Simulation Null data

Preload code and set parameters

```
source("~/project/reproducibility/code/rep_pval.R")
N = 5000
se = 0.5
```

Simulate the consistent null data

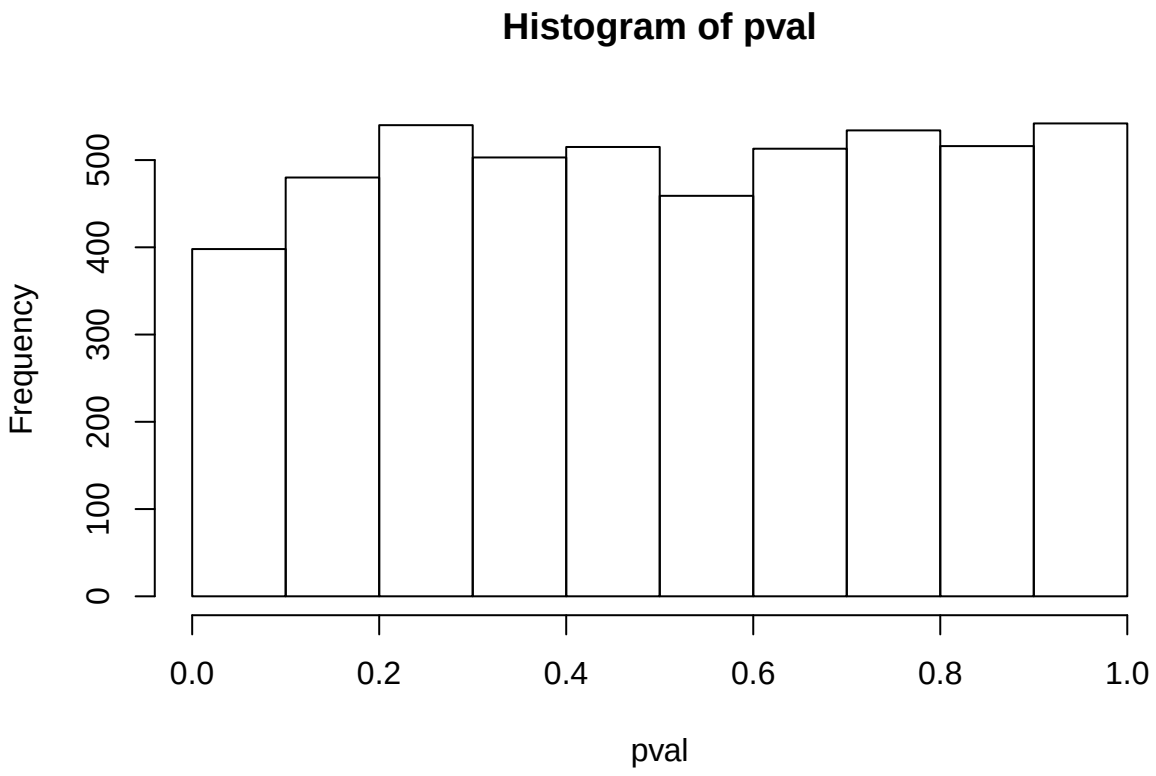
```
bhat1 = rnorm(N,sd=se)
bhat2 = rnorm(N,sd=se)
```

Analyze data

The default two-sided p-values

```
##      Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## 0.0005464 0.2685891 0.5136131 0.5152829 0.7645907 0.9996298
```

```
## [1] 185
```

