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Introduction to Categorical Data Analysis

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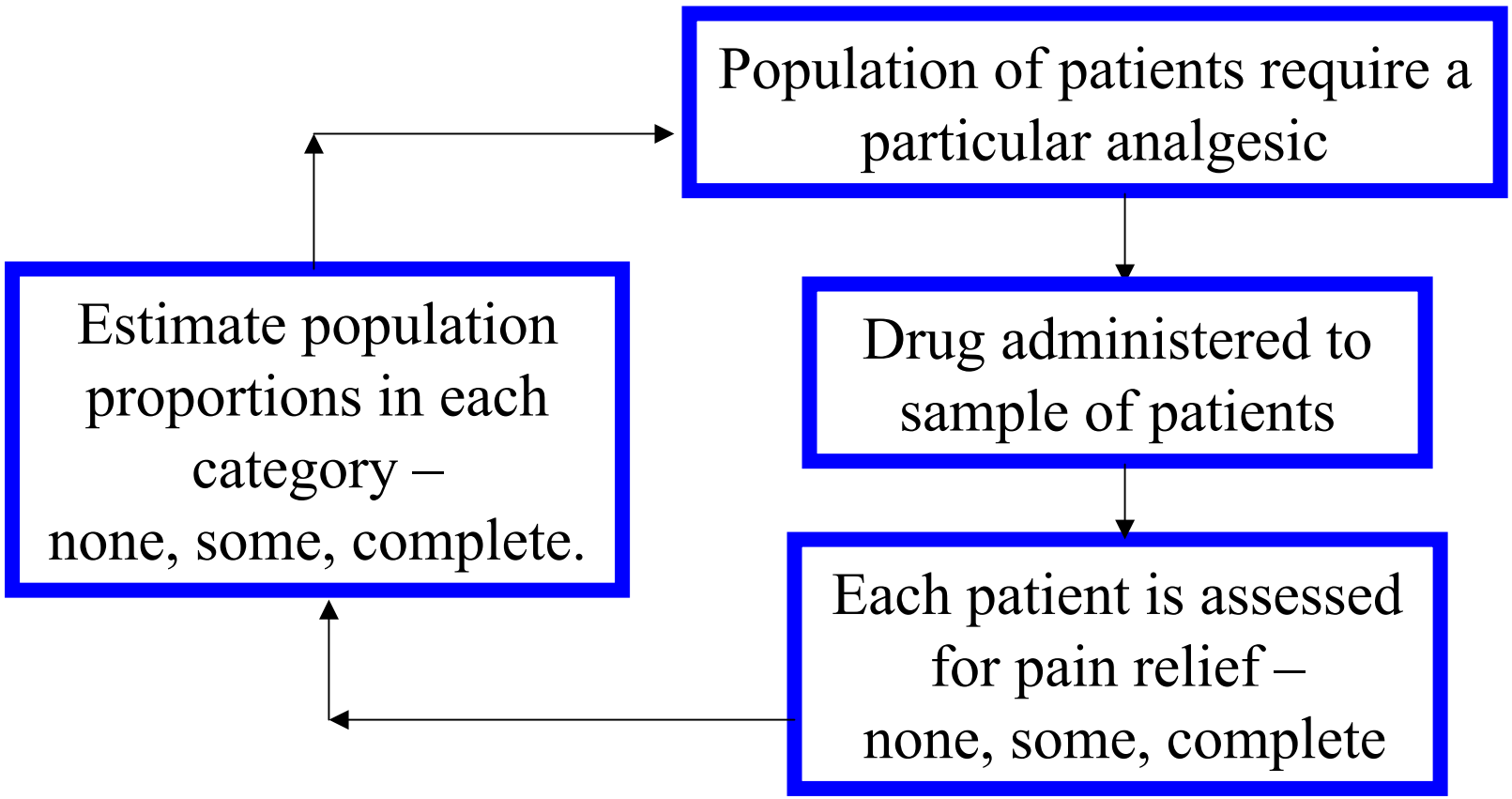
Data Types

- Quantitative
  - Continuous — Plasma drug conc., BP, Muscle Tension, Time
  - Discrete — Number of blood cells, Number of heart attacks
- Categorical
  - Nominal — Religion, Nationality, Gender
  - Ordinal — Social class, Treatment outcome
  - Binary — Gender, Dead/Alive

Example: Categorical Data



Binary Data

- Describe the two categories as "Success" (S) and "Failure" (F).

- Code

$$Z = 0 \quad \text{for } F$$

$$Z = 1 \quad \text{for } S$$

Binary Data

- Proportion of S in population.
- Randomly select a member of the population – probability of S.
- Proportion = Probability

Binary Data

- Z has the Bernoulli Distribution

$$\Pr(Z = 1) = \pi \quad \text{Prob of } S$$

$$\Pr(Z = 0) = 1 - \pi \quad \text{Prob of } F$$

$$\Pr(Z = r) = \pi^{r}(1-\pi)^{(1-r)} \qquad r = 0,1$$

Estimation: Method of Maximum Likelihood

- Likelihood

$$L(\pi) = \prod_{i=1}^{n} \pi^{z_i} (1-\pi)^{(1-z_i)}$$

- $\hat{\pi}$ is the value of π that maximises the likelihood

Simple Example

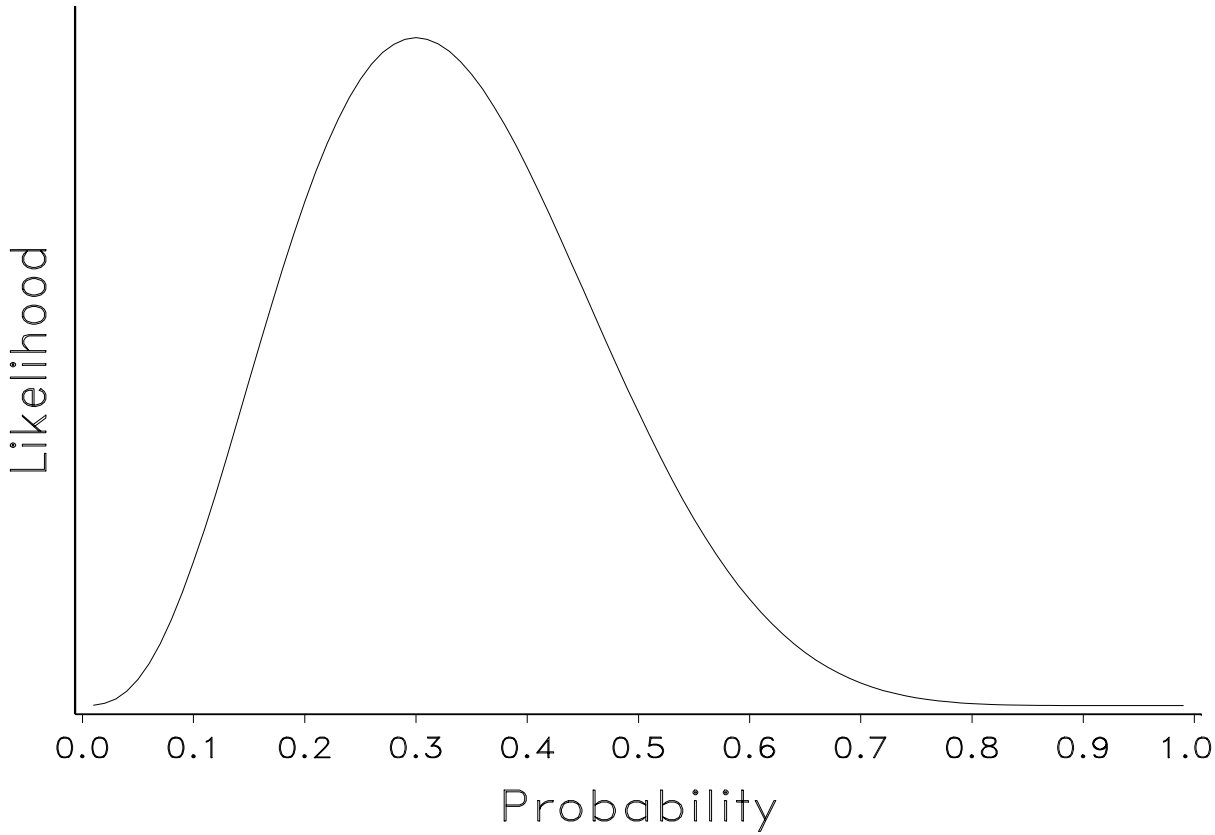
10 observations:- 3S's 7F's

Simple model with no structure

$$Z \sim Bernoulli(\pi)$$

$$L(\pi) = \prod_{i=1}^{n} \pi^{z_i} (1-\pi)^{(1-z_i)}$$

Example: Likelihood



Data Modelling

- Previous example had no structure in the data.
- Consider the case where the subjects were administered different doses of drug and the response depends on dose.
- Another example would be where response changes with time following drug administration (PK-PD).

