MA40198 Coursework

**Model Checking**

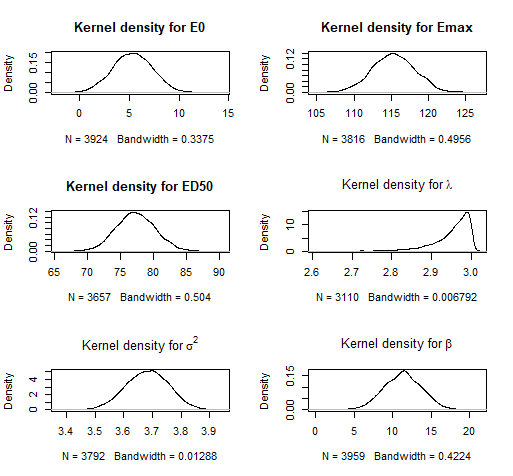
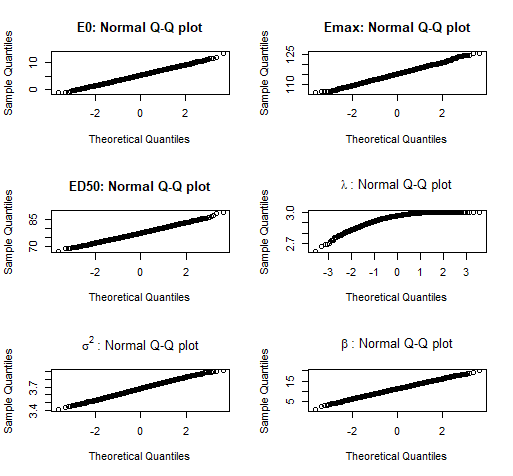
After choosing the second output of the Metropolis-Hastings sampler (which included the posterior correlation between parameters), as it provided a slightly better fit, we move on to produce some model checking calculations.

First, we verify that each parameter estimate is significant, i.e., different than zero. To determine this significance, we compute the 95% Credible Intervals (CI’s) and check whether these intervals contain zero or not.

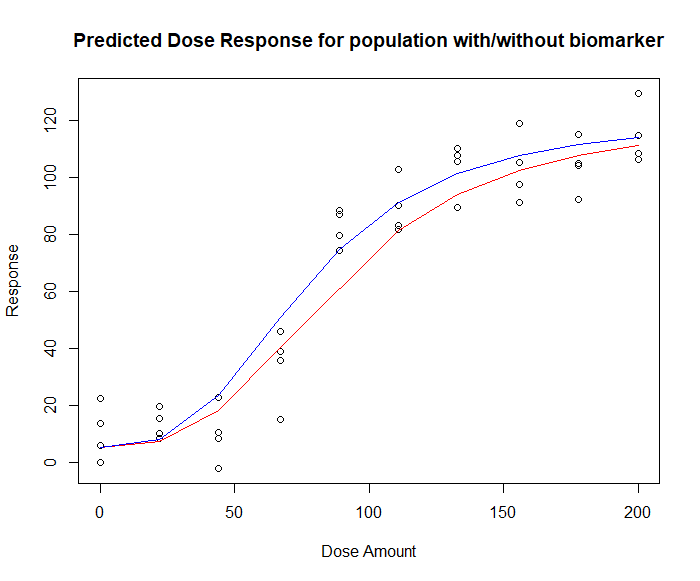
* 95% CI for E0: 1.437- 9.079
* 95% CI for Emax: 109.695-120.766
* 95% CI for ED50: 71.780-82.997
* 95% CI for λ: 2.833-2.998
* 95% CI for σ2: 3.533-3.823
* 95% CI for β: 6.505-16.018

Thus, we can conclude that each parameter is significantly different than zero. In particular, the parameter β, which is associated with a different response to the treatment in presence of the biomarker is different than zero. So we can also add to out conclusions that the presence of the biomarker affects the effectivity of the treatment.

We are also interested in determining if the marginal posterior distribution of each parameter is a normal distribution, given that we constructed the posterior distribution from samples of a multivariate normal distribution. The following quantile and density plots provide visual evidence that all the parameters, except for λ, might be normally distributed. These suspicions are confirmed after performing the Cramer-von Mises Normality test and observing that each test yields a p-value greater than 5%. This test also confirms that λ is not normally distributed, as it is highly skewed.

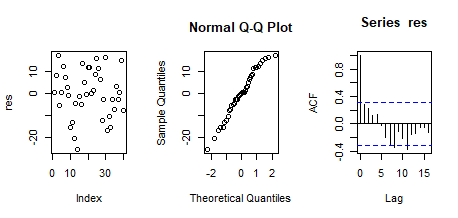


Using the estimated parameter values, we calculate the predicted response to treatment. We can confirm that the presence of the biomarker provides a significant difference in the response to treatment.



To assess if the model is proving a significant fit, we compute the residuals between the predicted and the observed responses to the treatment. The following plots show:

* A scatter plot of the residuals, showing there is no discernible pattern. This provides evidence of independence between the residuals.
* A quantile plot of the sample quantiles vs quantiles from a Normal distribution. The linear trend provides evidence that the residuals might be normally distributed. This suspicion is later confirmed by performing the Cramer-von Mises test and observing that it yielded a p-value greater than 5%.
* An autocorrelation plot between the residuals, showing further evidence of no correlation between the residuals, as only the 0-th order lag is statistically significant.



Combining this visual evidence and the result from the Cramer-von Mises test, we can conclude that the residuals are normally distributed and uncorrelated, hence they are independent.

As consequence, we can conclude that the proposed posterior distribution along with the parameter value estimates are relevant and provide a robust fit.

<http://www.math.chalmers.se/~rootzen/finrisk/reportwriting0315.pdf> : for how to write a report

<https://www.wikihow.com/Write-a-Statistical-Report>

<http://file.zums.ac.ir/ebook/75-Dose%20Finding%20in%20Drug%20Development%20(Statistics%20for%20Biology%20and%20Health)-Naitee%20Ting-0387290745-Sp.pdf>