hw11

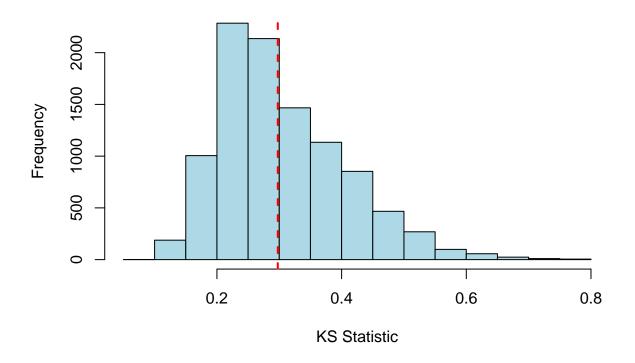
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Q1 (a)

```
# Data
soybean <- c(158, 171, 193, 199, 230, 243, 248, 248, 250, 267, 271, 316, 327, 329)
linseed <- c(141, 148, 169, 181, 203, 213, 229, 244, 257, 260, 271, 309)
z <- c(soybean, linseed)</pre>
group <- c(rep(1, length(soybean)), rep(2, length(linseed)))</pre>
# Kolmogorov-Smirnov statistic function
ks_statistic <- function(x, group) {</pre>
  Fn <- ecdf(x[group == 1]) # Empirical CDF for group 1
  Gm <- ecdf(x[group == 2]) # Empirical CDF for group 2</pre>
  \max(abs(Fn(x) - Gm(x)))
# Observed statistic
obs_stat <- ks_statistic(z, group)</pre>
# Randomization distribution
set.seed(123) # Ensure reproducibility
perm_stats <- replicate(10000, {</pre>
  perm_group <- sample(group)</pre>
                                 # Randomize group labels
# Compute KS statistic for permuted data
  ks_statistic(z, perm_group)
})
# Plot the randomization distribution
hist(perm_stats, main = "Randomization Distribution of KS Statistic",
     xlab = "KS Statistic", col = "lightblue")
abline(v = obs_stat, col = "red", lwd = 2, lty = 2)
```

Randomization Distribution of KS Statistic



Q1 (b)

```
# Compute p-value
p_value <- mean(perm_stats >= obs_stat)
cat("The p-value is:", p_value)
```

The p-value is: 0.4574

Q2 (a)

##

```
# Load the data
data(alfalfa, package = "faraway")

# Fit the model
model <- aov(yield ~ inoculum + shade + irrigation, data = alfalfa)

# Summary of the model
summary(model)</pre>
```

Df Sum Sq Mean Sq F value Pr(>F)

```
## inoculum
               4 155.89
                          38.97 12.709 0.000284 ***
## shade
               4 87.40
                          21.85
                                 7.125 0.003533 **
## irrigation
                  16.56
                           4.14
                                  1.350 0.307872
## Residuals
              12
                  36.80
                           3.07
                  0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1
## Signif. codes:
```

From the ANOVA table:

The treatment factor *inoculum* has a significant effect on yield (F = 12.709, p = 0.000284), as the p-value is less than the significance level of 0.05.

The blocking factor *shade* also has a significant effect on yield (F = 7.125, p = 0.003533), as its p-value is below 0.05.

The blocking factor *irrigation*, however, does not have a significant effect on yield (F = 1.350, p = 0.307872), as its *p-value is greater than 0.05*.

Thus, the treatment factor and the shade blocking factor are significant, while the irrigation blocking factor is not.

Q2 (b)

##

diff

lwr

upr

```
# Tukey's Honest Significant Difference Test
tukey_results <- TukeyHSD(model, "inoculum", conf.level = 0.95)</pre>
# Display results
print(tukey_results)
##
     Tukey multiple comparisons of means
##
       95% family-wise confidence level
##
## Fit: aov(formula = yield ~ inoculum + shade + irrigation, data = alfalfa)
##
## $inoculum
##
       diff
                    lwr
                              upr
                                      p adj
## B-A -0.72 -4.250202 2.810202 0.9633433
## C-A -0.08 -3.610202 3.450202 0.9999928
## D-A -0.86 -4.390202 2.670202 0.9326392
## E-A -6.60 -10.130202 -3.069798 0.0005166
## C-B 0.64 -2.890202 4.170202 0.9759059
## D-B -0.14 -3.670202 3.390202 0.9999332
## E-B -5.88 -9.410202 -2.349798 0.0014163
## D-C -0.78 -4.310202 2.750202 0.9515868
## E-C -6.52 -10.050202 -2.989798 0.0005764
## E-D -5.74 -9.270202 -2.209798 0.0017334
# Significant pairwise differences
significant <- tukey_results$inoculum[tukey_results$inoculum[, "p adj"] < 0.05, ]
significant
```

p adj

```
## E-A -6.60 -10.130202 -3.069798 0.0005166455

## E-B -5.88 -9.410202 -2.349798 0.0014163428

## E-C -6.52 -10.050202 -2.989798 0.0005764154

## E-D -5.74 -9.270202 -2.209798 0.0017334480
```

From the Tukey HSD test results:

Pairwise comparisons reveal that $inoculum\ E$ is significantly different from several other levels $at\ an\ experiment-wise\ significance\ level\ of\ 0.05$:

```
• E-A: p = 0.0005166
```

• E-B: p = 0.0014163

• E-C: p = 0.0005764

• E-D: p = 0.0017334

No other pairwise comparisons show significance as their adjusted p-values exceed 0.05. In conclusion, inoculum level E stands out as being significantly different from levels A, B, C, and D, while the other pairwise differences are not statistically significant.