UKSta18_Liang_Ex06

August 13, 2018

1 Planning an experiment: Test the quality of a die

An experiment is to be conducted where the proper behavior of a die is checked. The probability of rolling a "one" is measured for checking against the expected probability for a fair die (p = 1/6). The experiment is performed in the following way: the die is rolled N = 10 times and the number of "ones" in these N rolls r is recorded. This counting is repeated K-times. The data that you nally have available are r_k counts where k = 1,...,K. For a fair die the r_k should obviously follow a binomial distribution $P(r_k|N,p) = \binom{N}{r_k} p^{r_k} (1-p)^{N-r_k}$.

• a: For this set-up, show that the ML estimators for the probability \hat{p} and its variance $Var[\hat{p}]$ are $\hat{p} = \frac{1}{KN} \sum r_k$ and $Var[\hat{p}] \ge \frac{\hat{p}(1-\hat{p})}{KN}$

Hint: An algebra program might be useful for handling some of the algebra. For instance, Mathematica is installed on the machines of the CIP pool. Moreover, there are also R-packages (e.g., *rSymPy*) for symbolic calculation.

The Log-likelihood function is:

$$\frac{\partial \ln \left(\prod_{k=1}^{K} P(r_{k}|N,p) \right)}{\partial p} = \frac{\partial \left(\sum_{k=1}^{K} \ln P(r_{k}|N,p) \right)}{\partial p} = \frac{\partial \left(\sum_{k=1}^{K} \left\{ \ln \left(\binom{N}{r_{k}} \right) + r_{k} \ln p + (N-r_{k}) \ln (1-p) \right\} \right)}{\partial p} = \sum_{k=1}^{K} \left\{ \ln \left(\binom{N}{r_{k}} \right) + \frac{r_{k}}{p} - \frac{N-r_{k}}{1-p} \right\} = \sum_{k=1}^{K} \left(\ln \left(\binom{N}{r_{k}} \right) \right) + \frac{1}{p(1-p)} \sum_{k=1}^{K} r_{k} - \frac{N^{2}}{1-p} = \sum_{k=1}^{K} r$$

- b: Before actually conducting the experiment, to economize resources, we want to predict how many countings K are actually necessary. Making the assumption that the die is indeed fair: How large has $K = K_1$ to be so that one can constrain p/p to 1%?
- c: Like in previous problem sheets we want to check the performance of the derived estimators by Monte Carlo simulation (in the computer not by hand, of course): perform the whole experiment with a fair die and calculate p. Repeat the experiment 10^4 times with $K_1/4$, K_1 , and compare the dispersion of p with the ML predictions. Is the Cramér-Rao bound reached?

2 Fitting a straight line with known uncertainties in y

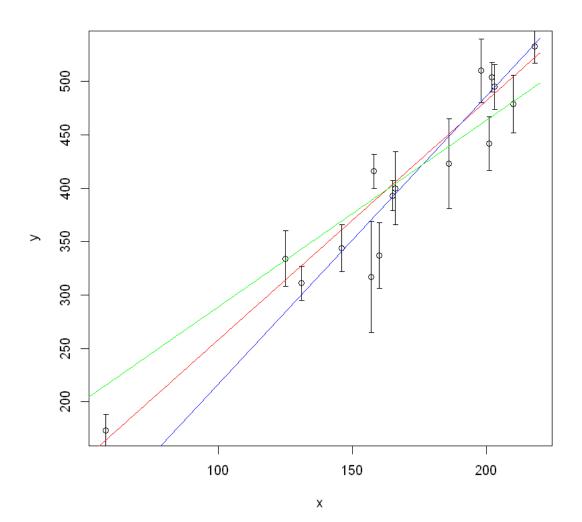
The next two exercises are taken from the paper of Hogg et al. "Fitting a straight line to data". Have perhaps a look at their section 1 for verifying your solutions. Using the linear algebra as given in the lecture, or the formulation in the article by Hogg et al. (in Moodle), t a straight line y = mx + b to the x, y, and y values for data points 5 through 20 in the table in the le *hogg table1.txt* (in Moodle). That is, ignore the rst four data points, and also ignore the columns for x and Cor[x, y].

