Assignment 3

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Question 1

a)

A Runs Test tests a set of binary variables $X_1, ..., X_n$ to verify if the variables occur randomly.

H_0: variables occur randomly, i.e. knowing $X_1, ..., X_n$ does not help predict X_{n+1}.

H_A: variables are not random, i.e. knowing some part of the sequence can help predict subsequent variables.

As the variables are binary, they will take the value 0 or 1. The number of 0s is n_0 and the number of 1s is n_1, where:

$n_0 = n - \sum_{i=1}^{n} X_i$

$n_1 = \sum_{i=1}^{n} X_i$

To perform a Runs Test the observations are combined into one collection of $n = n_0 + n_1$ observations and arranged in increasing order of magnitude or observation. They are labeled according to which set they originally came from. A run is a group of two or more sequential values of 0 or 1.

Let R denote the number of runs in the combined ordered sample of $X \in \{0, 1\}$. Under H_0, R can be approximated as a normally distributed random variable, assuming both n_0 and n_1 are sufficiently large.

$R = 1 + \sum_{i=2}^{n} I_{(X_i, X_{i-1})}$, where $I_{(X_i, X_{i-1})} = 0$ if $X_i = X_{i-1}$ and $I_{(X_i, X_{i-1})} = 1$ if $X_i \neq X_{i-1}$

$\bar{R} = \dfrac{2n_0n_1}{n} + 1$

$Var(\bar{R}) = \dfrac{2n_0n_1(2n_0n_1 - n)}{n^2(n-1)}$

With test statistic $Z = \dfrac{R - \bar{R}}{\sqrt{Var(\bar{R})}}$ where $Z \sim N(0, 1)$

b)

A small number of runs (a small value for R) would indicate that X_i is more likely to be the same as X_{i-1}. A large number means that X is fluctuating regularly between values and X is less likely to be the same as X_{i-1}.

c)

```
## 0 healthy, 1 diseased
X <- "HHHDDDHDDHHHHHDHHHHHHHHHHHDDDHHHHDDDHHHHDHHHDHH" %>%
  stringr::str_split("") %>% unlist() %>% `==`("D") %>% as.integer()

n <- length(X)
n_0 <- n - sum(X)
n_1 <- sum(X)
```

```
R <- 1 + sum(X[2:n] != X[1:n-1])
R_est <- 1 + 2*n_0*n_1/n
R_var <- (2*n_0*n_1*(2*n_0*n_1 - n))/(n^2*(n - 1))
Z <- (R - R_est)/sqrt(R_var)
p <- pnorm(Z)
cbind(R, R_est, R_var, Z, p)
```

```
##        R    R_est    R_var         Z          p
## [1,] 15 20.65957 7.974767 -2.004125 0.02252834
```

