Paul Kogan-HW3

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```r
rjct <- function(lvl) paste("<", lvl,
                            "so reject the null hypothesis that the\n")
fail <- function(lvl) rjct(lvl) %>%
    str_replace_all(c("<" = ">", "so" = "so fail to"))
conc <- function(test, lvl = 1 - attr(test$conf.int, "conf.level")) {
  lvl <- ifelse(length(lvl) == 0, 0.05, lvl)
  ifelse(test$p.value > lvl, fail(lvl), rjct(lvl))
}
```

1

```r
stock <- read.table("d_logret_6stocks.txt", T)
intel <- stock$Intel
pfizer <- stock$Pfizer
ip_var <- var.test(intel, pfizer)
t_i <- t.test(intel)
w_i <- wilcox.test(intel, pfizer, conf.int = T)
t_ip <- t.test(intel, pfizer, var.equal = ip_var$p.value > 0.05)
w_ip <- wilcox.test(intel, pfizer, conf.int = T)

cat("a:\n")
t_i
cat("conclusion: p-value =", t_i$p.value, conc(t_i),
    "mean of intel return is zero\n\n")

cat("b:\n")
w_i
cat("conclusion: p-value = ", w_i$p.value, conc(w_i),
    "mean of intel return is zero\n\n")

cat("c:\n")
t_ip
cat("conclusion: p-value =", t_ip$p.value, conc(t_ip),
    "mean returns of pfizer and intel are the same\n\n")

cat("d:\n")
w_ip
cat("conclusion: p-value =", w_ip$p.value, conc(w_ip),
    "mean returns of pfizer and intel are the same\n\n")

cat("e:\n")
```

```
ip_var
cat("conclusion: p-value =", ip_var$p.value, conc(ip_var),
    "variances of returns of pfizer and intel are the same\n\n")
```

```
## a:
##
##  One Sample t-test
##
## data:  intel
## t = -0.70588, df = 63, p-value = 0.4829
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  -0.02293067  0.01095951
## sample estimates:
##    mean of x
## -0.005985579
##
## conclusion: p-value = 0.482864 > 0.05 so fail to reject the null hypothesis that the
##  mean of intel return is zero
##
## b:
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  intel and pfizer
## W = 2077, p-value = 0.892
## alternative hypothesis: true location shift is not equal to 0
## 95 percent confidence interval:
##  -0.01347123  0.01871938
## sample estimates:
## difference in location
##            0.001019999
##
## conclusion: p-value =  0.8919643 > 0.05 so fail to reject the null hypothesis that the
##  mean of intel return is zero
##
## c:
##
##  Welch Two Sample t-test
##
## data:  intel and pfizer
## t = -0.21707, df = 77.394, p-value = 0.8287
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.01977844  0.01588991
## sample estimates:
##    mean of x    mean of y
## -0.005985579 -0.004041315
##
## conclusion: p-value = 0.8287273 > 0.05 so fail to reject the null hypothesis that the
##  mean returns of pfizer and intel are the same
##
## d:
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  intel and pfizer
## W = 2077, p-value = 0.892
## alternative hypothesis: true location shift is not equal to 0
## 95 percent confidence interval:
##  -0.01347123  0.01871938
## sample estimates:
## difference in location
##            0.001019999
##
## conclusion: p-value = 0.8919643 > 0.05 so fail to reject the null hypothesis that the
##  mean returns of pfizer and intel are the same
##
## e:
##
##  F test to compare two variances
##
## data:  intel and pfizer
## F = 8.6379, num df = 63, denom df = 63, p-value = 3.553e-15
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##   5.247738 14.218152
## sample estimates:
## ratio of variances
##            8.63789
##
## conclusion: p-value = 3.552714e-15 < 0.05 so reject the null hypothesis that the
##  variances of returns of pfizer and intel are the same
```

2

```r
bp26 <- c(152, 157, 179, 185, 178, 149)
bp5 <- c(384, 369, 354, 367, 375, 423)
t_bp <- t.test(bp26, bp5, "greater",
               var.equal = var.test(bp26, bp5)$p.value > 0.05)
t_bp
cat("conclusion: p-value =", t_bp$p.value, conc(t_bp),
    "mean blood pressures are the same\n\n")
```

```
##
##  Two Sample t-test
##
## data:  bp26 and bp5
## t = -18.173, df = 10, p-value = 1
## alternative hypothesis: true difference in means is greater than 0
## 95 percent confidence interval:
##  -233.1437       Inf
## sample estimates:
## mean of x mean of y
##  166.6667  378.6667
##
```

