

Bayesian fractional polynomial model used to model the Bland–Altman limits of agreement

The Bayesian model applied to the Bland–Altman limits of agreement was:

$$\begin{aligned}\log_e(d_j) &\sim t(\mu_j, \sigma_j^2, 4), & j = 1, \dots, N, \\ \mu_j &= \alpha_0 + \alpha_1 f_1(a_j), \\ \sigma_j^{-2} &= \exp[\beta_0 + \beta_1 f_2(a_j)], \\ \alpha_k &\sim N(0, 1000), & k = 0, 1, \\ \beta_k &\sim N(0, 1000), & k = 0, 1.\end{aligned}$$

Where d_j is the difference in sample size for study j and there were N studies in total. This difference was modelled using a t-distribution with 4 degrees of freedom. The mean and variance were modelled using regression equations with an intercept and the study's average sample size a_j transformed using functions $f_1()$ and $f_2()$ which were fractional polynomials. We tested the same powers for the polynomials: $\{-2, -1, -0.5, 0, 0.5, 1, 2, 3\}$, but the mean and variance could have different best powers. The best pair of powers were chosen using the deviance information criterion.

The same model was used for the clinicaltrials.gov and ANZCTR databases.