- a: Write an R-program to calculate the best tting parameters m and b, their uncertainties, covariance, and ² of the t!
- b: Make a plot showing the points, their uncertainties, and the best-t line! Hint: error bars can be plotted by using arrows, e.g.: arrows(x, y-sigy, x, y+sigy, length=0.05, angle=90, code=3)
- c: Do you have an idea how to illustrate the uncertainty of the location of the tting line?
- d: Repeat the previous exercise but for all the data points in the table! Is there anything you do not like about the result?
- e: Of course, as statistics oriented programming language R has build in the tting of linear models with the command lm. Compare lm results to yours. Hint: lm might appear a bit cryptic. Have a look at the example below for inspiration. $lm(formula = y \sim x + I(x^2), data = table_hogg, subset = (5:20), weights=1.0/table_hogg$sigy^2)$

Note that the "std. error" in the output of lm() are not the 1 error bars but auxiliary quantities useful in combination with t-statistics.

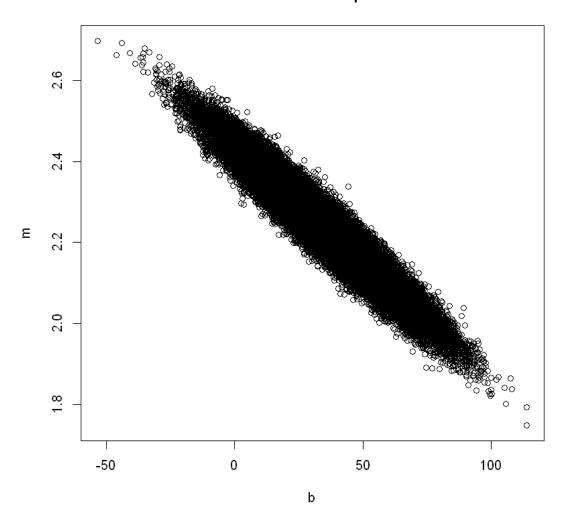
```
In [1]: data <- read.table("hogg_table1.txt", header=TRUE)</pre>
        # without first 4 points
        x <- data[-(1:4),2]
        y < - data[-(1:4),3]
        sigy <- data[-(1:4),4]
        inv_s_sq <- sigy^(-2)</pre>
        left <- matrix(c(sum(inv_s_sq),sum(x*inv_s_sq),sum(x*inv_s_sq),sum(x^2*inv_s_sq)), 2,</pre>
        right <- c(sum(y*inv_s_sq),sum(y*x*inv_s_sq))
        res <- solve(left, right)</pre>
        b <- res[1]
        m \leftarrow res[2]
        cat("the fitting result of m is: ", m, ", of b is", b, "\n")
        chi_sq <- sum((y-b-m*x)^2*inv_s_sq)</pre>
        cat("the chi_square of the fit is: ",chi_sq, "\n" )
        cat("the covariance matrix of fitted parameters is the inverse of the normal equations
        lsg <- solve(left, diag(2))</pre>
        print(lsg)
        cat("the variance(uncertainty) of m is: ", lsg[2,2], ", of b is: ", lsg[1,1])
the fitting result of m is: 2.239921, of b is 34.04773
the chi_square of the fit is: 18.68077
the covariance matrix of fitted parameters is the inverse of the normal equations matrix:
           [,1]
[1,] 332.922601 -1.88954491
[2,] -1.889545 0.01161663
the variance(uncertainty) of m is: 0.01161663, of b is: 332.9226
In [2]: # plot
        plot(x, y)
        arrows(x, y-sigy, x, y+sigy, length=0.03, angle=90, code=3)
```

```
t <- seq(40, 220, 1)
lines(t, b + m*t, col="red")
# uncertainty of the location of the fitting line
# m, b is correalted, so we use multivariate normal distribution for the two parameter
library(MASS)
paras <- mvrnorm(10^5, res, lsg)
min1 <- min(paras[,1])
min2 <- paras[which(paras[,1]==min1),2]
lines(t, min1 + min2*t, col="blue")
max1 <- max(paras[,1])
max2 <- paras[which(paras[,1]==max1),2]
lines(t, max1 + max2*t, col="green")
plot(paras, xlab="b", ylab="m", main="Correlation of 2 fitted parameters")
cat("The possible location of the fitting line is the region between the green and blue</pre>
```