Data Modelling

- Take account of the structure by recording the values of covariates (*x*'s) for each member of the sample e.g. dose, time.

- Then construct a model which describes how the parameters depend on the covariates.

Modelling Binary Data

- We model π_i e.g.

$$\pi_i = f(x_i, \theta)$$

- However,

$$0 \leq \pi_i \leq 1$$

- There is no guarantee that

$$0 \leq f(x_i, \hat{\theta}) \leq 1$$

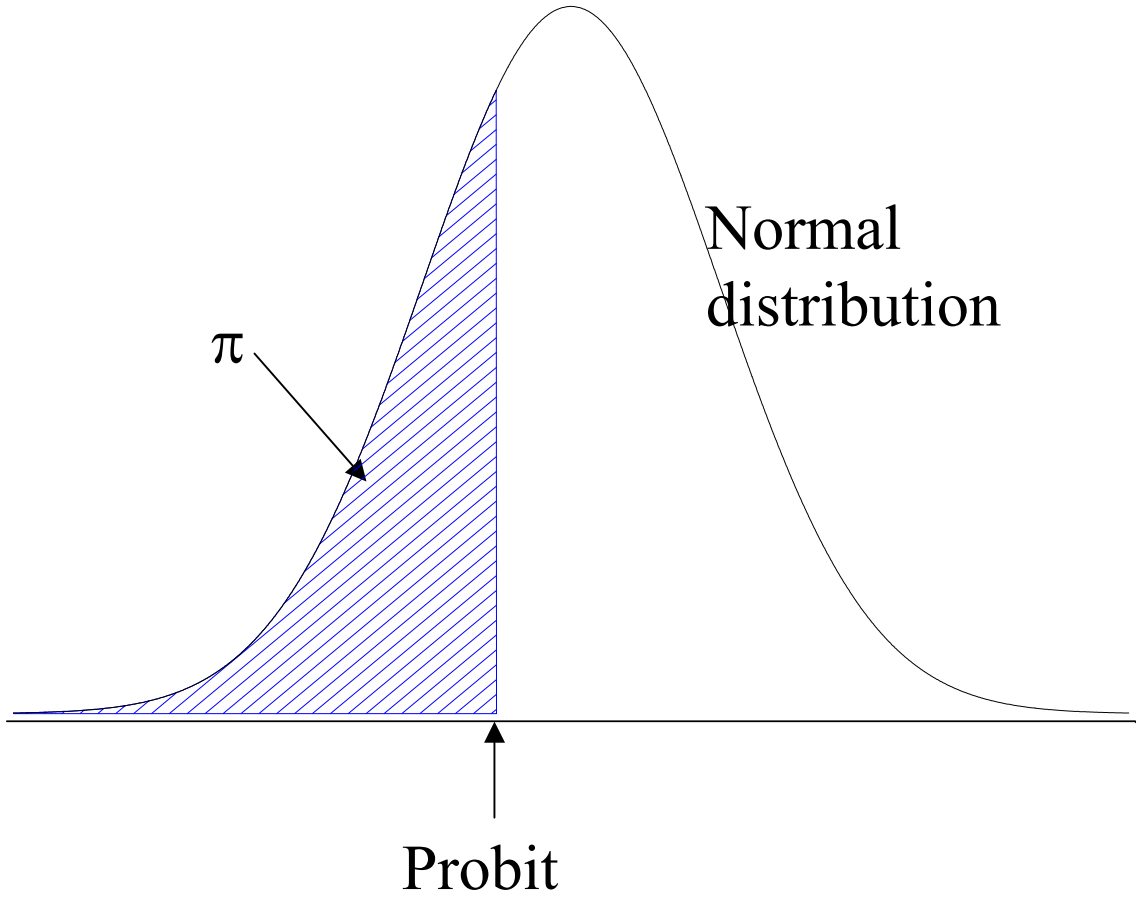
Modelling Binary Data

Transform π_i from (0,1) to $(-\infty,+\infty)$ and model the transformed value to ensure that model predicted probabilities lie in (0,1).

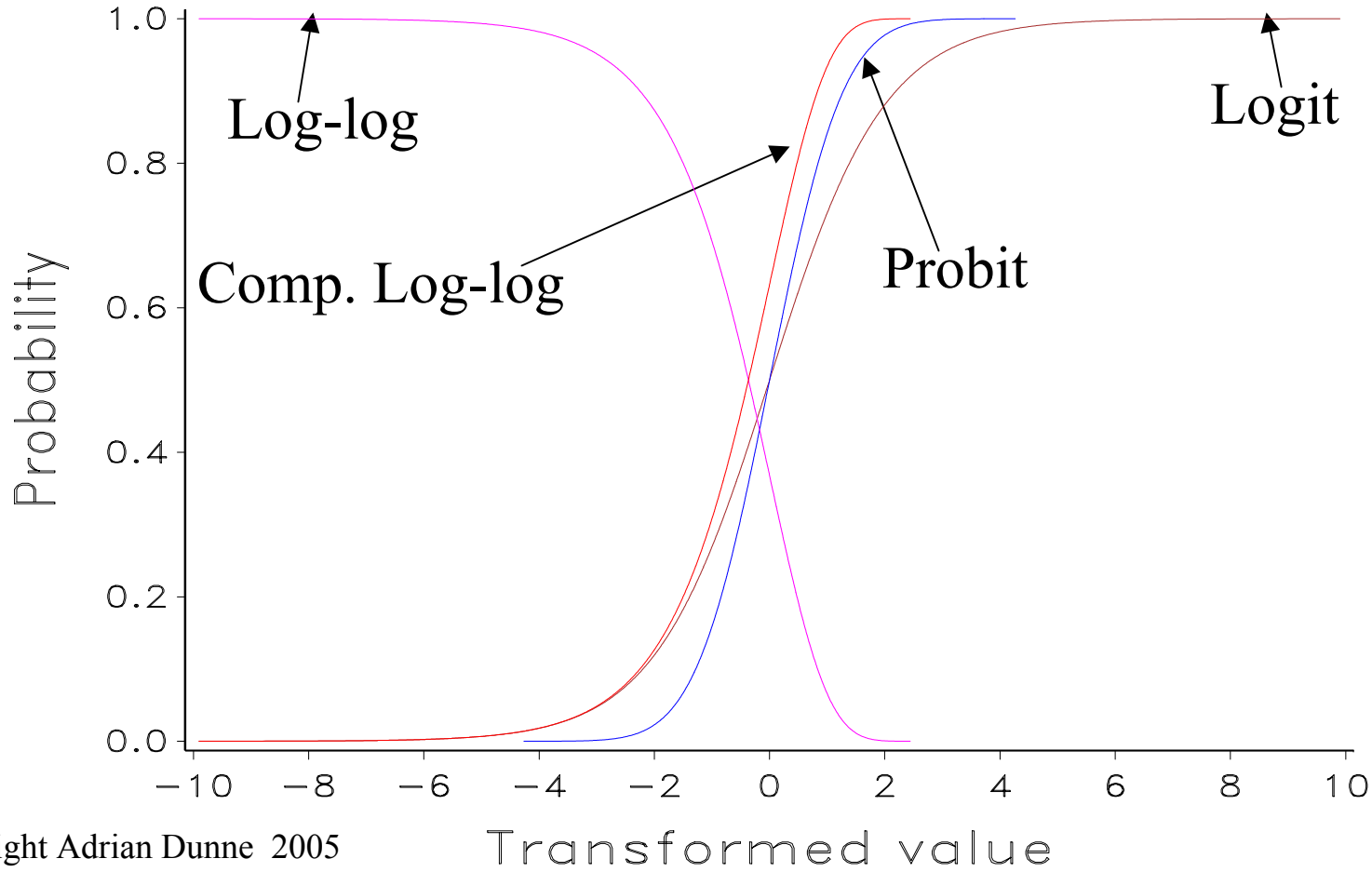
Transformations

- Logit $\text{logit}(\pi_i) = \log\left(\frac{\pi_i}{1-\pi_i}\right)$
- Probit $\text{probit}(\pi_i) = \Phi^{-1}(\pi_i)$
- Log-log $\log(-\log(\pi_i))$
- Complementary log-log $\log(-\log(1-\pi_i))$

