

Assignment 3
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Course: Statistical Inference
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1 Question 1

```
library(BSDA)

## Loading required package: lattice
##
## Attaching package: 'BSDA'
## The following object is masked from 'package:datasets':
##
##      Orange

brand1 <- c(10.62, 10.58, 10.33, 10.72, 10.44, 10.74)
brand2 <- c(10.50, 10.52, 10.58, 10.62, 10.55, 10.51, 10.53)

# Null hypothesis (H0): The mean viscosity of the two brands is equal (mean1 = mean2)
# Alternative hypothesis (HA): The mean viscosity of the two brands is different (mean1 != mean2)
# This is a two-tailed test

alpha1 <- 0.05
alpha2 <- 0.01

mean1 <- mean(brand1)
mean2 <- mean(brand2)
sd1 <- sd(brand1)
sd2 <- sd(brand2)
n1 <- length(brand1)
n2 <- length(brand2)

test_result <- tsum.test(mean.x = mean1, s.x = sd1, n.x = n1,
                          mean.y = mean2, s.y = sd2, n.y = n2,
                          alternative = "two.sided", var.equal = TRUE,
                          conf.level = 1 - alpha1)

print(test_result)

##
## Standard Two-Sample t-Test
##
```

```

## data: Summarized x and y
## t = 0.4371, df = 11, p-value = 0.6705
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.1104937 0.1652556
## sample estimates:
## mean of x mean of y
## 10.57167 10.54429

t_stat <- test_result$statistic
df <- n1 + n2 - 2

# Compute critical t-values for two-tailed test
critical_value_05 <- qt(1 - alpha1 / 2, df = df)
critical_value_01 <- qt(1 - alpha2 / 2, df = df)

cat("Test statistic (t) =", t_stat, "\n")

## Test statistic (t) = 0.4371004

cat("Critical value at alpha = 0.05:", critical_value_05, "\n")

## Critical value at alpha = 0.05: 2.200985

cat("Critical value at alpha = 0.01:", critical_value_01, "\n")

## Critical value at alpha = 0.01: 3.105807

if (abs(t_stat) > critical_value_05) {
  cat("Reject H0 at alpha = 0.05\n")
} else {
  cat("Fail to reject H0 at alpha = 0.05\n")
}

## Fail to reject H0 at alpha = 0.05

if (abs(t_stat) > critical_value_01) {
  cat("Reject H0 at alpha = 0.01\n")
} else {
  cat("Fail to reject H0 at alpha = 0.01\n")
}

## Fail to reject H0 at alpha = 0.01

```

In the above question, we fail to reject the null hypothesis in both the cases of significance level of 0.05 and 0.01.

2 Question 2

```
library(BSDA)

before <- c(1280, 1200, 1050, 1190, 1250, 1290, 1220, 1270, 1260)
after <- c(1380, 1310, 1090, 1240, 1290, 1360, 1270, 1330, 1310)

# Null hypothesis (H0): The mean increase in SAT scores is 50 (mean difference = 50)
# Alternative hypothesis (HA): The mean increase in SAT scores is greater than 50 (mean difference > 50)

# This is a right-tailed test

alpha1 <- 0.05
alpha2 <- 0.10
mu_0 <- 50

differences <- after - before

mean_diff <- mean(differences)
sd_diff <- sd(differences)
n <- length(differences)

test_result <- tsum.test(mean.x = mean_diff, s.x = sd_diff, n.x = n,
                        mu = mu_0, alternative = "greater", conf.level = 1 - alpha1)

## Warning in tsum.test(mean.x = mean_diff, s.x = sd_diff, n.x = n,
## mu = mu_0, : argument 'var.equal' ignored for one-sample test.

print(test_result)

##
## One-sample t-Test
##
## data: Summarized x
## t = 1.5689, df = 8, p-value = 0.07765
## alternative hypothesis: true mean is greater than 50
## 95 percent confidence interval:
## 47.53021 NA
## sample estimates:
## mean of x
## 63.33333

t_stat <- test_result$statistic
```

```
critical_value_05 <- qt(1 - alpha1, df = n-1)
critical_value_10 <- qt(1 - alpha2, df = n-1)

cat("Test statistic (t) =", t_stat, "\n")

## Test statistic (t) = 1.568929

cat("Critical value at alpha = 0.05:", critical_value_05, "\n")

## Critical value at alpha = 0.05: 1.859548

cat("Critical value at alpha = 0.10:", critical_value_10, "\n")

## Critical value at alpha = 0.10: 1.396815

if (t_stat > critical_value_05) {
  cat("Reject H0 at alpha = 0.05\n")
} else {
  cat("Fail to reject H0 at alpha = 0.05\n")
}

## Fail to reject H0 at alpha = 0.05

if (t_stat > critical_value_10) {
  cat("Reject H0 at alpha = 0.10\n")
} else {
  cat("Fail to reject H0 at alpha = 0.10\n")
}

## Reject H0 at alpha = 0.10
```

