(ri2_out)
```

Randomization Inference



Estimate Observed Value

In ri

```
library(ri)

# all possible permutations
perms <- genperms(data3.7$d)

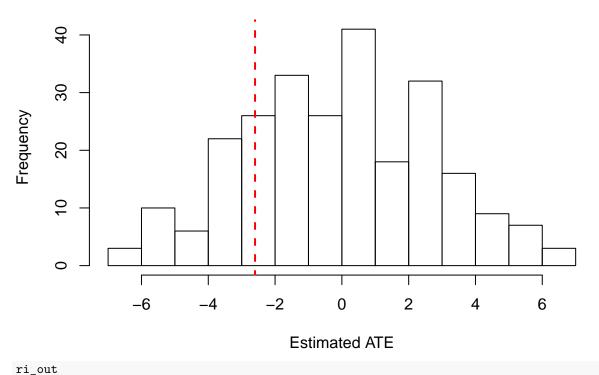
# probability of treatment
probs <- genprobexact(data3.7$d)

# estimate the ATE
ate <- estate(data3.7$y, data3.7$d, prob = probs)

## Conduct Sharp Null Hypothesis Test of Zero Effect for Each Unit

# generate potential outcomes under sharp null of no effect
Ys <- genouts(data3.7$y, data3.7$d, ate = 0)
# generate sampling dist. under sharp null
distout <- gendist(Ys, perms, prob = probs)
# display characteristics of sampling dist. for inference
ri_out <- dispdist(distout, ate)</pre>
```

Distribution of the Estimated ATE



```
ri_out
```

```
## $two.tailed.p.value
## [1] 0.4126984
##
## $two.tailed.p.value.abs
## [1] 0.4126984
##
## $greater.p.value
## [1] 0.8373016
##
## $lesser.p.value
## [1] 0.2063492
##
## $quantile
   2.5% 97.5%
##
   -5.4
         5.4
##
## $sd
## [1] 2.829213
##
## $exp.val
## [1] 0
```

By hand

```
perms <- combn(10, 5, tabulate, nbins = 10)
sims <- ncol(perms)</pre>
```

```
observed_ate <- with(data3.7, mean(y[d == 1]) - mean(y[d == 0]))
simulated_ates <- rep(NA, sims)

for (i in 1:sims){
    data3.7$Z_sim <- perms[,i]
    simulated_ates[i] <- with(data3.7, mean(y[Z_sim == 1]) - mean(y[Z_sim == 0]))
}

p_two_tailed <- mean(abs(simulated_ates) >= abs(observed_ate))
p_upper <- mean(simulated_ates >= observed_ate)
p_lower <- mean(simulated_ates <= observed_ate)

c(observed_ate, p_two_tailed, p_upper, p_lower)

## [1] -2.6000000  0.4126984  0.8373016  0.2063492

hist(simulated_ates, breaks = 10)
abline(v = observed_ate, col = "red")</pre>
```

Histogram of simulated_ates