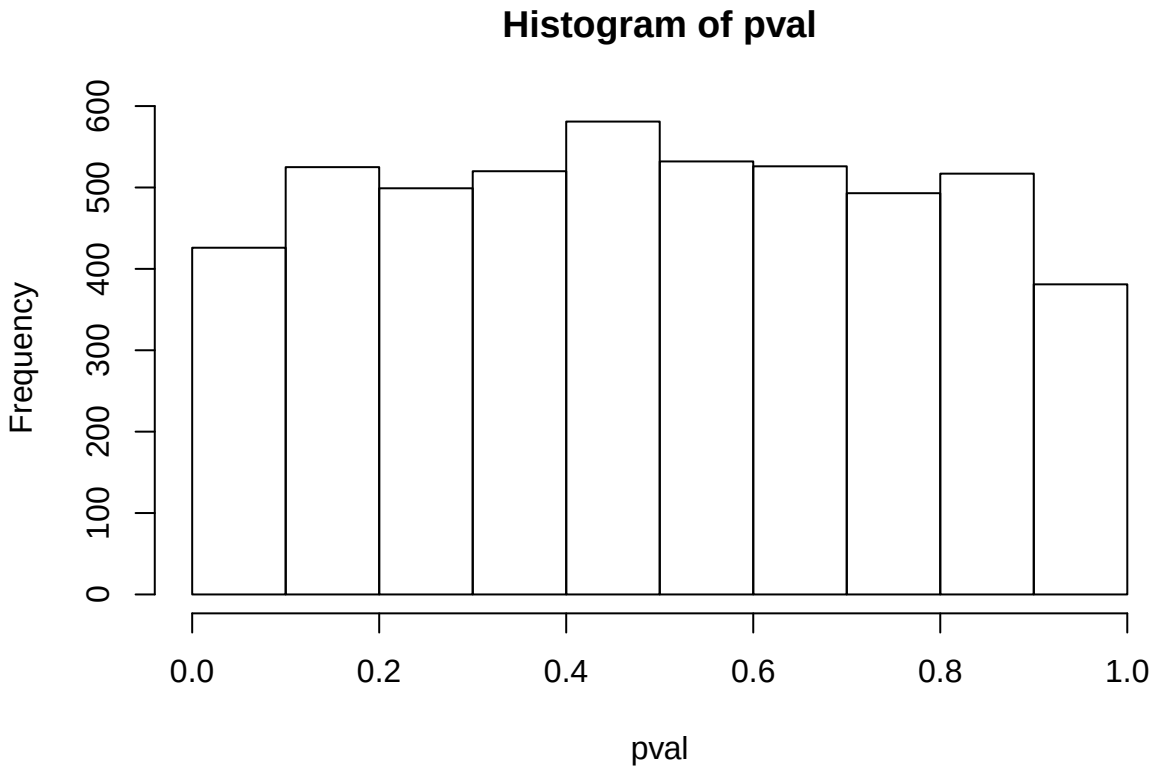


Left-tailed p-values

```
##      Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
```

```
## 0.001002 0.261338 0.489709 0.495591 0.733320 0.998201
```

