

# Lab 6

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## Contents

<b>Problem 1</b>	<b>2</b>
Problem 1a . . . . .	2
Problem 1b . . . . .	2
<b>Problem 2</b>	<b>2</b>
<b>Problem 3</b>	<b>3</b>
<b>Bonus Question 1</b>	<b>4</b>
<b>Bonus Question 2</b>	<b>5</b>

## Problem 1

Section 12.3.3 from your textbook refers to: The problem with replications of a meaningless experiment: ‘alpha and the captain’s age.’ The issue here is that if you run an ineffectual experiment enough times you can always find a significant result by chance. The textbook mentions that if you repeat an experiment 20 times, you are guaranteed to find a significant result with .64 probability, and the probability is .92 if you repeat the experiment 50 times.

### Problem 1a

Make use of the `rbinom()` function to show you can reproduce both probabilities. (1 point)

```
P1a <- replicate(10000, sum(rbinom(20,1,.05)))  
length(P1a[P1a > 0])/10000
```

```
## [1] 0.6367
```

```
P1a2 <- replicate(10000, sum(rbinom(50,1,.05)))  
length(P1a2[P1a2 > 0])/10000
```

```
## [1] 0.9236
```

### Problem 1b

If the ineffectual experiment was conducted 20 times, and there were four groups, and the experimenter would accept a significant result from any of the orthogonal linear contrasts, what would be the probability of finding a significant result here? (1 point)

```
P1b <- replicate(10000, sum(rbinom(20,3,.05)))  
length(P1b[P1b > 0])/10000
```

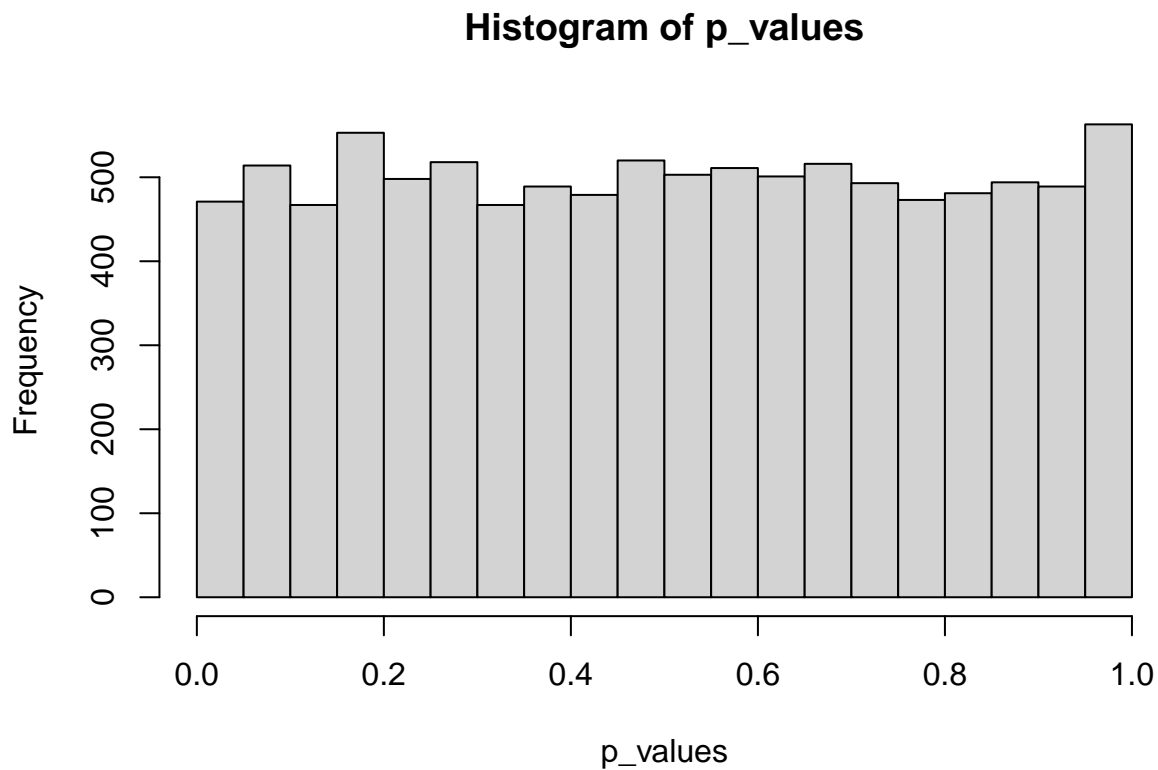
```
## [1] 0.9533
```

## Problem 2

The next two questions draw a connection to a technique we have not yet discussed called p-curve analysis (Simonsohn et al., 2014; Wallis, 1942). P-curve analysis is sometimes used for purposes of meta-analyses to determine whether there is “good” evidence for an effect in the literature.

