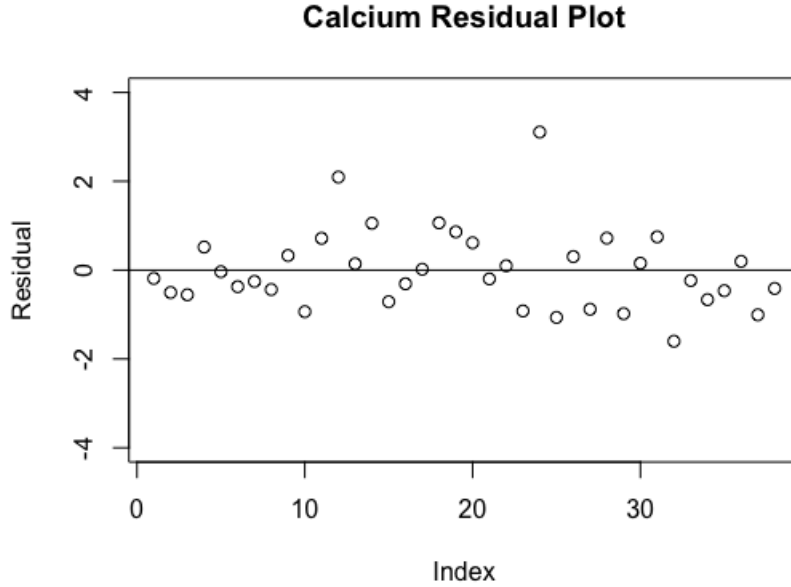


Q1-a

$R = (\frac{X_1 - \bar{X}}{\sigma\sqrt{1 - \frac{1}{n}}}, \frac{X_2 - \bar{X}}{\sigma\sqrt{1 - \frac{1}{n}}}, \dots, \frac{X_n - \bar{X}}{\sigma\sqrt{1 - \frac{1}{n}}})$ where \bar{X} denotes sample mean, S denotes sample standard deviation.



Most residuals fall in -2 to 2, which implies most data is included in 2 standard deviations from mean value. Residuals are denser when close to zero than away from zero. Though there is one extreme value that lies outside 3rd standard deviations away from the mean, the dataset seems to follow normal distribution.

(R code in Appendix)

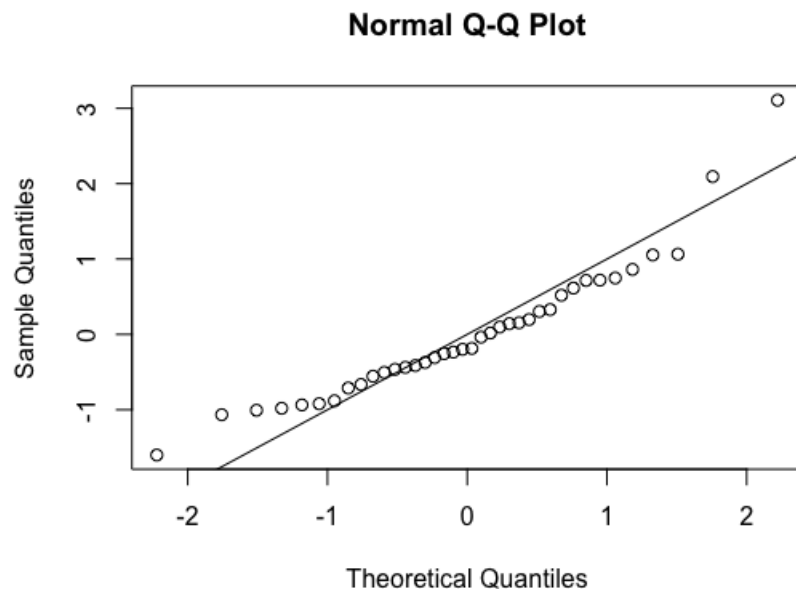
Q1-b

$Y - axis = R$ where R is the standardized residual for calcium value.

$$\begin{aligned} F_R(r) &= P(R \leq r) \\ &= P\left(\frac{X - \bar{X}}{\sigma\sqrt{1 - \frac{1}{n}}} \leq r\right) \end{aligned}$$

Since X is hypothesized to follow normal distribution, $\frac{X - \bar{X}}{\sigma\sqrt{1 - \frac{1}{n}}} = Z$, $F(r) = P(Z \leq r) = \Phi(r)$

$$\begin{aligned} Y - axis \text{ vs } X - axis &= \Phi(r_k) \text{ vs } \frac{k}{n+1} \\ &= r_k \text{ vs } \Phi^{-1}\left(\frac{k}{n+1}\right) \end{aligned}$$



From the QQ-plot, we can perceive that residuals in the middle match with expected values very well. However, a few data points on two tails is larger than expected value, since the density of standardized residual is lower in left tail and higher in right tail than of standard normal. Overall, the distribution of standardized residuals follows normal distribution.