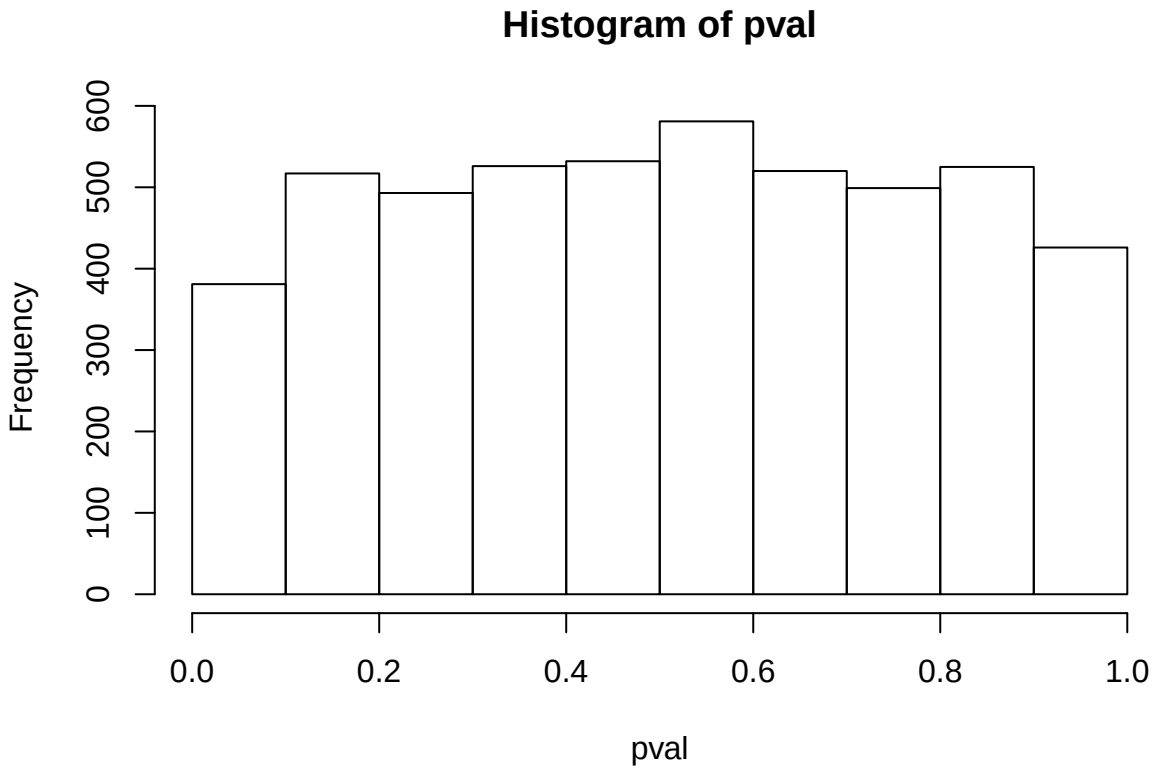
```
## [1] 189
```



right-tailed p-values

```
##     Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
## 0.001799 0.266680 0.510291 0.504409 0.738662 0.998998
```

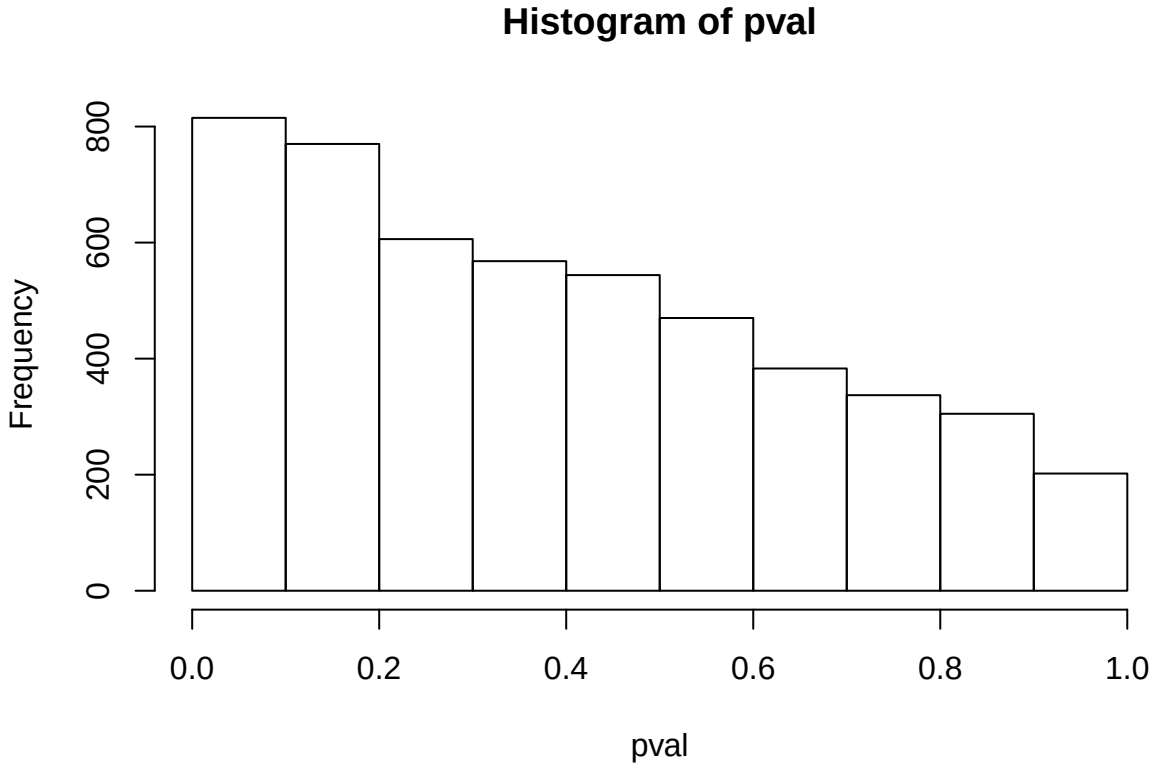
```
## [1] 177
```



The pubbias p-values

```
##      Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## 0.0001896 0.1514925 0.3561003 0.3916415 0.5946115 0.9988492
```

```
## [1] 403
```



Not quite right. The proposed test statistic is problematic.

Can we test how extreme is the observed $\frac{\hat{\beta}_r}{\hat{\beta}_o}$?