Probit transformation



Transformations



Logistic Regression Model

Now consider a model with structure

$$\text{logit}(\pi_i) = f(x_i, \theta)$$

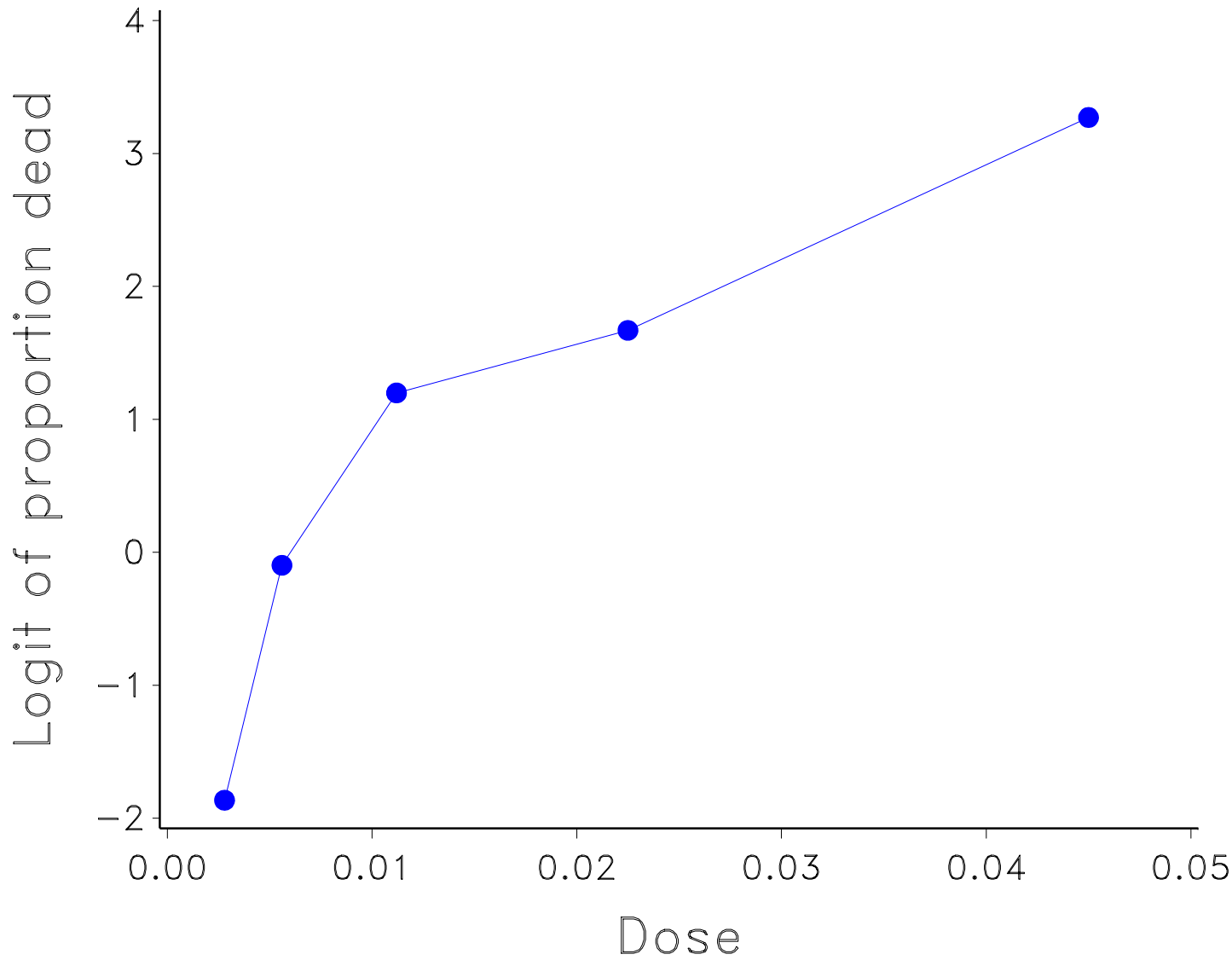
Example

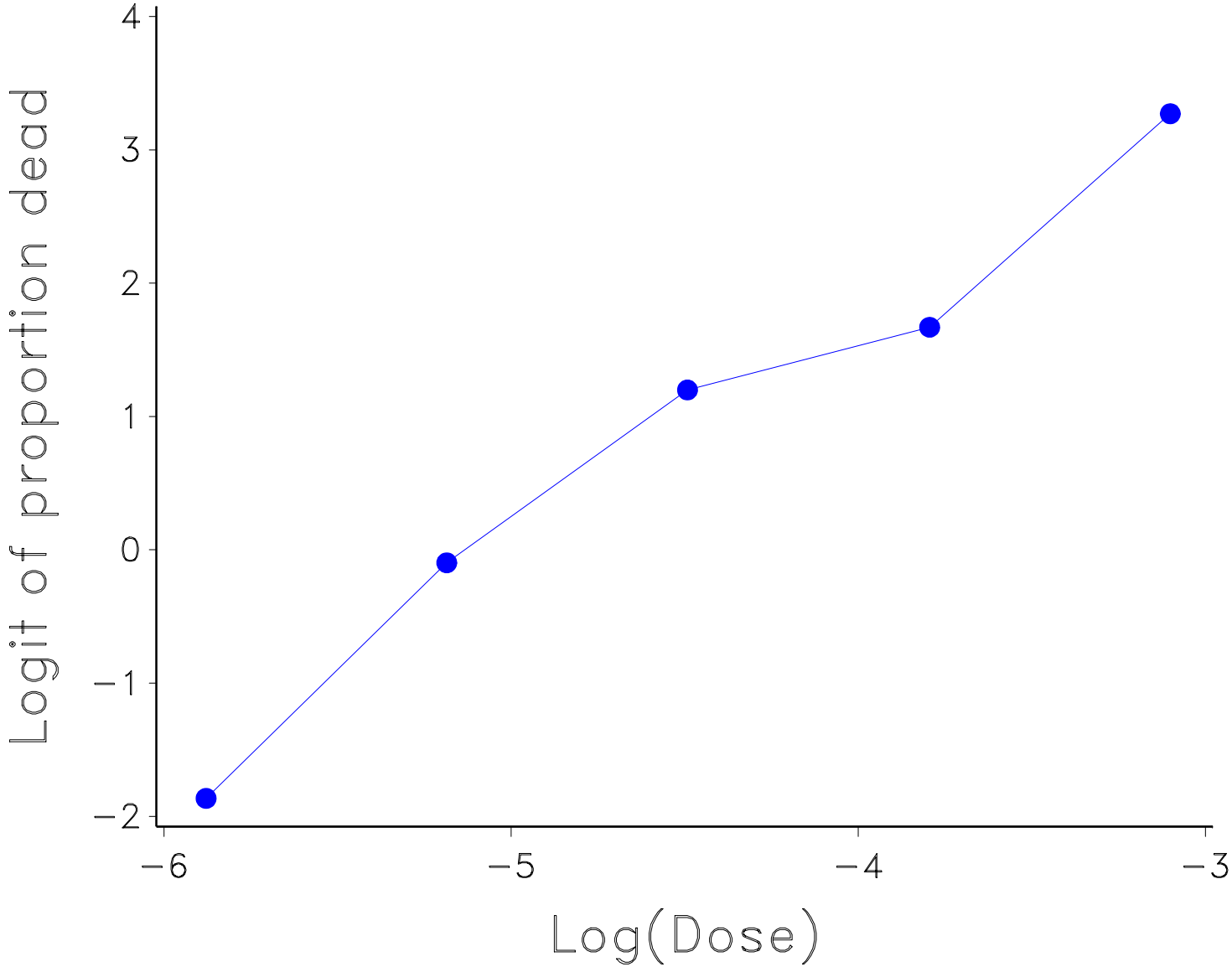
$$\text{logit}(\pi_i) = \theta_1 + \theta_2 x_{1i} + \theta_3 x_{2i} + \ldots$$

