MAST20005/MAST90058: Week 8 Lab Solutions

1. Using the same example data as in the tutorial solutions:

```
x <- c(0, 8, 42)           # observed
prob <- c(0.1, 0.2, 0.7)   # expected (prob)
chisq.test(x, p = prob)


##
##  Chi-squared test for given probabilities
##
## data:  x
## X-squared = 6.8, df = 2, p-value = 0.03337
```

   The p-value is small, which indicates the string of digits is unlikely to have been randomly generated.

2. First do the Wilcoxon test:

```
x <- c(41.195, 39.485, 41.229, 36.840, 38.050, 40.890, 38.345,
       34.930, 39.245, 31.031, 40.780, 38.050, 30.906)
wilcox.test(x, mu = 40, alternative = "less")

## Warning in wilcox.test.default(x, mu = 40, alternative = "less"):  cannot
compute exact p-value with ties


##
##  Wilcoxon signed rank test with continuity correction
##
## data:  x
## V = 18, p-value = 0.02955
## alternative hypothesis: true location is less than 40
```

   The p-value is small, we should reject H_0.

   Don't worry about the warning: it is simply alerting us to the fact that it is using a normal approximation rather than an exact calculation of the sampling distribution of the Wilcoxon test statistic.

   Now try the sign test:

```
binom.test(sum(x > 40), length(x), alternative = "less")


##
##  Exact binomial test
##
## data:  sum(x > 40) and length(x)
## number of successes = 4, number of trials = 13, p-value =
## 0.1334
## alternative hypothesis: true probability of success is less than 0.5
```

```
## 95 percent confidence interval:
##  0.0000000 0.5726193
## sample estimates:
## probability of success
##              0.3076923
```

Cannot reject H_0, p-value is too high.

3.
```
flies  <- c(254, 69, 87, 22)  # observed
ratios <- c(9, 3, 3, 1)       # expected probabilities (unnormalised)
chisq.test(flies, p = ratios, rescale.p = TRUE)


##
##  Chi-squared test for given probabilities
##
## data:  flies
## X-squared = 3.6461, df = 3, p-value = 0.3023
```

Cannot reject H_0, p-value is too high.

Here we have used a convenient feature of `chisq.test()`: by specifying `rescale.p = TRUE` we do not have to calculate the expected counts, it is enough to specify the relative amounts and R will work out the rest.

4.
```
nurses <- rbind(c(95, 36, 71, 21, 45, 32),
                c(53, 26, 43, 18, 32, 28))
chisq.test(nurses)


##
##  Pearson's Chi-squared test
##
## data:  nurses
## X-squared = 3.2305, df = 5, p-value = 0.6645
```

Cannot reject H_0, p-value is too high.