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1 Question 3

The contour probability for $H_0 : \theta_0 = 0.25$ is obtained with two computational approaches solving the same problem: measuring the area under the beta posterior density curve with limits defined such that $p(\theta|y) > p(\theta_0|y)$. When θ_0 is less than the mode of the posterior density, this area corresponds to $P(\theta_0 < \theta < \delta)$, with density $p(\delta|y) = p(\theta_0)$. In this scenario, the complement p_b of the probability $P(\theta_0 < \theta < \delta)$ can be interpreted as the counterpart of a two-sided p-value. This is the contour probability.

In the first approach, we simply look for δ such that $(P(\theta_0|y) - P(\delta|y))^2 = 0$. This is accomplished with the numerical optimization **R** program *optimize*. Again assuming θ_0 to be the lower limit of integration, the complement of p_b is then obtained from:

$$\begin{aligned} P(\theta_0 < \theta < \delta) &= \int_{\theta_0}^{\delta} P(\theta|y)d\theta \\ &= \int_{\theta_0}^{\delta} \frac{1}{\text{Beta}(\bar{\alpha}, \bar{\beta})}\theta^{\bar{\alpha}-1}(1-\theta)^{\bar{\beta}-1} \\ &= F(\delta|y) - F(\theta_0|y) \end{aligned} \tag{1}$$

with the **R** digital table for the beta cumulative distribution F. In the second approach, we first obtain the mode $\bar{\theta}$ of the posterior beta density with $\frac{\bar{\alpha}-1}{\bar{\alpha}+\bar{\beta}-2}$. Then, for the case where θ_0 is less than $\bar{\theta}$, we search for δ in the interval $[\bar{\theta}, 1]$ such that $P(\theta_0|y) = P(\delta|y)$. This is accomplished with the **R** program *uniroot*. Once δ is obtained, the complement of the contour probability p_b is measured by following Equation 1. Both approaches give return the same contour probabilities.

As in Questions 2 and 3,

2 Question 10

Our goal here is to find the dosage associated with an increase of 0.01 in excess risk q of foetus malformation. It is useful to reformulate the question in order to clarify the problem and its solution.

The excess risk q is associated with a probability of malformation $P(d^*)$ by:

$$P(d^*) = q(1 - P(0)) + P(0) \tag{2}$$

where $P(0)$ is the prevalence of foetus malformation at a dose 0 of diglyme. The logit of $P(d)$, the probability of malformation at a given dose, can be estimated with the linear model $\alpha + \beta * \text{dose}$. As such, the dose we are looking for can be deduced with simple algebra from

$$\text{dose} = \text{BMD} = \frac{\text{logit}(P(d^*)) - \alpha}{\beta} \tag{3}$$

provided we have estimates for α and β. This dose is called the benchmark dose (BMD). From Question 3, we posess samples from the posterior distributions of β and α. Thus, we can not only furnish a point estimate of the BMD, but also express its uncertainty with a certitude interval. Only, as the dose variable is standardized, Equation 3 becomes

$$\text{BMD} = \left(\frac{\text{logit}(P(d^*)) - \alpha}{\beta} \right) s_{\text{dose}} + \text{avg}(\text{dose}) \tag{4}$$

where s and avg respectively designate the standard deviation and mean of the dose covariate.

Assuming that the prevalence at dose 0, $P(0)$, is known and obtained from the proportion in the provided table (i.e. 0.238), we get a mean BMD of 32.17 with a 95% equal-tails certitude interval of 20.53 to 42.79.