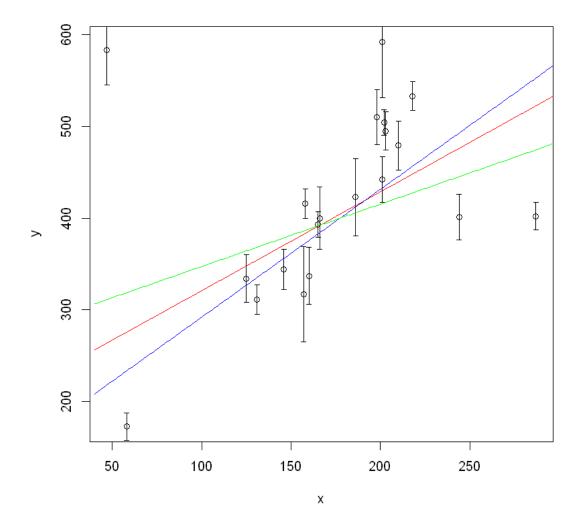
The possible location of the fitting line is the region between the green and blue lines.

Correlation of 2 fitted parameters



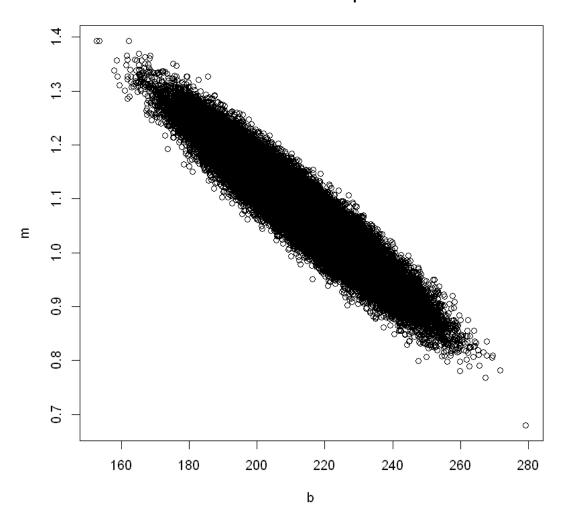
```
In [3]: # with first 4 points
    x <- data[,2]
    y <- data[,3]
    sigy <- data[,4]
    inv_s_sq <- sigy^(-2)
    left <- matrix(c(sum(inv_s_sq),sum(x*inv_s_sq),sum(x*inv_s_sq),sum(x^2*inv_s_sq)), 2, 1
    right <- c(sum(y*inv_s_sq),sum(y*x*inv_s_sq))
    res <- solve(left, right)</pre>
```

```
b <- res[1]
        m <- res[2]
        cat("the fitting result of m is: ", m, ", of b is", b, "\n")
        chi_sq \leftarrow sum((y-b-m*x)^2*inv_s_sq)
        cat("the chi_square of the fit is: ",chi_sq, "\n" )
        cat("the covariance matrix of fitted parameters is the inverse of the normal equations
        lsg <- solve(left, diag(2))</pre>
        print(lsg)
        cat("the variance(uncertainty) of m is: ", lsg[2,2], ", of b is: ", lsg[1,1])
the fitting result of m is: 1.076748 , of b is 213.2735
the chi_square of the fit is: 289.9637
the covariance matrix of fitted parameters is the inverse of the normal equations matrix:
           [,1]
                        [,2]
[1,] 207.188189 -1.05427206
[2,] -1.054272 0.00599181
the variance(uncertainty) of m is: 0.00599181, of b is: 207.1882
In [4]: # plot
        plot(x, y)
        arrows(x, y-sigy, x, y+sigy, length=0.03, angle=90, code=3)
        t < -seq(40, 300, 1)
        lines(t, b + m*t, col="red")
        # uncertainty of the location of the fitting line
        # m, b is correalted, so we use multivariate normal distribution for the two parameter
        library(MASS)
        paras <- mvrnorm(10^5, res, lsg)</pre>
        min1 <- min(paras[,1])</pre>
        min2 <- paras[which(paras[,1]==min1),2]</pre>
        lines(t, min1 + min2*t, col="blue")
        max1 <- max(paras[,1])
        max2 <- paras[which(paras[,1]==max1),2]</pre>
        lines(t, max1 + max2*t, col="green")
        plot(paras, xlab="b", ylab="m", main="Correlation of 2 fitted parameters")
        cat("The possible location of the fitting line is the region between the green and blue
        cat("Apparently the result shows us that the outliers have big influence on fitted pare
        very large and thus the fit seem to be very bad. \n")
```