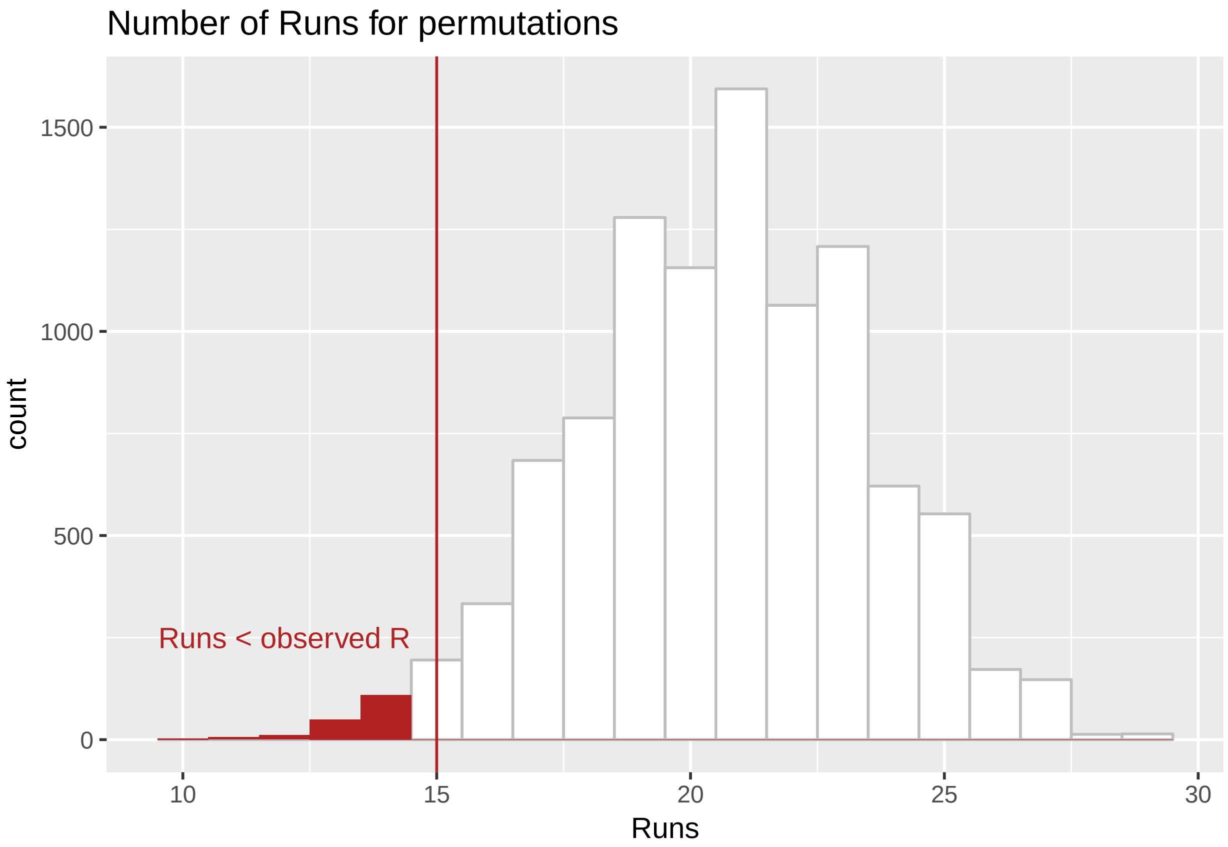
With p-value of 0.0225 we reject H_0 at the 5% level. We conclude that values are not randomly ordered.

d)

```
set.seed(101)

calc_R <- function(input)
  1 + sum(input[2:length(input)] != input[1:length(input)-1])

sample_R <- function(iter, input)
  input %>% sample() %>% calc_R()

obs_R <- calc_R(X)

N <- 1e4
perm_R <- 1:N %>% sapply(sample_R, input = X)

p <- sum(perm_R < obs_R)/length(perm_R)
p
```

```
## [1] 0.0179
```

```
ggplot() +
  geom_histogram(data = data.frame(x = perm_R[perm_R >= obs_R]),
                 aes(x = x), binwidth = 1, fill = "white", colour = "grey") +
  geom_histogram(data = data.frame(x = perm_R[perm_R < obs_R]),
                 aes(x = x), binwidth = 1, fill = "firebrick") +
  geom_vline(xintercept = obs_R, colour = "firebrick") +
  ggtitle("Number of Runs for permutations") +
  xlab("Runs") +
  geom_text(aes(x = 12, y = 250), label = "Runs < observed R", colour = "firebrick")
```



Because the number of runs is not a continuous variable, there is some ambiguity around whether the p-value should be calculated comparing values < or <= or even using some half point. I have decided to use < as it gives the test the highest power.

Given this we find a p-value of 0.0179. We reject H_0 at the 5% level. We conclude that values are not randomly ordered.