Example: Bioassay

Beetle deaths following dosing with an insecticide

Dose	# Exposed	# Dead
0.0028	40	5
0.0056	40	19
0.0112	40	31
0.0225	40	34
0.0450	40	39





Logit Model

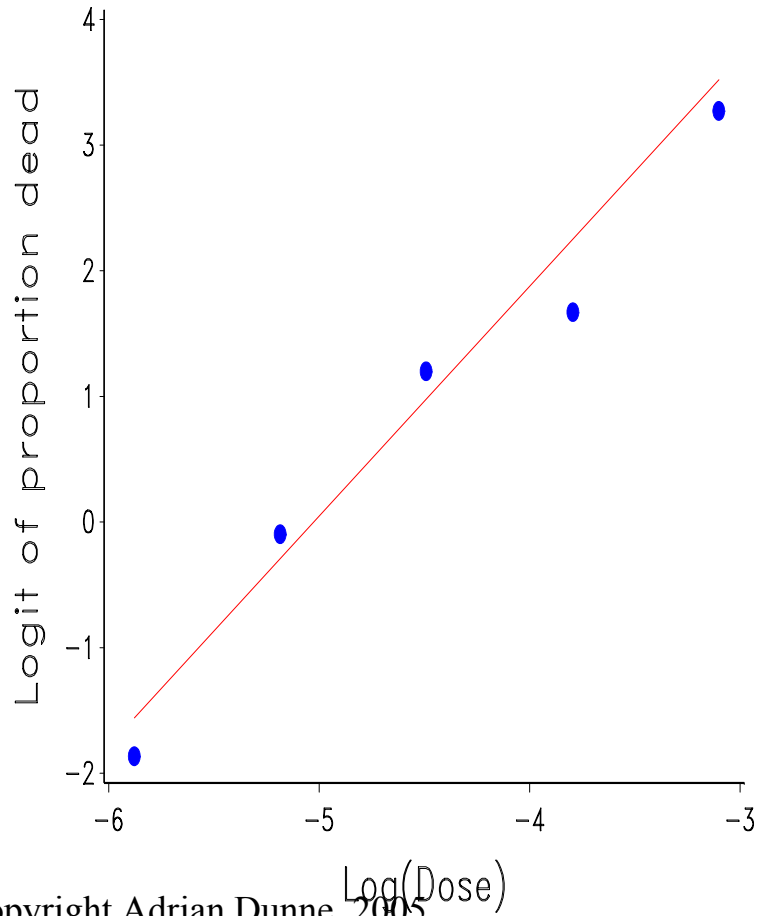
Linear logistic model with log(dose)