In the above question, we fail to reject the null hypothesis for 0.05 significance level whereas reject the null hypothesis at 0.1 level.

3 Question 3

```
library(BSDA)

coast1 <- c(18.8, 20.5, 20.0, 21.0, 17.8, 18.2, 17.8, 19.5, 20.0, 18.2, 18.4, 19.8, 19.8, 20.0)
coast2 <- c(19.8, 21.0, 20.0, 19.5, 18.9, 18.0, 18.5, 18.2, 20.2, 19.0, 19.2, 20.2, 19.2, 17.8)

# Null hypothesis (H0): Variability in fish size at both coasts is the same ( $\sigma_1^2 = \sigma_2^2$ )
# Alternative hypothesis (HA): Variability in fish size is different ( $\sigma_1^2 \neq \sigma_2^2$ )

# This is a two-tailed test
```

```

alpha1 <- 0.05
alpha2 <- 0.01

var_coast1 <- var(coast1)
var_coast2 <- var(coast2)

test_result <- var.test(coast1, coast2, alternative = "two.sided", conf.level = 1 - alpha1)
print(test_result)

##
## F test to compare two variances
##
## data: coast1 and coast2
## F = 1.0499, num df = 14, denom df = 19, p-value = 0.9031
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
## 0.3966568 3.0035342
## sample estimates:
## ratio of variances
## 1.049922

f_stat <- test_result$statistic

critical_value_05_low <- qf(alpha1 / 2, df1 = length(coast1) - 1, df2 = length(coast2) - 1,
critical_value_05_high <- qf(1 - alpha1 / 2, df1 = length(coast1) - 1, df2 = length(coast2)

critical_value_01_low <- qf(alpha2 / 2, df1 = length(coast1) - 1, df2 = length(coast2) - 1,
critical_value_01_high <- qf(1 - alpha2 / 2, df1 = length(coast1) - 1, df2 = length(coast2)

cat("Test statistic (F) =", f_stat, "\n")

## Test statistic (F) = 1.049922

cat("Critical values at alpha = 0.05:", critical_value_05_low, "and", critical_value_05_high)

## Critical values at alpha = 0.05: 0.3495622 and 2.646928

cat("Critical values at alpha = 0.01:", critical_value_01_low, "and", critical_value_01_high)

## Critical values at alpha = 0.01: 0.2445719 and 3.637756

if (f_stat < critical_value_05_low || f_stat > critical_value_05_high) {
  cat("Reject H0 at alpha = 0.05\n")
} else {
  cat("Fail to reject H0 at alpha = 0.05\n")
}

```

```
## Fail to reject H0 at alpha = 0.05

if (f_stat < critical_value_01_low || f_stat > critical_value_01_high) {
  cat("Reject H0 at alpha = 0.01\n")
} else {
  cat("Fail to reject H0 at alpha = 0.01\n")
}

## Fail to reject H0 at alpha = 0.01
```

In the above question, we fail to reject the null hypothesis at both the significance levels of 0.05 and 0.01.

