

Bioassay experiment

→ “We use a particularly simple simulation approach, approximating the posterior distribution by a discrete distribution supported on a two-dimensional grid of points, that provides sufficiently accurate inferences for this two-parameter example”

→ They give drugs to animals.

→ “The animals’ responses are typically characterized by a dichotomous outcome: for example, alive or dead, tumor or no tumor.”

→ “...we must model the outcomes of the five animals within each group i as exchangeable (...) and independent...”

$$y_i | \theta_i \sim \text{Bin}(n_i, \theta_i),$$

→ What about the prior?

“...noninformative density such as $p(\theta_i) \propto 1$ ”

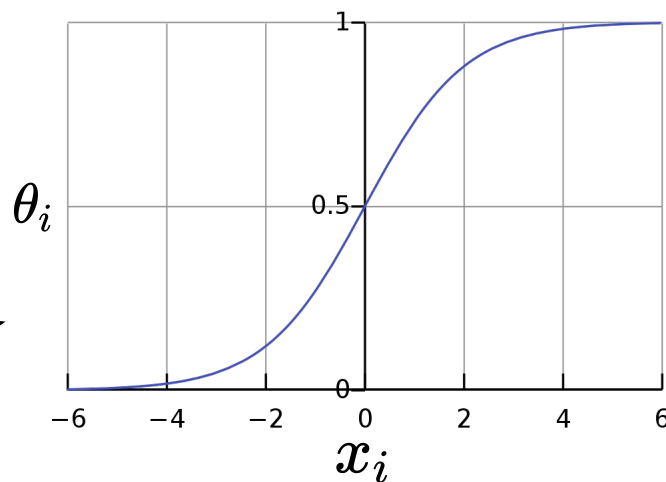
BUT

“...however; we know the dose level x_i for each group i , and one would expect the probability of death to vary systematically as a function of dose...”

“... θ_i , being a probability, must be constrained to lie between 0 and 1...”

$$\text{logit}(\theta_i) = \alpha + \beta x_i \longleftrightarrow \theta_i = \frac{\exp(\alpha + \beta x_i)}{1 + \exp(\alpha + \beta x_i)}$$

Dose, x_i (log g/ml)	Number of animals, n_i	Number of deaths, y_i
−0.86	5	0
−0.30	5	1
−0.05	5	3
0.73	5	5



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→ Dado el modelo de parámetros, el likelihood:

$$p(y_i|\alpha, \beta, n_i, x_i) \propto [\text{logit}^{-1}(\alpha + \beta x_i)]^{y_i} [1 - \text{logit}^{-1}(\alpha + \beta x_i)]^{n_i - y_i}$$

→ Y el posterior:

$$\begin{aligned} p(\alpha, \beta|y, n, x) &\propto p(\alpha, \beta|n, x) p(y|\alpha, \beta, n, x) \\ &\propto p(\alpha, \beta) \prod_{i=1}^k p(y_i|\alpha, \beta, n_i, x_i) \end{aligned}$$

→ “... *an analysis based on a prior distribution for (α, β) that is independent and locally uniform in the two parameters; that is, $p(\alpha, \beta) \propto 1$.*”

→ Es decir, usa un modelo para conectar tita (desconocido) con alfa y beta (modelo multiparamétrico, galerazo aceptable) y luego un prior no informativo para alfa y beta.

→ Vamos al código...

Bioassay experiment: normal approximation

→ “To begin, we compute the mode of the posterior distribution (using a logistic regression program) and the normal approximation evaluated at the mode.”

```
def bioassayfun(w):  
    a = w[0]  
    b = w[1]  
    et = np.exp(a + b * x)  
    z = et / (1 + et)  
    e = - np.sum(y * np.log(z) + (n - y) * np.log(1 - z))  
    return e  
  
# initial guess  
w0 = np.array([0.0, 0.0])  
  
# optimise  
optim_res = optimize.minimize(bioassayfun, w0)  
  
# extract desired results  
w = optim_res['x'] # mean  
S = optim_res['hess_inv'] # covariance matrix
```

$$p(\theta|y) \approx N(\hat{\theta}, [I(\hat{\theta})]^{-1})$$

$$I(\theta) = - \frac{d^2}{d\theta^2} \log p(\theta|y)$$

$$e = - \sum_i y_i \cdot \log\left(\frac{\exp(\alpha + \beta \cdot x_i)}{1 + \exp(\alpha + \beta \cdot x_i)}\right) + (n_i - y_i) \cdot \log\left(\frac{1}{1 + \exp(\alpha + \beta \cdot x_i)}\right)$$

$$\log p(\theta|y)$$

Bioassay experiment: LD50

A parameter of common interest in **bioassay** studies is the LD50—the dose level at which the probability of death is 50%. In our logistic model, a 50% survival rate means

$$\text{LD50: } E\left(\frac{y_i}{n_i}\right) = \text{logit}^{-1}(\alpha + \beta x_i) = 0.5;$$

thus, $\alpha + \beta x_i = \text{logit}(0.5) = 0$, and the LD50 is $x_i = -\alpha/\beta$.