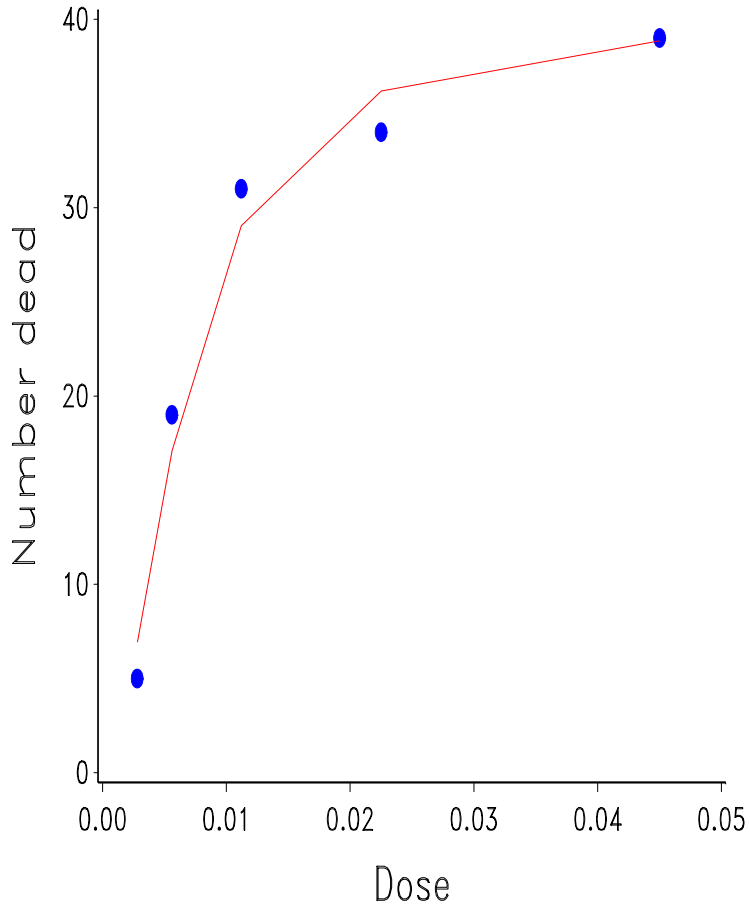
$$z_i \sim Bernoulli(\pi_i)$$

$$\text{logit}(\pi_i) = \theta_1 + \theta_2 \log(dose_i)$$

$$L(\boldsymbol{\theta}) = \prod_{i=1}^{n} \pi_i^{z_i} (1-\pi_i)^{(1-z_i)}$$

Observed & Predicted Values



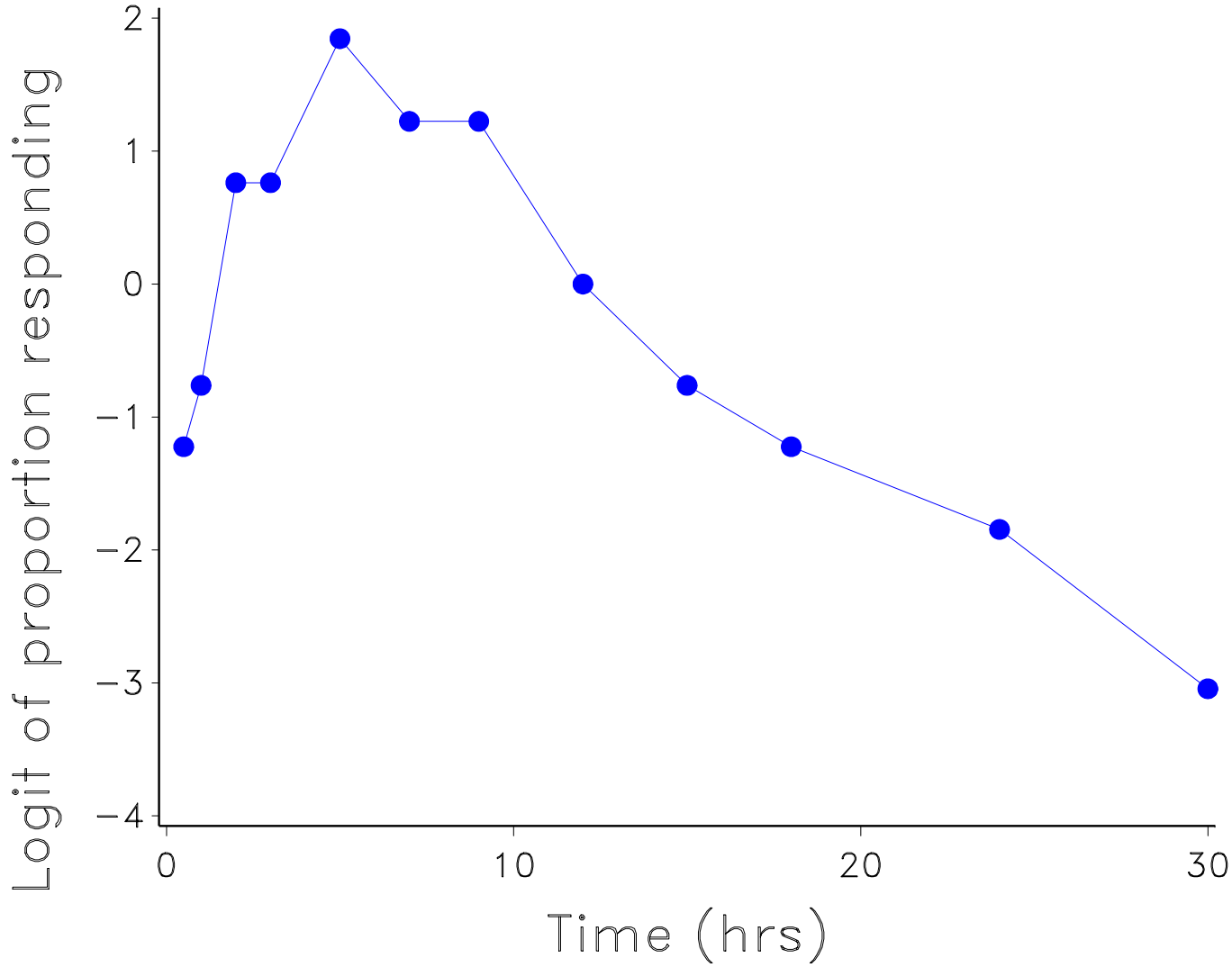


Mixed Effects Modelling

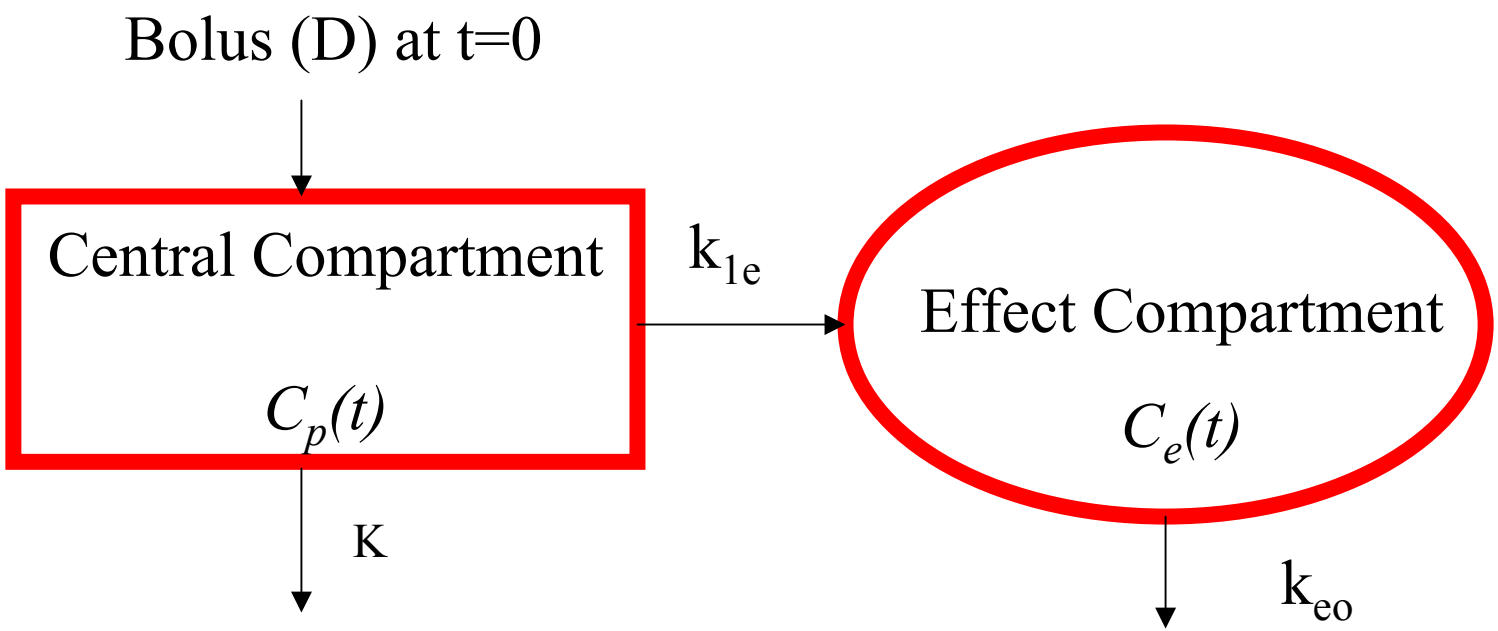
- Modelling correlation between responses/variation between groups.
  - Groups of related items
  - Repeated measures/Longitudinal data

Example: Binary PK-PD response

- 10 subjects all received dose of 100 units.
- Bolus iv administration.
- Binary response (dry mouth) recorded for each subject at times 0.5, 1, 2, 3, 5, 7, 9, 12, 15, 18, 24, 30 hours.



PK-PD Model



$$Eff\ (t) = f\ (C_e\ (t))$$

PK-PD Model

- Linear PD model

$$Eff(t) = \theta_1 + \theta_2 C_e(t)$$

$$\text{logit}(\pi(t)) = \theta_1 + \theta_2 C_e(t)$$

Example: Binary Population PK-PD model

- Variation between subjects
- Longitudinal (repeated measures) data – observations on same subject are correlated
- Model intrasubject correlation and intersubject variation using random effects