The possible location of the fitting line is the region between the green and blue lines. Apparently the result shows us that the outliers have big influence on fitted parameters, which very large and thus the fit seem to be very bad.

Correlation of 2 fitted parameters



Now we compare our fitting result with the fit model using functions in r:

```
Call: lm(formula = y ~ x, data = data, subset = (5:20), weights = 1/sigy^2)
```

Weighted Residuals:

```
Min 1Q Median 3Q Max -1.7882 -0.9639 -0.4158 0.6911 1.7528
```

Coefficients:

```
Estimate Std. Error t value Pr(>|t|)
(Intercept) 34.0477 21.0768 1.615 0.129
x 2.2399 0.1245 17.991 4.49e-11 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

Residual standard error: 1.155 on 14 degrees of freedom Multiple R-squared: 0.9585, Adjusted R-squared: 0.9556 F-statistic: 323.7 on 1 and 14 DF, p-value: 4.493e-11

3 Fitting a quadratic model

Generalize the method of this Section to t a general quadratic (second order) relationship $g(x) = qx^2 + mx + b$. Then re-do the tting for the case without outliers. What is the best quadratic relationship?

With quadratic relationship the Log-likelihood function is then:

$$l(q, b, m) = \sum_{i=1}^{N} \{-\ln s_i - \ln \sqrt{2\pi} - \frac{1}{2} \frac{(y_i - qx_i^2 - mx_i - b)^2}{s_i^2}\}$$

Thus the partial derivatives are:

$$\frac{\partial l}{\partial b} = \sum_{i=1}^{N} (y_i - qx_i^2 - mx_i - b)s_i^{-2}$$

$$\frac{\partial l}{\partial m} = \sum_{i=1}^{N} (y_i - qx_i^2 - mx_i - b)x_is_i^{-2}$$

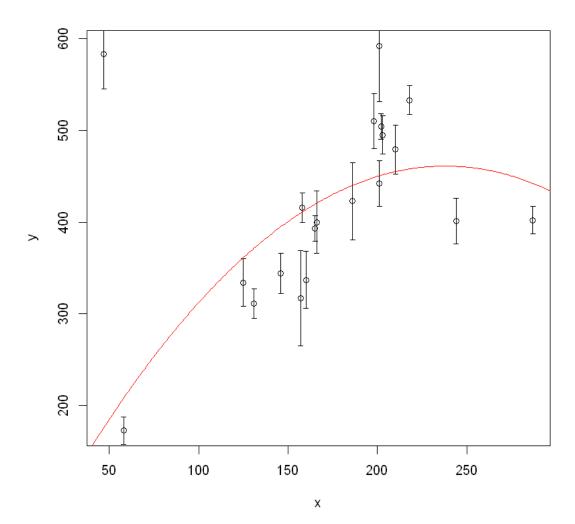
$$\frac{\partial l}{\partial q} = \sum_{i=1}^{N} (y_i - qx_i^2 - mx_i - b)x_i^2s_i^{-2}$$

So we get a 3*3 linear system of equations

$$\begin{pmatrix} \sum_{i} s_{i}^{-2} & \sum_{i} x_{i} s_{i}^{-2} & \sum_{i} x_{i}^{2} s_{i}^{-2} \\ \sum_{i} x_{i} s_{i}^{-2} & \sum_{i} x_{i}^{2} s_{i}^{-2} & \sum_{i} x_{i}^{3} s_{i}^{-2} \\ \sum_{i} x_{i}^{2} s_{i}^{-2} & \sum_{i} x_{i}^{3} s_{i}^{-2} & \sum_{i} x_{i}^{4} s_{i}^{-2} \end{pmatrix} \begin{pmatrix} b \\ m \\ q \end{pmatrix} = \begin{pmatrix} \sum_{i} y_{i} s_{i}^{-2} \\ \sum_{i} y_{i} x_{i} s_{i}^{-2} \\ \sum_{i} y_{i} x_{i}^{2} s_{i}^{-2} \end{pmatrix}$$

And the following steps are pricinpally the same.