Consider that a researcher publishes a study showing a significant effect,  $p < .05$ ; but, in reality the researcher makes a type I error, and the manipulation did not cause any difference. If many other researchers replicated the study, what kind of p-values would they find? Use R to create a sampling distribution of p-values that would be expected in this situation. What shape does this distribution have? (2 points)

```
p_values <- replicate(10000, t.test(rnorm(20,0,1), rnorm(20,0,1), var.equal=TRUE)$p.value)  
hist(p_values)
```

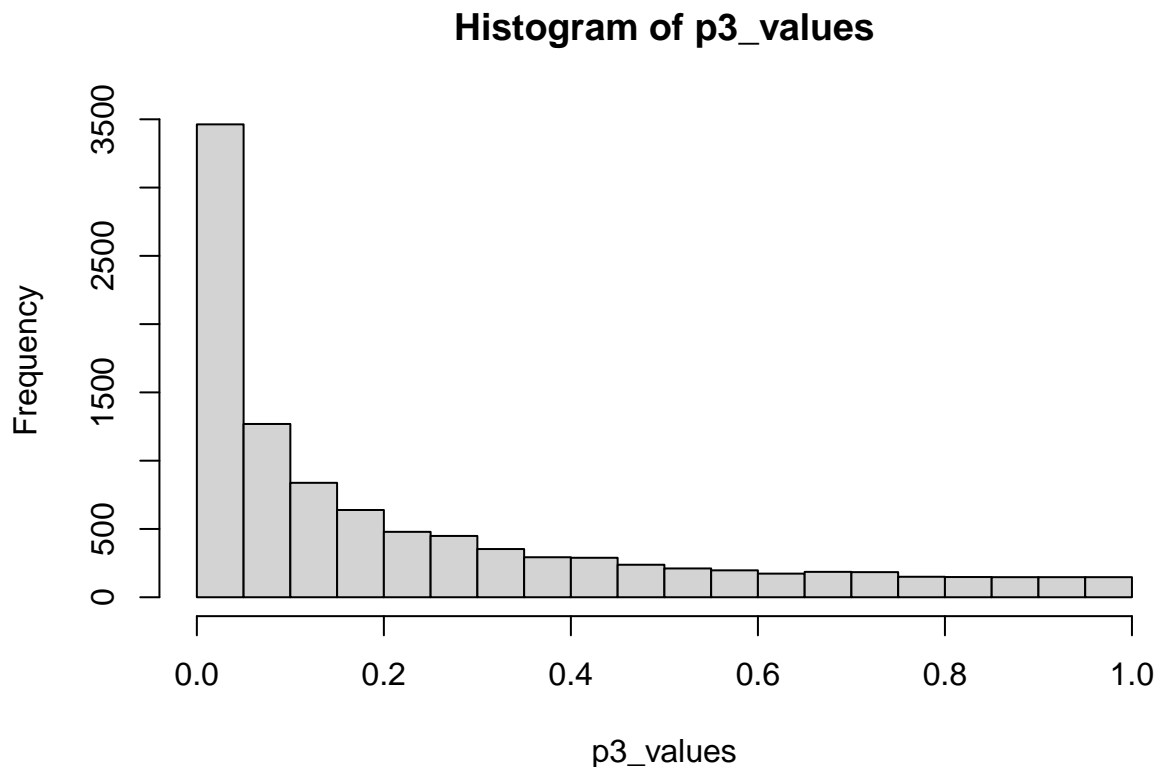


The shape of the distribution is flat, there is an equal chance for any p-value to occur.

### Problem 3

Now assume that the published result reflects a true effect. Specifically, let's imagine the study had two groups (between-subjects), with 20 subjects in each group. Assume that scores for subjects are all sampled from a normal distribution, and that group A has larger mean than group B by .5 standard deviations (e.g., Cohen's  $d = .5$ ). If many other researchers replicated the study, what kind of p-values would they find? Use R to create a sampling distribution of p-values that would be expected in this situation. What shape does this distribution have? (2 points)

```
p3_values <- replicate(10000, t.test(rnorm(20,.5,1), rnorm(20,0,1),var.equal=TRUE)$p.value)
hist(p3_values)
```