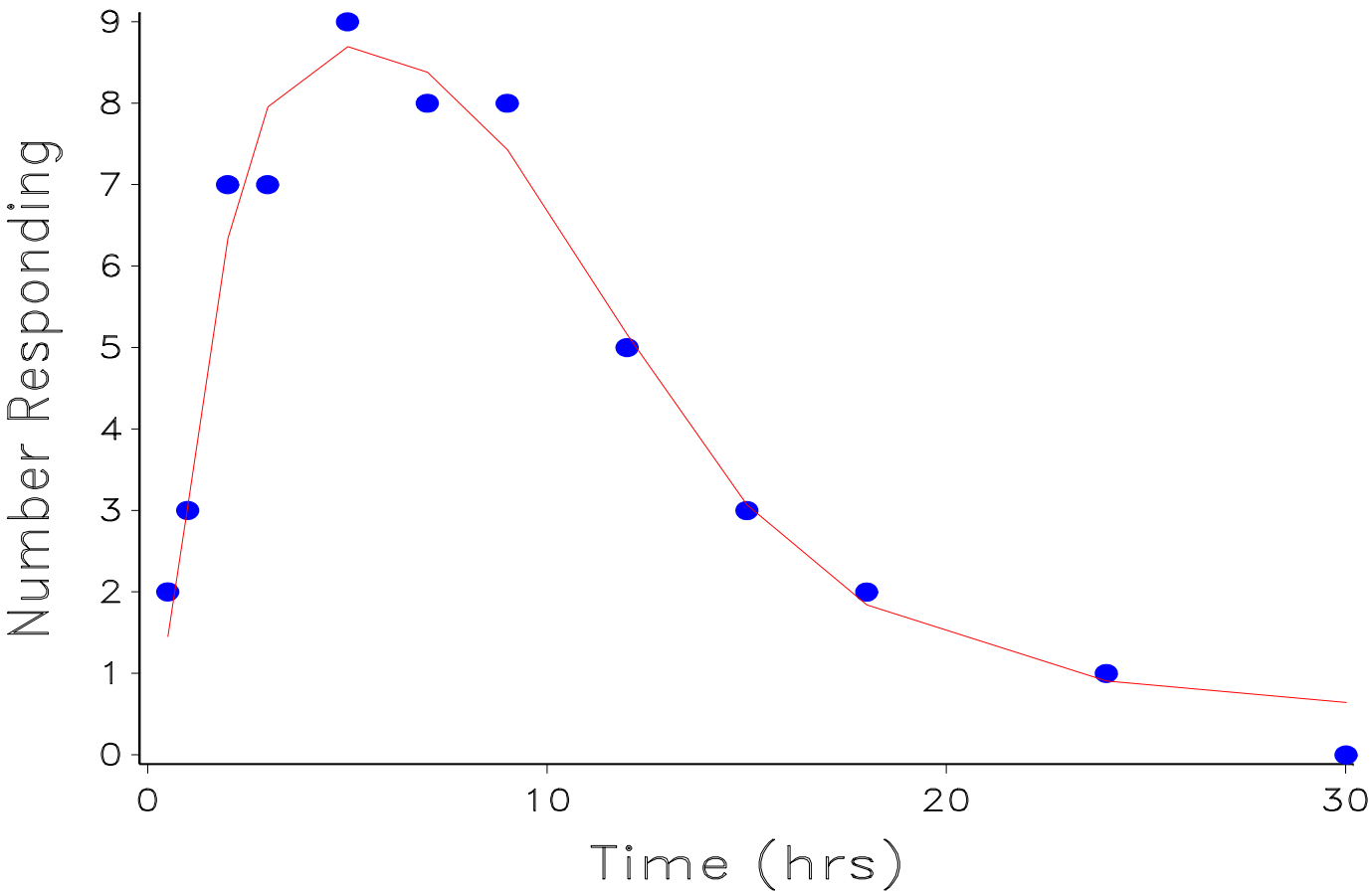
Example: Binary Population PK-PD model

$$\text{logit}\ (\pi_i(t_j)) = \theta_1 + \theta_2 C_e(t_j) + \eta_i$$

$$\eta_i \sim N(0, \Omega)$$

$$L(\boldsymbol{\theta}, \Omega) = \prod_{i=1}^{n} \int_{-\infty}^{+\infty} \prod_{j=1}^{m_i} \pi_i(t_j)^{z_i} (1 - \pi_i(t_j))^{(1-z_i)} f(\eta_i, \phi) d\eta_i$$

Observed & Predicted Values



Latent Variable

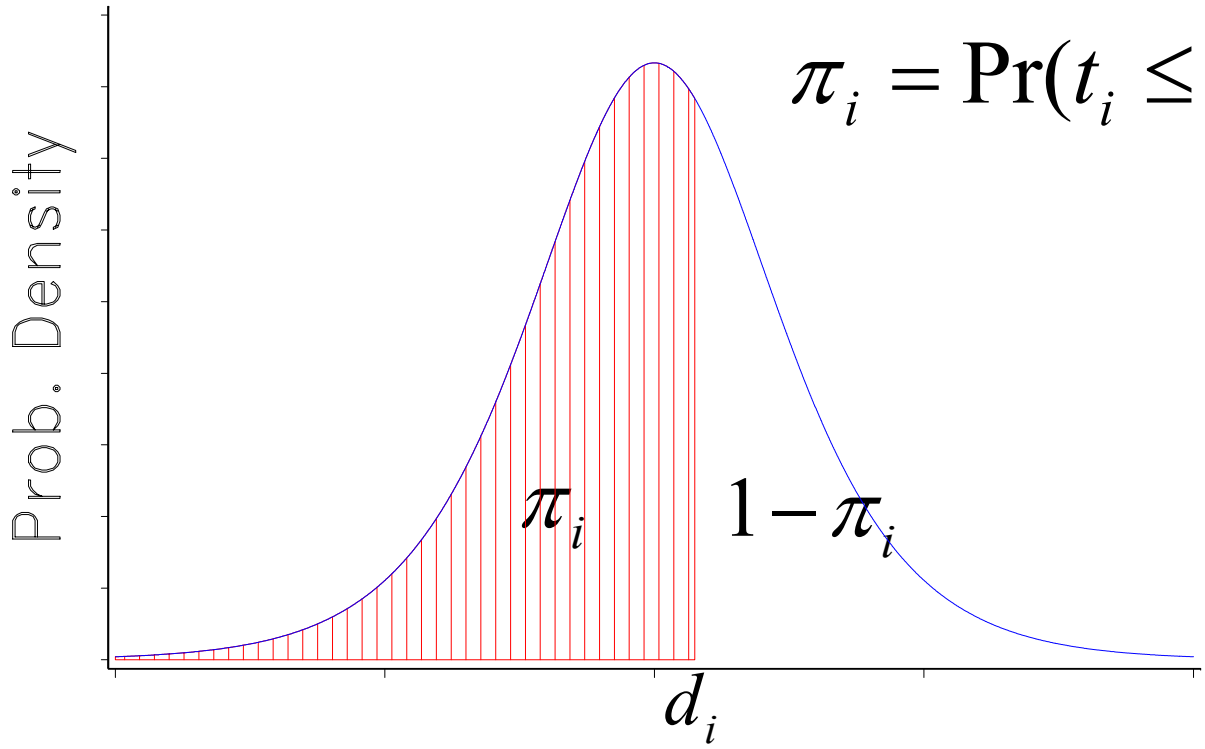
- Consider again the insecticide bioassay

- Assume that each insect has an (unobserved) tolerance t_i which varies randomly across the population of insects