```
right <-c(sum(y*inv_s_sq), sum(y*x*inv_s_sq), sum(y*x^2*inv_s_sq))
        res <- solve(left, right)</pre>
        b <- res[1]
        m <- res[2]
        q \leftarrow res[3]
        cat("the fitting result of m is: ", m, ", of b is", b, "\n", ", of q is", q, "\n")
        \label{eq:chi_sq}  \mbox{chi\_sq} \ \mbox{$<$-$ sum((y-b-m*x-q*x^2)^2*inv\_s\_sq)$} 
        cat("the chi_square of the fit is: ",chi_sq, "\n" )
        cat("the covariance matrix of fitted parameters is the inverse of the normal equations
        lsg <- solve(left, diag(3))</pre>
        print(lsg)
        cat("the variance(uncertainty) of m is: ", lsg[2,2], ", of b is: ", lsg[1,1], ", of q
the fitting result of m is: 3.715966, of b is 18.84583
 , of q is -0.007806819
the chi_square of the fit is: 218.49
the covariance matrix of fitted parameters is the inverse of the normal equations matrix:
                            [,2]
              [,1]
                                           [,3]
[1,] 736.08377181 -8.2336570507 2.123665e-02
[2,] -8.23365705 0.1034469043 -2.882726e-04
       0.02123665 -0.0002882726 8.527114e-07
[3.]
the variance(uncertainty) of m is: 0.1034469, of b is: 736.0838, of q is: 8.527114e-07
In [7]: # plot
        plot(x, y)
        arrows(x, y-sigy, x, y+sigy, length=0.03, angle=90, code=3)
        t < - seq(40, 300, 1)
        lines(t, b + m*t+q*t^2, col="red")
```



```
chi_sq \leftarrow sum((y-b-m*x-q*x^2)^2*inv_s_sq)
        cat("the chi_square of the fit is: ",chi_sq, "\n" )
        cat("the covariance matrix of fitted parameters is the inverse of the normal equations
        lsg <- solve(left, diag(3))</pre>
       print(lsg)
        cat("the variance(uncertainty) of m is: ", lsg[2,2], ", of b is: ", lsg[1,1], ", of q
the fitting result of m is: 1.59605, of b is 72.89463
 , of q is 0.002298888
the chi_square of the fit is: 17.40317
the covariance matrix of fitted parameters is the inverse of the normal equations matrix:
              [,1]
                           [,2]
                                         [,3]
[1,] 1514.10912766 -21.46719570 6.990046e-02
[2,] -21.46719570 0.33610764 -1.158570e-03
       0.06990046 -0.00115857 4.136581e-06
[3,]
the variance(uncertainty) of m is: 0.3361076, of b is: 1514.109, of q is: 4.136581e-06
In [9]: # plot
       plot(x, y)
       arrows(x, y-sigy, x, y+sigy, length=0.03, angle=90, code=3)
       t < - seq(40, 240, 1)
        lines(t, b + m*t+q*t^2, col="red")
```