Q1-c

Since we presume the population variance σ is known, the ancillary statistic R is defined as $(X_1 - \bar{X}, X_2 - \bar{X}, \dots, X_n - \bar{X})$.

Use $D(x) = \frac{1}{\sigma^2} \sum_{i=1}^n R_i^2$ as discrepancy statistic.

Under normality model, the discrepancy statistic follows chi-square distribution with degree of freedom $n - 1$ where n is sample size. In this case $D(x) \sim \chi_{37}^2$.

The observed discrepancy is 29.45 with its p-value of 0.806825. Under the test size $\sigma = 0.05$, the observed data failed to provide significant evidence to reject normal model.

(R code in Appendix)

Q1-d

Let p_1, p_2, p_3, p_4 denote multinomial probabilities for each interval based on presumed model. $\sigma = 500$ and θ is unknown

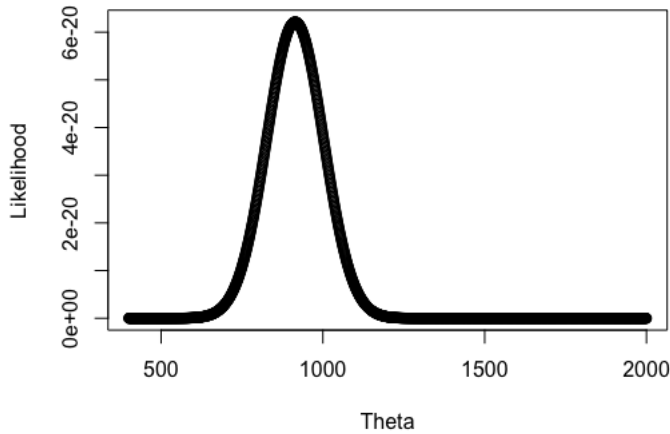
$$\begin{aligned}
 p_1 &= \int_{-\infty}^{600} \frac{1}{\sqrt{2\pi}\sigma^2} e^{-\frac{(x-\theta)^2}{2\sigma^2}} dx \\
 &= \Phi\left(\frac{600-\theta}{\sigma}\right), \text{ where } \Phi \text{ is cdf of standard normal} \\
 p_2 &= \Phi\left(\frac{1200-\theta}{\sigma}\right) - \Phi\left(\frac{600-\theta}{\sigma}\right) \\
 p_3 &= \Phi\left(\frac{1800-\theta}{\sigma}\right) - \Phi\left(\frac{1200-\theta}{\sigma}\right) \\
 p_4 &= 1 - \Phi\left(\frac{1800-\theta}{\sigma}\right)
 \end{aligned}$$

Let x_1, x_2, x_3, x_4 denote number of observed data that fall in each interval.

$$x_1 = 9, x_2 = 20, x_3 = 7, x_4 = 2$$

Then the likelihood function based on observed data and presumed multinomial probability can be represented as

$$\begin{aligned}
 L(\theta|x_1, x_2, x_3, x_4) &= \frac{n!}{\prod_{i=1}^4 (x_i)!} \prod_{i=1}^4 (p_i)^{x_i} \\
 &\propto \prod_{i=1}^4 (p_i)^{x_i} \\
 &\propto \Phi\left(\frac{600-\theta}{\sigma}\right)^9 \times [\Phi\left(\frac{1200-\theta}{\sigma}\right) - \Phi\left(\frac{600-\theta}{\sigma}\right)]^{20} \\
 &\quad \times [\Phi\left(\frac{1800-\theta}{\sigma}\right) - \Phi\left(\frac{1200-\theta}{\sigma}\right)]^7 \times [1 - \Phi\left(\frac{1800-\theta}{\sigma}\right)]^2
 \end{aligned}$$



Based on calculation, the MLE of θ is equal to 914.2893, with initial value 1000

Based on MLE, values in each interval are 10.122625 17.152466 9.286662 1.438248

The discrepancy statistic is calculated as

$$\begin{aligned} D(x) &= \sum_{i=1}^4 \frac{(x_i - np_i)^2}{np_i} \\ &= 1.379686 \end{aligned}$$

There are four categories and one unknown parameter, thus, degree of freedom is 2.

$$\begin{aligned} p - value &= P(\chi_2^2 \geq D(x)) \\ &= 0.5016549 \end{aligned}$$

chi-square test p-value of observed data is 0.5016549, therefore, under test size 0.05, observed data failed to provide significant evidence that normality model is incorrect.

(R code in Appendix)