4 Question 4

```
library(BSDA)

# Given data: Breakdown counts for different machines and shifts
breakdown_matrix <- matrix(c(41, 20, 12, 16,
                             31, 11, 9, 14,
                             15, 17, 16, 10),
                           nrow = 3, byrow = TRUE)
rownames(breakdown_matrix) <- c("Shift 1", "Shift 2", "Shift 3")
colnames(breakdown_matrix) <- c("Machine A", "Machine B", "Machine C", "Machine D")

# Null hypothesis (H0): Breakdowns are independent of the shift
# Alternative hypothesis (HA): Breakdowns are dependent on the shift

test_result <- chisq.test(breakdown_matrix, correct = FALSE)

print(test_result)

##
## Pearson's Chi-squared test
##
## data: breakdown_matrix
## X-squared = 11.649, df = 6, p-value = 0.07027

chi_sq_stat <- test_result$statistic
p_value <- test_result$p.value

chi_sq_stat <- test_result$statistic
p_value <- test_result$p.value
```

```

alpha1 <- 0.05
alpha2 <- 0.01
df <- (nrow(breakdown_matrix) - 1) * (ncol(breakdown_matrix) - 1) # Degrees of freedom

critical_value_05 <- qchisq(1 - alpha1, df)
critical_value_01 <- qchisq(1 - alpha2, df)

cat("Test statistic (Chi-Square) =", chi_sq_stat, "\n")

## Test statistic (Chi-Square) = 11.64909

cat("P-value =", p_value, "\n")

## P-value = 0.07027104

cat("Critical value at alpha = 0.05:", critical_value_05, "\n")

## Critical value at alpha = 0.05: 12.59159

cat("Critical value at alpha = 0.01:", critical_value_01, "\n")

## Critical value at alpha = 0.01: 16.81189

if (chi_sq_stat > critical_value_05) {
  cat("Reject H0 at alpha = 0.05\n")
} else {
  cat("Fail to reject H0 at alpha = 0.05\n")
}

## Fail to reject H0 at alpha = 0.05

if (chi_sq_stat > critical_value_01) {
  cat("Reject H0 at alpha = 0.01\n")
} else {
  cat("Fail to reject H0 at alpha = 0.01\n")
}

## Fail to reject H0 at alpha = 0.01

```

In the above question, we fail to reject the null hypothesis at both the significance levels of 0.05 and 0.01.

5 Question 5

```

library(BSDA)

x <- c(0, 1, 2, 3, 4)
f_obs <- c(24, 30, 31, 11, 6)

lambda_hat <- sum(x * f_obs) / sum(f_obs)

p_exp <- dpois(x, lambda_hat)

f_exp <- round(p_exp * sum(f_obs))

test_result <- chisq.test(f_obs, p = p_exp, rescale.p = TRUE)

## Warning in chisq.test(f_obs, p = p_exp, rescale.p = TRUE): Chi-squared
approximation may be incorrect

print(test_result)

##
## Chi-squared test for given probabilities
##
## data: f_obs
## X-squared = 2.4898, df = 4, p-value = 0.6465

chi_sq_stat <- test_result$statistic
p_value <- test_result$p.value

alpha <- 0.05
df <- length(x) - 1 - 1

critical_value <- qchisq(1 - alpha, df)

cat("Test statistic (Chi-Square) =", chi_sq_stat, "\n")

## Test statistic (Chi-Square) = 2.489796

cat("P-value =", p_value, "\n")

## P-value = 0.6464638

cat("Critical value at alpha = 0.05:", critical_value, "\n")

## Critical value at alpha = 0.05: 7.814728

```



```
if (chi_sq_stat > critical_value) {  
  cat("Reject H0 at alpha = 0.05\n")  
} else {  
  cat("Fail to reject H0 at alpha = 0.05\n")  
}  
  
## Fail to reject H0 at alpha = 0.05
```

Given the p-value is not less than 0.05, the data fits the poisson distribution.