$$t_i \leq d_i \Rightarrow z_i = 1$$

$$t_i > d_i \Rightarrow z_i = 0$$

Tolerance distribution



$z_i = 1$ $\qquad$ $z_i = 0$

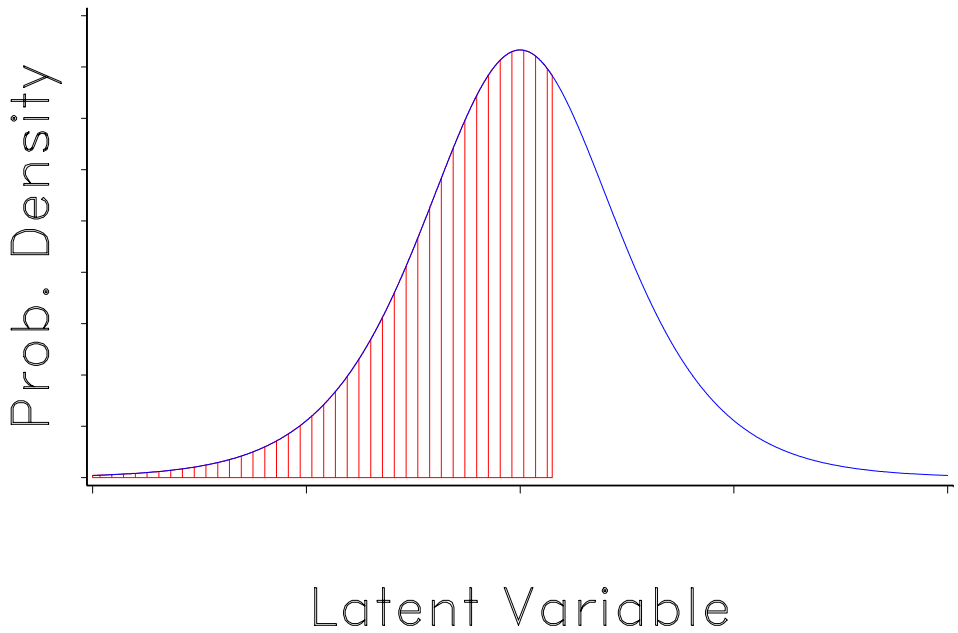
Latent Variables

- d_i is known as the cut-point
- Here the latent variable is tolerance

$$\pi_i = \Pr(t_i \leq d_i)$$

$$\pi_i = \int_{-\infty}^{d_i} f(t_i, \boldsymbol{\beta}) dt_i$$

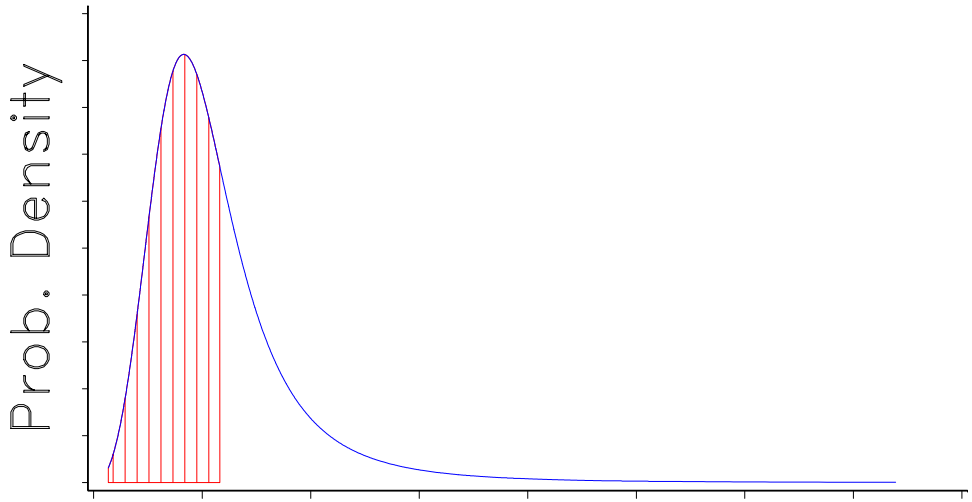
Logistic distribution



$$f(t_i, \boldsymbol{\beta}) = \frac{\exp((t_i - \beta_0)/\beta_1)}{\beta_1\left(1+\exp((t_i - \beta_0)/\beta_1)\right)^2}$$

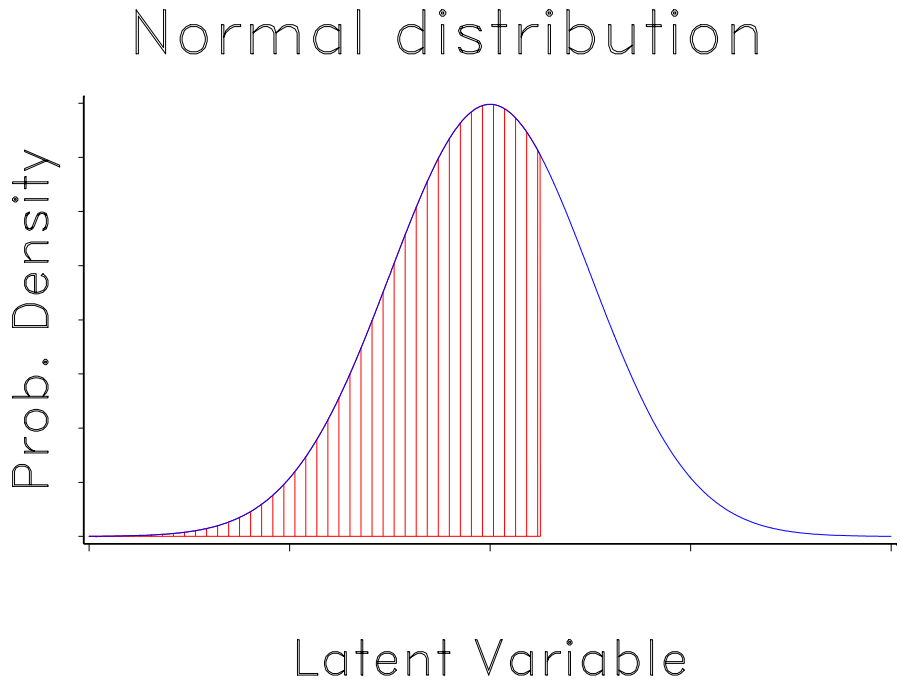
$$\text{logit}(\pi_i) = \theta_1 + \theta_2 d_i$$

Log–logistic distribution



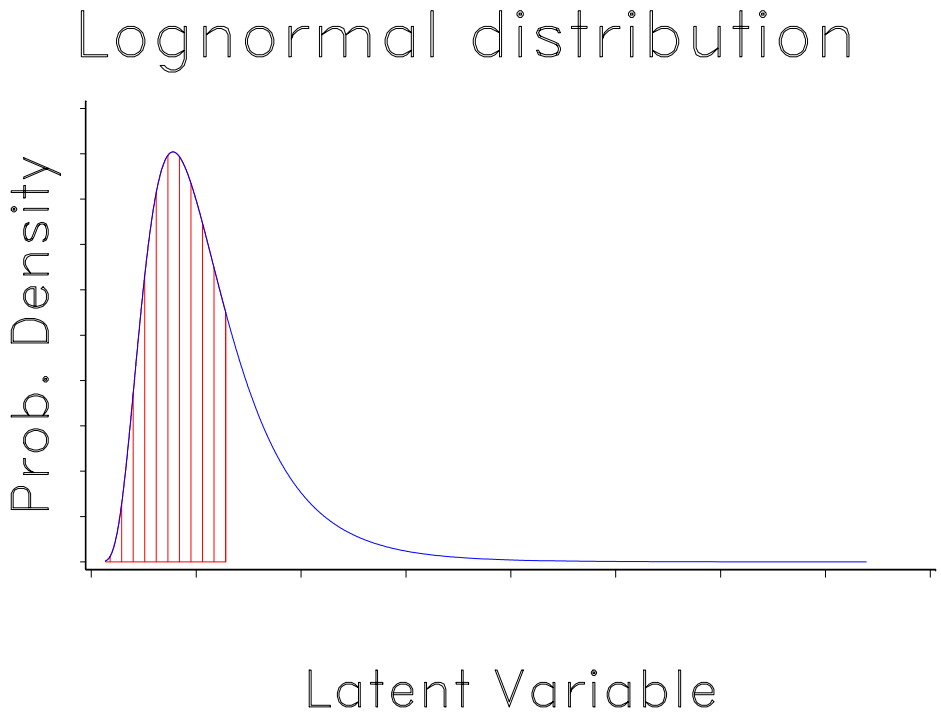
$$f(t_i, \boldsymbol{\beta}) = \frac{\exp((\log(t_i) - \beta_0)/\beta_1)}{t_i \beta_1 \left(1 + \exp((\log(t_i) - \beta_0)/\beta_1)\right)^2}$$

$$\text{logit}(\pi_i) = \theta_1 + \theta_2 \log(d_i)$$



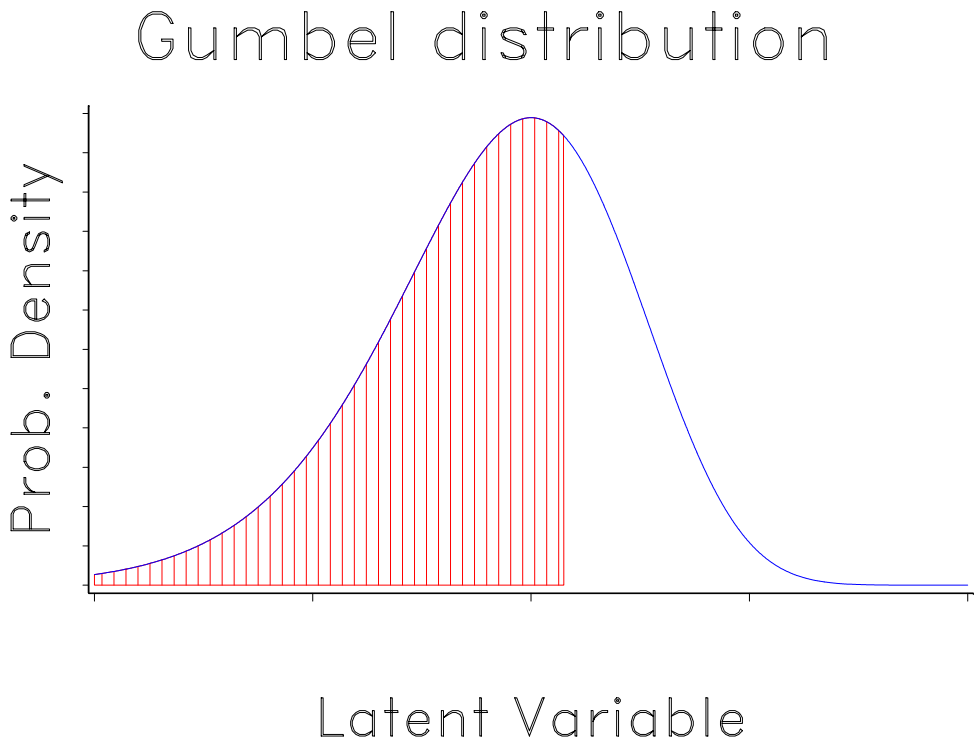
$$f(t_i, \boldsymbol{\beta}) = \frac{\exp(-0.5((t_i - \beta_0)/\beta_1)^2)}{\sqrt{2\pi}\beta_1}$$

