# Non-Linear Modeling for Ca Bioassays

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For the binary problems the outcome, for the $n$ experiments is $Y_i$=0 or 1, $i$ = 1,2,…,$n$ and this outcome is linked with the covariate or input variable $x \in X$ and the parameter vector $\theta$, from the parameter space $\Theta \subseteq \Re^p$, through a probability model PM, which assigns probability $p$ on the "success" as:

$$p = p(x;\theta) = p(Y_i=1 \mid x) = \mathrm{PM}(x;\theta) = 1 - P(Y_i=0 \mid x).$$

In Bioassay the typical situation is to consider *logit*, *probit* or *exponential models* (known also as *one-hit*) as PM i.e.

$\mathrm{PM}_L = \log \{p(x;\theta)\,(1-p(x;\theta))\}$, $\mathrm{PM}_P = \Phi^{-1}\{p(x;\theta)\}$, $\mathrm{PM}_E = \exp(-\theta x)$, respectively, with "$\Phi$" being the cumulative distribution function of the standard normal distribution.

For regression models, the input variable $x$, is linked with the involved parameter $\theta$, through a (deterministic) function, $f(x;\theta)$. In practice the responses or readings $y$ are only observed with the experimental error $e$. This result in a (stochastic) nonlinear regression model of the form: $y_i = f(x_i,\theta) + e_i$, for the $i$=1,2,…,$n$ experiments.

The function $f$ (typical example the Michaelis-Menden model) is, in principle, a smooth, nonlinear regression function and the errors are assumed independent identically distributed random variables with mean $E(e_i)=0$ and variance $V(e_i)=\sigma^2>0$. But when a Bioassay is performed the crucial problem in both cases remains: the nonlinear design points depend on the unknown parameters we design to estimate them! Typical example being the logistic model of the form

$$\mathrm{PM}_L = \{1+\exp[-\theta_1(x-\theta_2)]\}^{-1},$$

the optimal design allocates half observations at the optimal design points

$$(1.54-\theta_1)/\theta_2 \ , \ (-1.54-\theta_1)/\theta_2 \ .$$

The target of this paper is to link the main nonlinear models with optimal experimental theory, when a Bioassay is formed, for, mainly, Ca problems.