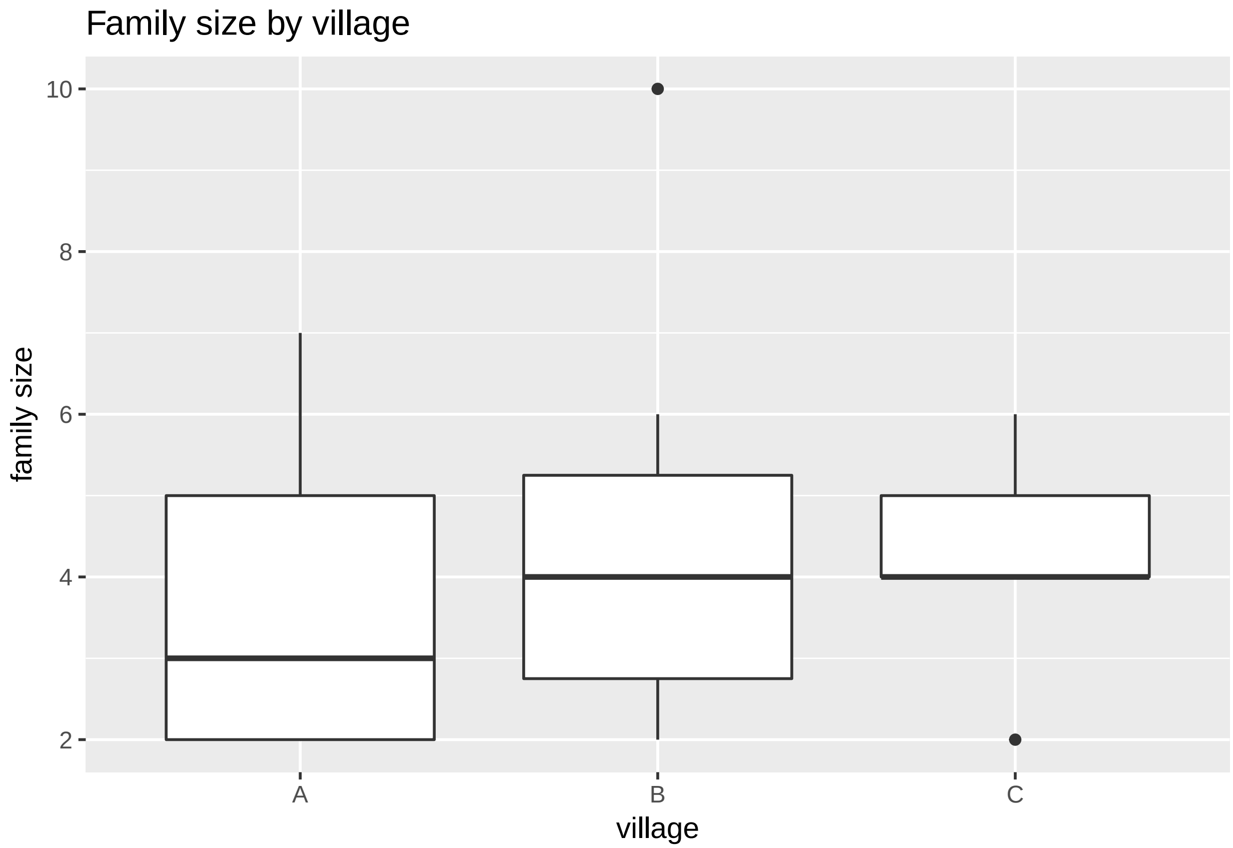
Question 2

a)

We could use a Poisson distribution

b)

```
dataset <- data.frame(
  size = c(2, 3, 2, 7, 5, 5, 3, 2, 6, 10, 3, 2, 2, 5, 6, 4, 4, 5, 4, 4, 6, 5, 4, 2),
  village = rep(c("A", "B", "C"), c(9, 8, 7))
)

ggplot(dataset, aes(x = village, y = size)) +
  geom_boxplot() +
  ggtitle("Family size by village") +
  ylab("family size")
```



```
## village means
tapply(dataset$size, dataset$village, mean) %>% round(digits = 4)
```

