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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, we give dose 0 an informative conjugate prior with $\alpha = y - 1 = 29$ and $\beta = n - y - 1 = 193$. The other doses are given vague beta priors with $\alpha = 1$ and $\beta = 1$ which correspond to a uniform distribution

with support from 0 to 1. In Table 1, the contour probabilities are presented for each dose. The probability at dose 500 couldn't converge because 1 is the maximum of the beta distribution and the posterior mode as a value of 1. Convergence could have be obtained with an informative prior. For every dose, the probability of the true θ being 0.25 is less than 0.05. Thus, we conclude that the H_0 is implausible and reject it. Remarkably with dose 0, we would have kept H_0 had the prior been non-informative (i.e. $p_b = 0.68$).

Table 1: Contour probabilities for H_0:$\theta_0 = 0.25$ per dose level

Dose	θ_0	δ	p_b	1 - p_b	Obj.
0	0.25	0.137	0.001	0.999	0
62.5	0.25	0.140	0.035	0.965	0
125	0.25	0.947	0.000	1.000	0
250	0.25	1.000	0.000	1.000	0
500	0.25	1.000	0.000	1.000	NA

In Figure 1, the complement of the contour probabilities are illustrated for each dosage. These are coloured in grey and the plotted curves are the posterior beta distributions.
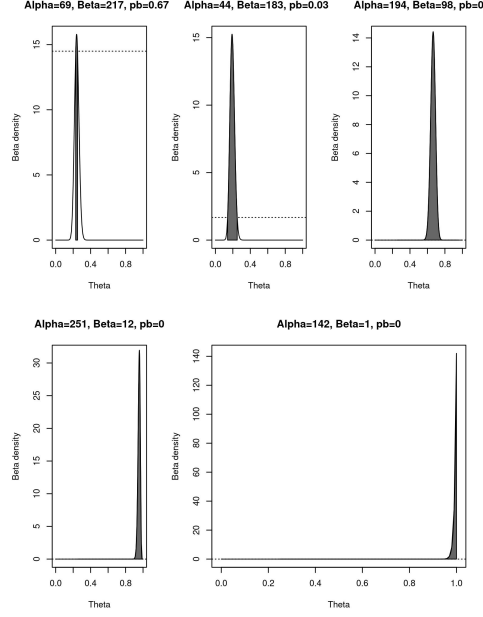
Figure 1: Contour probability plots per dose

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

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

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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.