$$\text{probit}(\pi_i) = \theta_1 + \theta_2 d_i$$



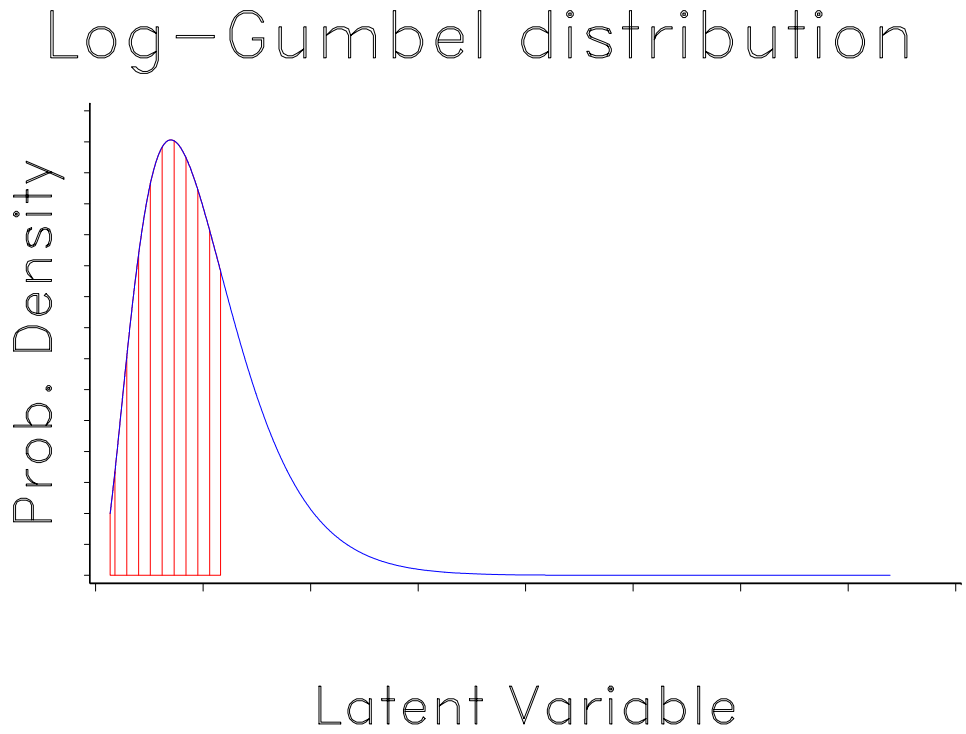
$$f(t_i, \boldsymbol{\beta}) = \frac{\exp(-0.5((\log(t_i) - \beta_0)/\beta_1)^2)}{t_i \sqrt{2\pi}\beta_1}$$

$$\text{probit}(\pi_i) = \theta_1 + \theta_2 \log(d_i)$$



$$f(t_i, \boldsymbol{\beta}) = \frac{\exp((t_i - \beta_0)/\beta_1)\exp(-\exp((t_i - \beta_0)/\beta_1))}{\beta_1}$$

$$\log(-\log(1-\pi_i)) = \theta_1 + \theta_2 d_i$$



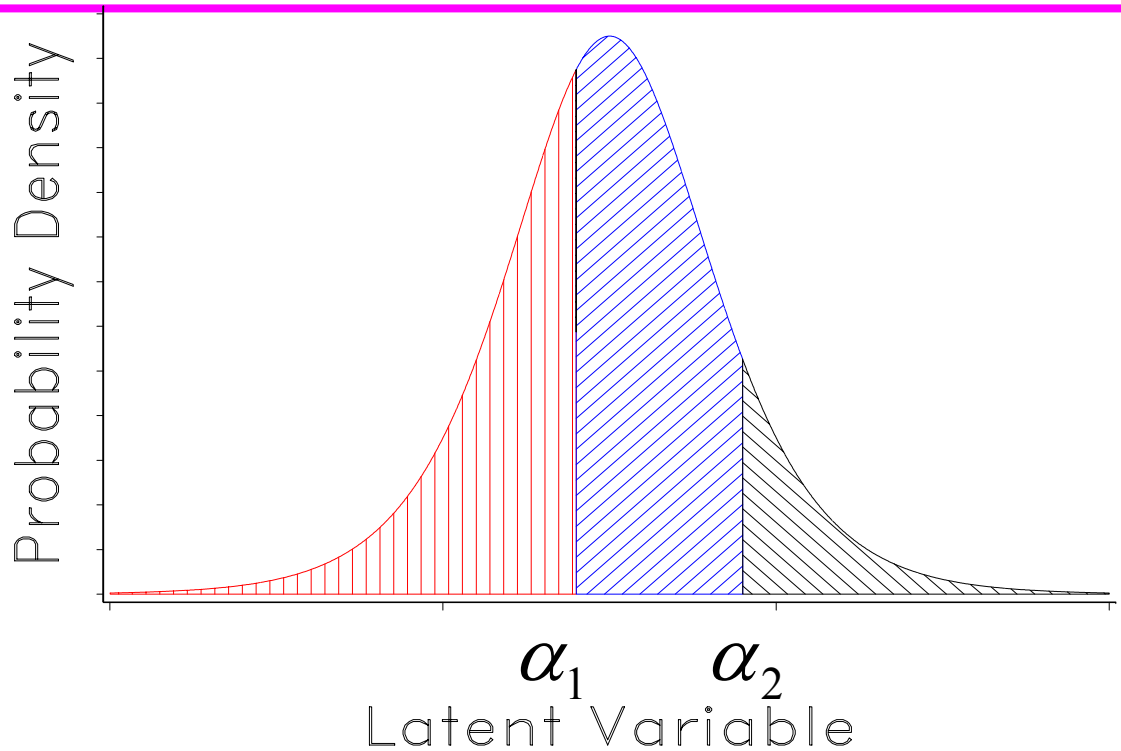
$$f(t_i, \boldsymbol{\beta}) = \frac{\exp((\log(t_i) - \beta_0)/\beta_1)\exp(-\exp((\log(t_i) - \beta_0)/\beta_1))}{t_i \beta_1}$$

$$\log(-\log(1-\pi_i)) = \theta_1 + \theta_2 \log(d_i)$$

Ordinal Data

- Ordered categories e.g. severity of symptoms, none, mild, moderate, severe.
- Ordered categories $Z = 1,2,\ldots, K$
- Probabilities $\pi_1, \pi_2, \ldots, \pi_K$

Latent Variable



$Z = 1 \qquad Z = 2 \qquad Z = 3$

Cumulative Logits

- Cumulative probabilities

$$F_k = \pi_1 + \pi_2 + \ldots + \pi_k$$

- Cumulative Logits

$$L_k = \text{logit}(F_k) = \log\left(\frac{F_k}{1-F_k}\right) \qquad k = 1,2,\ldots,K-1$$

- A model for L_k is a logit model for a binary response.
- We need *K-1* logit models

Cumulative Logits

Based on *K-1* dichotomizations.

- (1) and (2 to K)
- (1 and 2) and (3 to K)
- (1 to 3) and (4 to K)
- etc.

Proportional Odds Model

- Covariate x influences all cumulative logits equally

$$\text{logit}(F_k) = \alpha_k - f(x, \theta)$$

- Such a model is equivalent to x influencing the location (but not the spread) of the distribution of the latent variable.

Proportional Hazards Model

- Covariate x influences all cumulative complementary log-logs equally

$$\log(-\log(1-F_k)) = \alpha_k - f(x,\theta)$$

- Such a model is equivalent to x influencing the location (but not the spread) of the distribution of the latent variable.