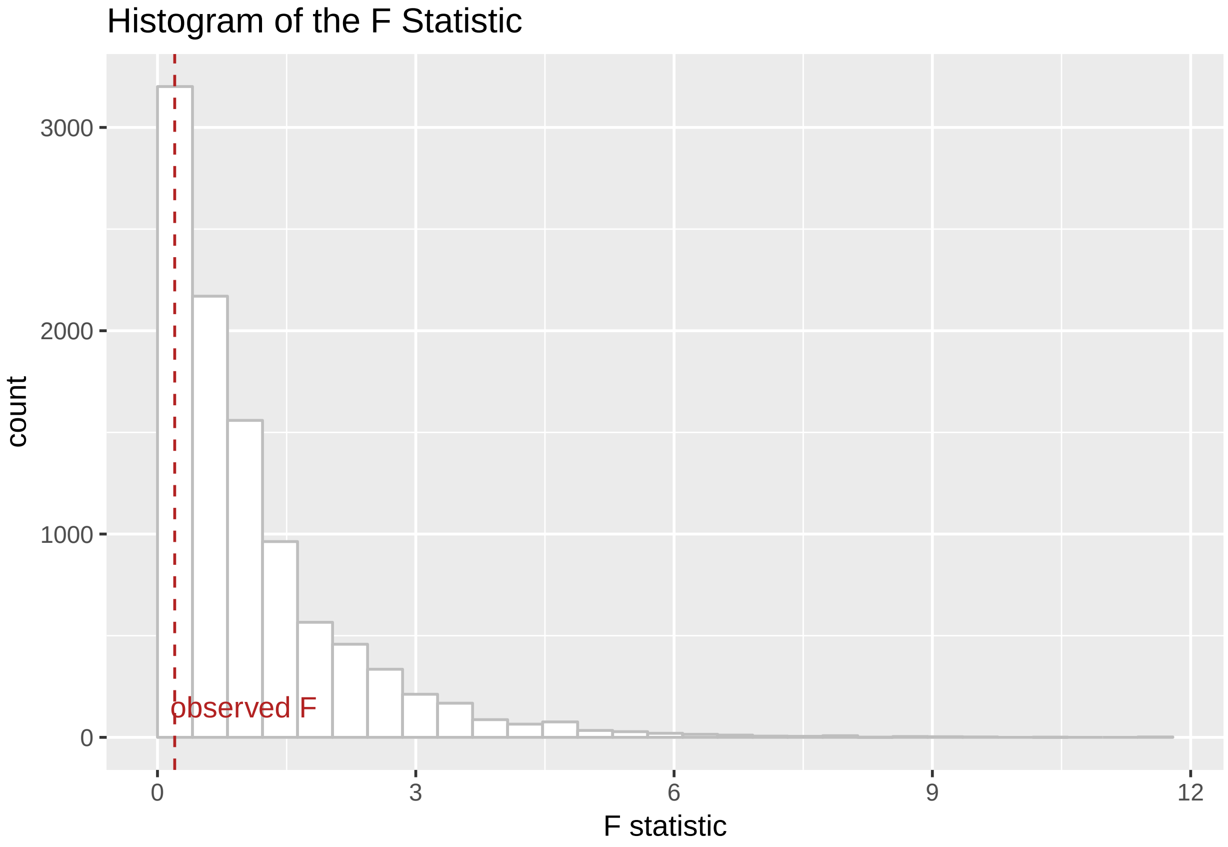
```
##      A      B      C
## 3.8889 4.5000 4.2857
```

c)

```
calc_F <- function(input)
  input[["fstatistic"]]["value"]

obs_F <- lm(size ~ village, data = dataset) %>%
  summary() %>% calc_F() %>% round(digits = 3)

N <- 1e4
set.seed(150)
perm_F <- 1:N %>%
  lapply(function(i) sample(dataset$village)) %>%
  lapply(function(groups) lm(dataset$size ~ groups)) %>%
  lapply(summary) %>%
  sapply(calc_F) %>%
  round(digits = 3)

p <- sum(perm_F >= obs_F)/N
p
```

```
## [1] 0.8319
```

```
ggplot() +
  geom_histogram(data = data.frame(x = perm_F), aes(x = x),
                 breaks = seq(from = 0, to = max(perm_F), length.out = 30),
                 fill = "white", colour = "grey") +
  geom_vline(xintercept = obs_F, colour = "firebrick", linetype = "dashed") +
  ggtitle("Histogram of the F Statistic") +
  xlab("F statistic") +
  geom_text(aes(x = 1, y = 150), label = "observed F", colour = "firebrick")
```



Given a p-value of 0.8319 we fail to reject H_0 and find that there is not difference in the village mean family sizes.

d)

```
draw_hist <- function(perm_values, observed) {
  print(
    ggplot() +
      geom_histogram(data = data.frame(x = perm_values), aes(x = x),
                     breaks = seq(from = 0, to = max(perm_values), length.out = 10),
                     fill = "white", colour = "grey") +
      geom_vline(xintercept = observed, colour = "firebrick", linetype = "dashed") +
      ggtitle("Histogram of permutation values") +
      xlab("test statistic"))
}

permutation_test = function(test_func, dataset, niter, comparator) {
  test_stat <- lm(size ~ village, data = dataset) %>%
    summary() %>% test_func() %>% round(digits = 3)
  set.seed(150)
  perms <- 1:niter %>%
    lapply(function(i) sample(dataset$village)) %>%
    lapply(function(groups) lm(dataset$size ~ groups)) %>%
    lapply(summary) %>%
    sapply(test_func) %>%
    round(digits = 3)

  draw_hist(perms, test_stat)
  sum(comparator(perms, test_stat))/niter
}
```