The shape of this distribution is skewed right

## Bonus Question 1

Same as #3, except that we now assume the design has four groups (between-subjects). Assume that group A has a mean that is .5 standard deviations larger than groups B, C, and D. Use R to create a sampling distribution of p-values that would be expected for the linear contrast evaluating the research hypothesis that  $A > B = C = D$ . (1 point)

```
bonus_pvalues <- c()
for(i in 1:1000){
  IV <- factor(rep(1:4,each=20))
  DV<- c(rnorm(20,.5,1), rnorm(20,0,1), rnorm(20,0,1), rnorm(20,0,1))

  bonus_data <- tibble(IV,DV)

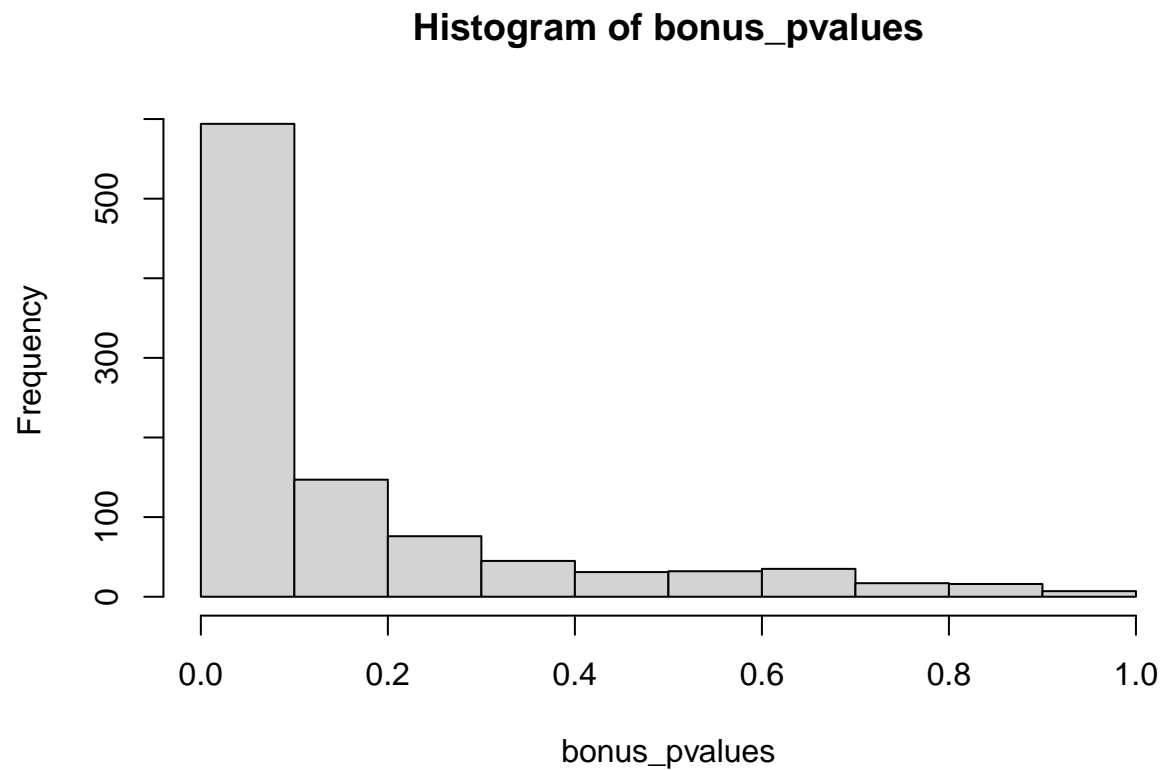
  c1 <- c(3,-1,-1,-1)

  contrasts(bonus_data$IV) <- c1

  bonus_aov <- aov(DV~IV,bonus_data)
  save_results <- summary.aov(bonus_aov, split = list(IV=list("c1" = 1)))

  bonus_pvalues[i] <- save_results[[1]]$`Pr(>F)`[2]
```

```
}  
  
hist(bonus_pvalues)
```



## Bonus Question 2

Consider a one-factor between subjects ANOVA with four groups. Run two simulations of the null-hypothesis, one for the omnibus test, and one for the specific linear contrast mentioned above  $A > B = C = D$ . Is the probability of rejecting a type I error (for rejecting the null with  $\alpha < .05$ ) the same for the omnibus test versus a specific contrast? (1 point)

```
omnibus_pvalues <- c()  
contrast_pvalues <- c()  
  
for(i in 1:1000){  
  IV <- factor(rep(1:4,each=20))  
  DV<- c(rnorm(20,0,1), rnorm(20,0,1), rnorm(20,0,1), rnorm(20,0,1))  
  
  bonus_data <- tibble(IV,DV)  
  
  c1 <- c(3,-1,-1,-1)  
  
  contrasts(bonus_data$IV) <- c1
```

```

bonus_aov <- aov(DV~IV,bonus_data)
save_results <- summary.aov(bonus_aov, split = list(IV=list("c1" = 1)))

omnibus_pvalues[i] <- save_results[[1]]$`Pr(>F)`[1]
contrast_pvalues[i] <- save_results[[1]]$`Pr(>F)`[2]
}

length(omnibus_pvalues[omnibus_pvalues < .05])/1000

```

```
## [1] 0.053
```

```
length(contrast_pvalues[contrast_pvalues < .05])/1000
```

```
## [1] 0.06
```

I'm not too sure if the probability of rejecting a type I error is the same for the omnibus or a contrast, the omnibus p-value is .041 and the contrast p value is .057 so I would think that its not the same? (not sure though because in the video you said they are the same)