```
## conclusion: p-value = 1 > 0.05 so fail to reject the null hypothesis that the
##  mean blood pressures are the same
```

3

```r
lvl <- .1
affected <- c(488, 478, 480, 426, 440, 410, 458, 460)
not_a <- c(484, 478, 492, 444, 436, 398, 464, 476)
s_aff <- shapiro.test(affected)
s_not <- shapiro.test(not_a)
s_affc <- conc(s_aff, lvl)
s_notc <- conc(s_not, lvl)
v_a <- var.test(affected, not_a)
t_aff <- t.test(affected, not_a, conf.level = 1 - lvl,
                var.equal = v_a$p.value > lvl)
assumptions <- c(paste("data in each group are ", sep = "",
ifelse(grepl("<", s_affc, F, F, T) || grepl("<", s_notc, F, F, T), "not ", ""),
"normal"), paste("variances of the groups are ",
ifelse(!v_a$p.value > lvl, "not ", ""), "equal", sep = ""))

cat("a:\n\tAffected")
s_aff
cat("conclusion: p-value =", s_aff$p.value, s_affc,
    "data are normal\n\n\tNot Affected")
s_not
cat("conclusion: p-value =", s_not$p.value, s_notc,
    "data are normal\n")
v_a
cat("conclusion: p-value =", s_not$p.value, s_notc,
    "variances are equal\n\nassumptions checked:\t")
for (assumption in assumptions) cat(assumption, "\n\t\t\t\t\t\t")
t_aff
cat("conclusion: p-value =", t_aff$p.value, conc(t_aff),
    "corneal thickness is equal for affected versus unaffected eyes\n\n")
cat("b:\t", t_aff$conf.int[1:2], "\n\n")
```

```
## a:
##  Affected
##  Shapiro-Wilk normality test
##
## data:  affected
## W = 0.9402, p-value = 0.6131
##
## conclusion: p-value = 0.6130593 > 0.1 so fail to reject the null hypothesis that the
##  data are normal
##
##  Not Affected
##  Shapiro-Wilk normality test
##
## data:  not_a
## W = 0.90211, p-value = 0.3018
##
## conclusion: p-value = 0.301824 > 0.1 so fail to reject the null hypothesis that the
```

```
##  data are normal
##
##  F test to compare two variances
##
## data:  affected and not_a
## F = 0.78205, num df = 7, denom df = 7, p-value = 0.7539
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  0.1565697 3.9062752
## sample estimates:
## ratio of variances
##          0.7820513
##
## conclusion: p-value = 0.301824 > 0.1 so fail to reject the null hypothesis that the
##  variances are equal
##
## assumptions checked: data in each group are normal
##                      variances of the groups are equal
##
##  Two Sample t-test
##
## data:  affected and not_a
## t = -0.27065, df = 14, p-value = 0.7906
## alternative hypothesis: true difference in means is not equal to 0
## 90 percent confidence interval:
##  -30.03098  22.03098
## sample estimates:
## mean of x mean of y
##       455       459
##
## conclusion: p-value = 0.7906108 > 0.1 so fail to reject the null hypothesis that the
##  corneal thickness is equal for affected versus unaffected eyes
##
## b:    -30.03098 22.03098
```

4

```r
mean <- 25
time <- c(28, 25, 27, 31, 10, 26, 30, 15, 55, 12, 24, 32, 28, 42, 38)
s_time <- shapiro.test(time)
t_time <- t.test(time, alternative = "greater", mu = mean, conf.level = .95)

cat("a:\n")
s_time
cat("conclusion: p-value =", s_time$p.value, conc(s_time),
    "data are normal\n\n")

cat("b:\n")
t_time
cat("conclusion: p-value =", t_time$p.value, conc(t_time),
    "mean time for a warehouse to fill a buyers order is", mean, "minutes\n\n")
```

```
## a:
```

```
##
##  Shapiro-Wilk normality test
##
## data:  time
## W = 0.94167, p-value = 0.4038
##
## conclusion: p-value = 0.4037724 > 0.05 so fail to reject the null hypothesis that the
##  data are normal
##
## b:
##
##  One Sample t-test
##
## data:  time
## t = 1.0833, df = 14, p-value = 0.1485
## alternative hypothesis: true mean is greater than 25
## 95 percent confidence interval:
##  22.99721      Inf
## sample estimates:
## mean of x
##      28.2
##
## conclusion: p-value = 0.1484898 > 0.05 so fail to reject the null hypothesis that the
##  mean time for a warehouse to fill a buyers order is 25 minutes
```