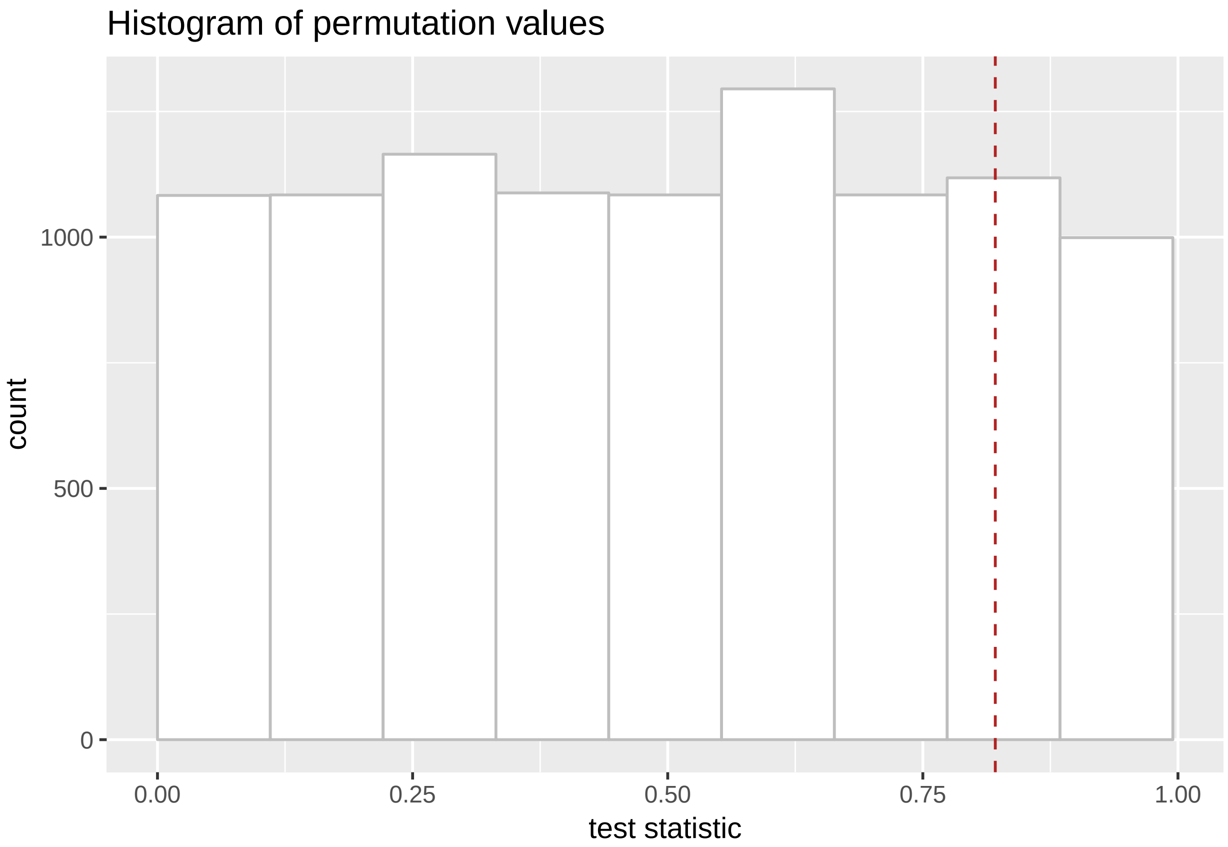
e)

A p-value is the probability of obtaining a test statistic as, or more, extreme than the test statistic observed under the null hypothesis. The p-value is a suitable test statistic to use in a permutation test as the relationship between the F statistic and the p-value means that the result of the ANOVA is preserved. Increasing the F statistic will always result in a decrease in the p-value so long as the degrees of freedom remain the same. Meaning that for all $F_x > F_y$, there will be $p_x < p_y$.

Using the same `set.seed` value will mean that the permutations of grouping values will be the same across tests even where the test statistic in question changes. Given the case above, the ratio of cases above/below the observed statistic will remain the same, giving the same final p-value.

The generated p-values appear to be drawn from a uniform distribution, and this is what we would expect under a null hypothesis.

```
calc_p <- function(input)
  pf(input$fstatistic, input$df[1]-1, input$df[2], lower.tail = FALSE)["value"]

p <- permutation_test(calc_p, dataset, 1e4, `<=`)
```



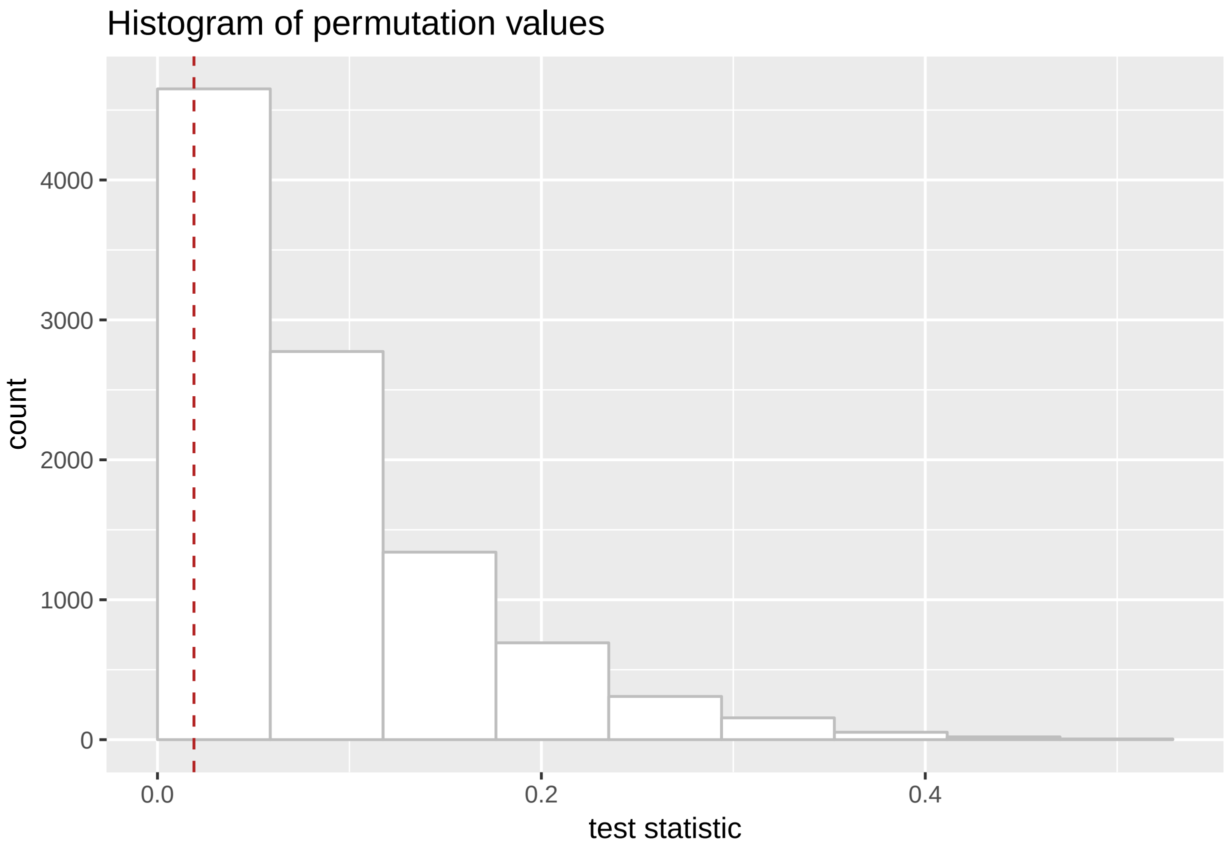
```
p
```

```
## [1] 0.8319
```

f)

A large R^2 value means the linear model fits the data well. This would also indicate that the F-statistic would be large as at least one of the coefficients in the model would be non-zero. This would mean that for all $F_x > F_y$ we have $R^2_x > R^2_y$.

```
calc_r2 <- function(input)
  input[["r.squared"]]

r2 <- permutation_test(calc_r2, dataset, 1e4, `>=`)
```


Histogram of permutation values
count
4000
3000
2000
1000
0
0.0
0.2
0.4
test statistic

```
r2
```

```
## [1] 0.8319
```